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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2003, 17:10:24 ; Search time 11.7002 Seconds (without alignments) 3367.676 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-009-332-1 5164 1 Miligiltlafagrtaggfe......DQCNLHRKPQELDFCVLRPC 950

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	mus popular	, œ
SUMMARIES	ATSL_MOUSE ATSL_HUMAN ATSL_HUMAN ATSB_MOUSE ATSS_HUMAN ATSL_HUMAN ATSL_HUMAN ATSL_HUMAN ATSL_HUMAN ATSL_HUMAN ATSL_BOVIN ADSL_BOVIN ADSL_B	
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Score	2480.5 2480.5 2135.5 2135.5 2135.5 2247.1 2247.5 22487.5 2	314
Result No.		33

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308	297	296	288.5	286	284	277.5	277	274.5	273.5	268	260.5

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIZB.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.

CAUTION: REP. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 7.
                                                                                             CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-1-LEU-1692
SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN.
COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
MATRIX.
                                                                                                                                                                                                                                                                               INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA CELLS OF PREOVULATORY FOLLICLES.
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA, MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
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CYSTEINE SWITCH (POTENTIAL)
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N -> S (IN REF. 2).
T -> S (IN REF. 2).
Y; 42EBDA55499FB6C1 CRC64;
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TSP TYPE-1 3.
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ZINC (CATALYTIC) (
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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EMBL, D67076; BAA11088.1; ALT_FRAME.
MERDPS; M12.222; AGAMTS1.
MGD; MGI:109249; Adamts1.
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                                                                                                                                                                              EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161
                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMKKKTES------FINAIPTFS------EWVIEEWGECSKTCGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSF
                                                                                                                                                                                                                                                                                                                                                                                 383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 ILSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
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                                                                          :| | ||:||| |:|||| :||| :| || || DPGSAAALSLCEGVRGAFYLQEEFFIQPAPGVATERLAPAVPEEESSARPQFHILRRR-
                                                                                                                                                                                                                                                                      ----RRGSGGAKCGVMD------DETLPTSDSRPESONTRNOWPVRDPTPQDAGKP
                                                                                                                                                                                                                                                                                                     ---SGRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI
                                                                                                                                                                                                                                                                                                                                                                 NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC
                                                                                                                                                                                                                                         162 VPGCPSGDPTSRCGVASCWNPAILRALDPYKPRRAGFGESRSRR--------
Length 968;
                              Indels
                 Pred. No. 1.3e-167
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48.1%; Score 2482.5;
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   Query Match

Best Local Similarity 48.0%; Pro
Matches 478; Conservative 158;
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NECENTRY OF SECURATION OF SECURATION OF SECURATE FROM N.A.

RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,

RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,

RA Hattori M., Fujiyama A., Ishil K., Totoki Y., Choi D.-K., Soeda E.,

RA Hattori M., Fujiyama A., Ishil K., Totoki Y., Choi D.-K., Soeda E.,

Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

RA Senthal A., Kump A., Schillhabel M., Schudy A., Zimmermann W.,

RA Rosenthal A., Saloho J., Shibuya K., Mitsuyama S., Antonarakis S.E.,

Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,

Schaffe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,

RA Memser J., Beck A., Klagas S., Hennig S., Riesselmann L., Dagand E.,

RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

Lehrach H., Reinhardt R., Yaspo M.-L.;

RA Lehrach H., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Olkemus S.,
Lombardo M., Iruela Arispe M.L.;
"METH-1, a human ortholog of ADAMTS-1, and METH-2 are members of a new
family of proteins with anglo-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CLEAVES AGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE
INVOLVED IN ITS TURNOVER (BY SIMILARITY). HAS ANGIOGENIC INHIBITOR
ACTIVITY. ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER
                                                                                                                                                     metalloproteinase
                                                                                                                                                                                                                                                                                                               Casas C., Pritchard M.A., Estivill X., Arbones M.L.;
Casas C., Pritchard M.A., Estivill X., Arbones M.L.;
"Cloning, characterization and mapping on human chromosome 21 of the orthologue of murine Adamts-1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-2018; PubMed-10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagaseltion of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
Na Res. 7:65-73(2000).
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Endothelial cells;
TISSUE-Endothelial cells;
MEDLINE-20247184; PubMed-10785405;
Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,
Rosenthal A., Thierauch K.H.;
"Differential gene expression by endothelial cells in distinct
                                   ATS1_HUMAN STANDARD; PRT; 967 'AA.
09UH181, Q9UP80; Q9UH83; Q9PR0; Q9NSJ8;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloprot with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
MEDLINE=99367466; PubMed=10438512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 418-967 FROM N.A.
                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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RESULT 2
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                    matrix (By similarity).

DOMIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE. CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLU-1-LEU-1939 SITE, WITHIN THE CHONDROITHIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS I ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IRR001890; Reprolysin.

R InterPro; IRR001890; Reprolysin.

R InterPro; IRR001894; Tapl.

R InterPro; IRR001894; Tapl.

R InterPro; IRR001894; Tapl.

R InterPro; IRR001894; Tapl.

R Pfam; PF00090; tsp_1; 6.

R Pfam; PF001562; Pep_M12B_propep; 2.

R RART; SM00209; TSPl; 3.

R PROSITE; PS00427; DISINTERNIA, 1: FALSE_NEG.

R ROSITE; PS00427; DISINTERNIA, 1: FALSE_NEG.

R PROSITE; PS00427; DISINTERNIA, 1: Heparin-binding.

STROMAL 1 49 POERWIAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 POLY-LYS. . . . . (POTENTIAL).
170 N-LINKED (GLCNAC. . .) (POTENTIAL).
171 N-LINKED (GLCNAC. . .) (POTENTIAL).
172 N-LINKED (GLCNAC. . .) (POTENTIAL).
173 P -> A (IN REF. 4 AND 5).
174 N-LINKED (GLCNAC. . .) (POTENTIAL).
175 N-D (IN REF. 1).
175 N-D (IN REF
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48.0%; Score 2480.5; DB 1; Length 967;
Best Local Similarity 48.9%; Pred. No. 1.8e-167;
Matches 485; Conservative 154; Mismatches 251; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                     SIMILARITY).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTECRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
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ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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TSP TYPE-1 3.
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CARBOHYD
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   SOLUTION TO THE SECOND TO THE
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24;

Gaps

251; Indels 101;

us-10-009-332-1.rsp

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                                                                                                                                                                                                                                  137 AALSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGG
                                                                                                                                                    197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS------PQDPALQGVGQP-TGTGS
                                                                                                                                                                          GRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
                                                                                                                                                                                                                     KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
 MILLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
                      -----RAP---GHGTTRLRLHAF
                                          QEDFYLHLTPDAQFLAPAFSTEHLG------VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
                                                                                      115 AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG
                                                                                                                                PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS
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967 AA.

PRT;

STANDARD;

ATS1\_RAT Q9WUQ1; Q9ERI1;

RESULT 3
ATS1\_RAT
ID ATS1
AC Q9WU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTECCLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEKIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1683-GLU-|-LEU-1684 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                        metalloproteinase
                                                                                                                            nartus nuzveptuus (mar.).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; pF00090; tsp_1; 6.
pfam; pF00090; tsp_1; 6.
pfam; pF01421; Reprolysin; 2.
pfam; pF01452; Pep_M12B_propep; 2.
SMART; SM00209; TSP1; 3.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00042; ZISP1; 2.
PROSITE; PS00042; DISINTEGRIN_1; FALSE_NBG:
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix (By similarity).
-i- INDUCTION: DOWN-REGULATED IN ENDOTHELIAL CELLS DERIVED FROM
                                                                                                                                                                                                                                                         Clemens
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-20304099, PubMed=10847486,
Diamantis I., Luethi M., Hoesli M., Reichen J.;
"Cloning of the rat ADAMTS-1 gene and its down regulation endothelial cells in cirrhottic rats.";
                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                              "Induction of a disintegrin and metalloprotease with the thrombospondin type I motif (ADAMIS)."; Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWYS-1 precursor (EC 3.4.24..) (A disintegrin and mwith thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i-SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                       Tu Y., Yin T., Johnstone E.M., Stephenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS, M12.222; -.
InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000184; TSPI.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF149118; AAD34012.1; -. EMBL; AF304446; AAG29823.1; -.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 18-967 FROM N.A.
                                                                                                                      (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIRRHOTIC LIVER
                                                                                                                        Rattus norvegicus
                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                               Liu X., Tu Y
Little S.P.;
                                                                                               ADAMTS1
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848 808

868

925 940

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ATS8_HUMAN STANDARD; PRT; 890 AA.
09UP79; 09NZS0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES.
-i- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a
                                                                                                                                                                       KPMHGYNFVVAIPAGASSIDIRQRGYRGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDL
                                                                                                                                                                                                            VVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPK--EPREDK
                                                                                                                                                                                                                                                                                                                       SAGQRTVPACDAAH -- RPVETQACGE - PCPTWELSAWSPCSKSCGRGFQRRSLKCVGHGG
                    FATPVHGSWGPWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNIEDC
                                              PSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYV
                                                                                                  LAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFT
                                                                                                                                                                                                                                                                  SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWYAGSWGPCSASCGSGLQKRAVDCRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.F., Apte S.S.;
the ADAM-TS family located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matrix (By similarity).
TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG,
       Vazquez F., Hastings G., Ortega M. A., Lane T.F., Olkemus S., Lombardo M., Iruela-Arispe M.L.;
"METH-1, a human ortholog of ADAMTS-1, and METH-2 are members family of proteins with anglo-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20079168; Pubmed-10610729; Georgiadis K.E., Hirohata S., Seldin M.F., Ag movel metalloprotease of the ADF mouse chromosome 9 and human chromosome 11."; Genomics 62:312-315(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
MEDLINE=99367466; Pubmed=10438512;
       RLLARDQCNLHRKPQE-LDFCVLRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAMTS8 OR METH2
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AFGQOLHLKLQPDSGFLAPGFTLQTV----GRSPGSEAQHLDPTGDLAHCFYSGTVNGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLL--QRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLASITMLLCVRGAHGRPTEEDEELVL----PSLERARGH-----DSTTLLRLD
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                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                        CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                  SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 47.9%; Score 2471; DB 1; Length 967; Local Similarity 48.4%; Pred. No. 8.6e-167; Lonservative 161; Mismatches 256; Indels 9:
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
I -> V (IN REF. 2).
KFRSSQ -> RSRGSL (IN REF V -> A (IN REF. 2).
K -> P (IN REF. 2).
K -> P (IN REF. 2).
L -> TR (IN REF. 2).
L -> TR (IN REF. 2).
K -> P (IN REF. 2).
L -> TR (IN REF. 2).
K -> P (IN REF. 2).
L -> TR (IN REF. 2).
TH (IN REF. 2).
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TH -> MLLK (IN REF. 2).
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S -> F (IN REF. 2)
L -> V (IN REF. 2).
I -> T (IN REF. 2).
M; F93C864F6DCD84CF CRC(
                                                                                                                                                                                                           (GLCNAC. . .)
                                                                               ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
               BY SIMILARITY. ADAMTS-1.
                                                                                                                                                             TSP TYPE-1 2.
TSP TYPE-1 3.
POLY-ARG.
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252
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ASGWNPAILRALDPYKPR---RAGFGESRSR----
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Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
E -> R (IN REF. 2).
YLTELLDGGHGDCLLDAPGAALPLPTGL -> FSGCHLQGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                R InterPro; IPR001762; Disintegrin.
R InterPro; IPR0012870; Pep_M12B_propep.
R InterPro; IPR001280; Reprolysin.
R InterPro; IPR001280; Reprolysin.
R InterPro; IPR00130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R Pfam; PF001421; Reprolysin: 1.
R Pfam; PF01421; Reprolysin: 1.
R Pfam; PF01421; ADAM_MEPRO; 1.
R PROSITE; PS50125; ADAM_MEPRO; 1.
R PROSITE; PS50125; ISP1; 2.
R PROSITE; PS50012; TSP1; 1.
R PROSITE; PS50012; TSP1; 1.
R PROSITE; PS50012; TSP1; 1.
R PROSITE; PS60127; DISINTEGRIN_1; FALSE_NEG.
W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; W Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLLLGILTLAFA----GRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQ
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SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHFKYLCKCVSELKCDLMP (IN REF. 2)
57D70EE03D5739D3 CRC64;
               SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 45.3%; Pred. No. 3.9e-143;
Matches 426; Conservative 150; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (ZINC (CATALYTIC) (DISINTEGRIN-LIKE. TSP TYPE-1 1. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY. ADAMTS-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.4%; Score 2135.5;
45.3%; Pred. No. 3.9e
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POLY-PRO.
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EMBL; AF175283; AAF25806.1; -.
HSSP; P34179; 11AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96671 MW;
                                                                                                                                                                                                            Genew; HGNC:224; ADAMTS8.
MIM; 605175; -.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-DCT-2005 (Rel. 41, 1ast annotation update)
4-DAWTS-8 precursor (EC 3-4, 24, -1) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKGACVERHNLNKHR--VDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                               SQQCELAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLC.
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                                                                                                                                387 NHMASPILIQIDRANDWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG--ASYIL
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MEDLINE-20079168; PubMed-10610729;
Georgiadis K.E., Hirohate S., Seldin M.F., Apte S.S.;
RADM-TSB, a novel metalloprotease of the ADAM-TS family located mouse chromosome 9 and human chromosome 11.";
---WGPAGARPL-PRGPEWEVETGEGORQERGDHQEDSEEESQEEEAEGASEPPPLGAT
                                                                                     GRAKREVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
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                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
             FUNCTION: HAS ANTI-ANDIGENIC PROPERTIES (BY SIMILARITY).

COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN ADULT LUNG AND HEART AND LOW EXPRESSION DURING MOUSE DEVELOPMENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXPRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R HSSP; D: 2.26; -...

R MEROPS; M12.226; -...

R MGD: MGI:1353468; Adamts8.

B InterPro: IPR001562; Disintegrin.

InterPro: IPR001562; Reprolysin.

B InterPro: IPR001884; TsP1.

BR Fign; PF00009; tsp_1.2.

BR Fign; PF00009; tsp_1.2.

BR MSITE; SM0209; TSP1; 2.

BR PROSITE; PS50014; ZINC_PROTEASE; 1.

BR ROSITE; PS50014; ZINC_PROTEASE; 1.

BR ROSITE; PS50014; ZINC_PROTEASE; 1.

BR ROSITE; PS50042; DISINTEGRIN_1; FALSE_NEG.

BR ROSITE; PS0042; DISINTEGRIN_1; FALSE_NEG.

BR ROSITE; PS0042; DISINTEGRIN_1; FALSE_NEG.

BR Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 IFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDS 113
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(POTENTIAL).
(POTENTIAL).
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZING (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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Mismatches 260; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF175282; AAF25805.1; -.
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                                                                                                                                                                261 PINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 AS--YILSQQCELAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTS 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSV-GKM 789
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                                                                                             161 REDP----GLAAAEVFPLPQGLEWEVEMGNGQGQERSDNEEDRKQDKEGLLKETEDSRKV
                                                       -----RAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILN
                                                                                                                                                                                                                                                                           321 LCG-ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE
                                                                                                                                                                                                                                                                                                                                                                                       380 VFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 HSTLYELDQQCKQIFGPDFRHCPNTSVEDICVQLCARHRDSDEPICHTKNGSLLWADGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 FPPKVRYTFFVPND--MDFSVQNSKERATT---NIIQSL------PSAEWVLGDWS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           895
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09P2N4; Q9NT29;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24..) (A disintegrin and naith thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
ADAMTS9 OR KIAA1312.
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TISSUE-Fetal;
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                                                         DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-I DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS50092; TSP1, 9.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.
                                                                                                                                                                                                                                       PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).
 laki R.A.;
ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISINTEGRIN-LIKE TSP TYPE-1 1.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001870; Pep_MI2B_propep.
InterPro; IPR001890; Reprolysin.
InterPro; IPR001894; TSP1.
InterPro; IPR001894; TSP1.
InterPro; IPR0010190; Zn_MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_MI2B_propep; 1.
SMART; SM00209; TSP1; 12.
PROSITE; PS50215; ADAM_MERRO; 1.
PROSITE; PS50215; ADAM_MERRO; 1.
                                              SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM)
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BY SIMILARITY.
ADAMIS-9.
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TSP TYPE-1
TSP TYPE-1
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                            Senomics 67:343-350(2000).
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1629
587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHKN----RHSKDKKKTRARKWGERINLAGDVAALNSGLATEAFSAYGNKTDNTREKRTHR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVA 177
                                                                                                                                                                                                                                                                                                                                                                                                                               EYEIVSPIRVNALGEPFPTNVHFKRTRRSINSATDPWPAFASSSSSSTSSOAHYRLSAFG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDFYLHLTPDAQFLAPAFSTEHLGVP----LQGLTGGSSDLRRCFYSGDVNAEPDSFAAV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA-TTC
                                                                                                                           ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
CLYTCGKGH -> VEWEGCEPP (IN
SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                          351; Indels 122;
                                                                                                  ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                            Query Match
38.1%; Score 1965; DB 1; Length 1629;
Best Local Similarity 39.9%; Pred. No. 8.8e-131;
Matches 411; Conservative 145; Mismatches 351; Indels 122,
                                                                                                                                                                                                                                                                                       MISSING (IN SHORT ISOFORM).
F -> L (IN REF. 1).
W; C1C4CEFF58B8941F CRC64;
                                                                                       (POTENTIAL)
TSP TYPE-1 7.
TSP TYPE-1 8.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 11.
POLY-SER.
                                                                                       CYSTEINE
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1439
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1612
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1267
1072
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CARBOHYD
VARSPLIC
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METAL
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804 PREDK---SSHPKDPRGP------ 840
684 KVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVV 743
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TMAKREIRIGNAVVEYSGSETAVERINSTDRIEQELLLQVLSVGKLYNPDVRYSFNIPIE 873
                                                                                                                                           874 DKPQQFYWNSH-----GPWQACSKPCQGERKRKLVCTRESDQLTVS----DQRCDKLPQPG 925
                                                                                                                                                                                    926 HITEPCGTDCDLRWHVASRSECSAQCGLGYRTLDIYCAKYSRLDGKTEKVDDGFCSSHPK 985
                                                                                                                                                                     ------GSAGORTVPACSASCGSGLOKRAVDCR-----GSAGORTVPACDAAHR 883
                                                                                                                                                                                                                PVETQACGEPCPT -- WELSAWSPCSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQE 941
                                                                                                                                                                                                                                                                                                                                                                                                   metalloproteinase
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16-0CT-2001 (Rel. 40, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
15-UTN-2002 (Rel. 41, Last annotation update)
MDAMYS-4 precursor (EC 34.24-7) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99286303; PubMed=10356395;
Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M.,
Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicoo C.P., Wynn R.,
Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
Nagase H., Itch Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K.,
Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
"Purification and cloning of aggrecanase-1: a member of the ADAMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                            SAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98403880; PubMed-9734811;
Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Saklatvala J., Clark A.R.; Sawaji Y., Nagase H., Saklatvala J., Clark A.R.; "ADAMTS-4 genomic locus."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                            837 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE, AND CHARACTERIZATION. MEDLINE-20400518; Pubmed-10827174;
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 284:1664-1666(1999).
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAMTS4 OR KIAA0688,
                                                                                                                                                                                                                                                                                 1045 IQRCSEFPC 1053
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SEQUENCE FROM N.A.
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            COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                         LUNG AND HEART. EXPRESSED
                                                                                                                                                                                      CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00000; tsp_1; 1.
Pfam; PF00121; Reprolysin; 1.
SMART; SM00109; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50015; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50047; DISINFECKIN, 1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .) (POTENTIAL).
fortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                 matrix (By similarity).
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HE
AT VERY LOW LEVEL IN PLACENTA AND SKELETAL MUSCLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5DF9C9AC137DF41F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A -> T (IN REF. 1).
R -> Q (IN REF. 3).
G -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP TYPE-1.
CYS-RICH.
SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB014588; BAA31663.1; --
EMBL; AF148213; AAD41494.1; --
EMBL; AY044481; AAL02262.1; --
MEROPS; M12.221; --
Genew; HGNC:220; ADAMTS4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626
682
837 AA;
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ACT_SITE
METAL
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DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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37.1%; Score 1917; DB 1; Length 837;

Query Match

Mus

Murinae;

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Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
(GLCNAC.
(GLCNAC.
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R MGD: MGI:1346321; Adamts5.

R InterPro; IPR001870; Disintegrin.

R InterPro; IPR001890; Pep_MI2B_propep.

R InterPro; IPR001890; Reprolysin.

R InterPro; IPR000814; TsP1.

R InterPro; IPR000130; Zn_MTpeptdse.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01421; Reprolysin; 1.

R PR0SITE; SW00209; TsP1; 2.

R PROSITE; PS50092; TsP1; 1.

R PROSITE; PS50092; TsP1; 1.

R PROSITE; PS00147; DISINTEGRIN_1; FALSE_NEG.

R PROSITE; PS00447; DISINTEGRIN_1; FALSE_NEG.

R PROSITE; PS00447; DISINTEGRIN_1; FALSE_NEG.

R REPEAT; Extracellular matrix.

R POTORIA:

R PROSITE; PS00147; DISINTEGRIN_1; POTENTIAL.

R PROSITE; PS00147; DISINTEGRIN_1; PROFENTIAL.

R PROSITE; PS00147; DISINTEGRIN_1; PATRIX PROFENTIAL.

R PROFERM PROSITE; PS00147; DISINTEGRIN_1; PATRIX PROFENTIAL.

R PROFERM PROFER
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CYS-RICH.
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N-LINKED
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209
411
411
420
526
    Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  -!- PTM: THE PRE SIMILARITY).
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485
567
624
732
875
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CARBOHYD
CARBOHYD
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METAL
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   16;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2005 (Rel. 41, Last annotation update)
ADAMYS-5 precursor (EC 3.4, 24.-) (A dishintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS5) (Aggrecanase-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSL-LRYSGTGTAVESLQA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 VQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTN 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIR 712
                                                                                                                                                                                                                                                 61 QEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120
                                                                                                                                                                                      HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL 299
                                                                                                                                                                                                                                                                                                                                                      NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                     HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                      Gaps
                                                                               88
                                                 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWGPWGPWGDCSRTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLTL---AVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                    GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG
                                                                                                                                                                                                                                                                                                           AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG
                                                                                                                                                                                                                                 180 WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLE
                      52;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRPILEPLIVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKD 814
      9.7e-128;
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      930
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9
         Pred.
                      381; Conservative 123;
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       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATS5_MOUSE
Q9R001;
       Best Local :
Matches 381
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ID ATS2_M

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DT 16-OCT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
MEDLINE=99395124; PubMed=10464288;
MEDLINE=99395124; PubMed=10464288;
MEDLINE=99395124; PubMed=10464288;
MEDLINE=99395124; Dawaras, and ADM-TS7, novel members of a new family of zinc metalloproteases.";
J. Biol. Chem. 274:25555-2553(1999).
I. Biol. Chem. 274:25555-2553(1999).
IFUNCION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI:IMPLANTATION PERIOD.
--- CATALXTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-[-Ala-393]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1- DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-
IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR UNDECTABLE LEVEL THEREAFTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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16-OCT-2001 (Rel. 40, Last sequence update)
    13;
                                                      90 GLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQR 149
                                                                  TLRNFCAWQKKLNKVSDKHPEVWDTAILFTRQDLCGATTCDTLGMADVGTWCDPKRSCSV 347
                                                                                                                                                                                                                                                               218 -POESPSVHSRSRRRSALAPQLLDHSAFSPSGNAGPQTWWRRRRRSISRARQVELLLVAD 276
                                                                                                                                                                                                  IEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACS 407
                                                                                                                                                                                                                               DPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREE 582
                                                                                                                                                                                                                                                                                                                               QCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCS 642
                                                                                                                                                                                                                                                                                                                                                                                                                               GTAVESL----QASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKS---SHPKD 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHRDDFLHGMGYSATKEL---LIVQILATDPTKALGVRYSFFVPKKTTQKVNSVISHGSN 868
                                                                                        ----NSQGAHLLQRRG------VPGGPSGDPTSRCGVASGWNPAILRALDPY 191
                                                                                                                                                        ESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLKDRDSGPKVTGNAAL 287
                                                                                                                                                                                                                                                       AAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTK 467
                                                                                                                                                                                                                                                                                       LWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER----HNLNKHRVDGSWAKW 522
                                                                                                                                                                                                                                                                                                      LWCAVVROGOMVCLTKKLPAVEGTPCGKGRVCLQGKCVDKTKKKYYSTSSH---GNWGSW 573
                                                                                                                                                                                                                                                                                                                                                                 PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAI 702
                                                                                                                                                                                                                                                                                                                                                                                               PAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    815 PRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRT 874
                                                                                                                         ---RAKREVSIPRYVETLVVAD
                                                                                                       181 IYGDGSSRILHVYNREGFSFEALPPRASCETPASPSG------
N-LINKED (GLCNAC. .) (POTENTIAL).
                         930;
                                          Indels
                         Length
                                        370; Conservative 115; Mismatches 265;
                        Score 1856; DB 1;
Pred. No. 2.2e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               930 AA
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        101780 MW;
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        930 AA;
                                Local Similarity
CARBOHYD
        SEQUENCE
                        Query Match
                                                                                        150
                                         Matches
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MEDLINE-20289799; PubMed=10830953;
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MEDLINE-202897999; PubMed=10830953;
Menter H. S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,
A. Anki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schlilhabel M., Schudy A., Zimmermann W.,
A. Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
T. The DNA sequence of human chromosome 21.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update)
ADAWTS-5 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TSS) (Aggrecanase-2) (ADAM-TS 11).
ADAMTS5 OR ADAMTS11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA BUT ALSO IN OTHER TISSUES, SUCH AS HEARY AND BRAIN, AND ALSO CERVIX, UTERUS, BLADDER, ESOPHAGUS, RIB CARTILLAGE,

CHONDROBLASTOMA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abbaszade I., Liu R.-Q., Yang F., Rosenfeld S.A., Ross O.H., Link J.R., Ellis D.M., Tortorella M.D., Pratta M.A., Hollis J.M., Wynn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K., Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H. Ito Y., Newton R.C., Magolda R.L., Trzaskos J.M., Hollis G.F., Arner E.C., Burn T.C., "Cloning and characterization of ADAMTS11, an aggrecanase from the
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAMTS family.";
J. Biol. Chem. 274:23443-23450(1999).
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MEDLINE=99395124; Pubmed=10464288;
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STANDARD;
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e by non-profit institutions as long as its content is in no way ililied and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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R Interpro; IPR000130; Zn_Wrpeptdse.

R Pfam; PF001421; Reprolysin; 1.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01562; Pep_M12B_ropep; 1.

R MRAT; SM00209; TSF1; 2.

R PROSITE; PS500142; DISINFGRIN_1; PALSE_NEG.

R PROSITE; PS500142; ZINC_PROTEASE; 1.

R PROSITE; PS500142; ZINC_PROTEASE; 1.

R PROSITE; PS50142; ZINC_PROTEASE; 2.

R PROSITE; PS50144; ZINC_PROTEASE; ZINC_PROTEASE; ZINC; SIGNATE, ZINC_PROTEASE; ZINC; ZINC_PROTEASE; ZINC_PROTEASE;
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINFECTIVE.
TSP TYPE-1 1.
CYS-RICH.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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1.4 R -> H (IN REF. 2).
92 P -> L (IN REF. 2).
101715 MW; B64281502F28193B
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TSP TYPE-1 2.
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InterPro; IPR001590; Reprolysin.
                                                                                                                                                                                         InterPro; IPR001762; Disintegrin
                                                                   EMBL; AF142099; AAD49577.1; -. EMBL; AP001698; BAA95504.1; -. EMBL; AF001697; BAA95503.1; -. EMBL; AF141293; AAF02493.1; -. HSSP; Q9PW35; IBUD.
                                                                                                                                                     Genew; HGNC:221; ADAMTS5.
MIM; 605007; -.
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Q9ESP7; Q9ESP8; Q9ESP6; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 4 precursor (Rcl. 41, 4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS 4) (Aggrecanase 1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDILINE-20415811; PubMed-10961658;
Satoh K., Suzuki N., Yokota H.;
"ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin
motifs) is transcriptionally induced in beta-amyloid treated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurosci. Lett. 289:177-180(2000).

-i- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY INVOLTON: CLEAVES INTROVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGRECAN IN ARTHRITIC DISEASES.

-i- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                       HIST HILL HISTORY STREAMSSILTSIDASKPWSKCTSATITEFLDDGHGNCLLDLPRKQ
                                                                                                                                                                                                                                                                                                                                                                                                             LALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESL----QASRPILEPLT
                                                                                                                                                                                                                                                                                                            TSCGEGKICLKGACVER----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNY
                                                                                                                                                                           HDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP
                                                                                                                                                                                                                                                                               ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARMVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPACDAAHRPVETQAC 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-10 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matrix (By similarity).
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombospondin type I repeats.";
Submitted (Jun.1999) to the EMBL/GenBank/DDBJ databases.
-i- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |:|: |:: |||| | |:: |||| | |:: ||| |: ||| |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: |:| |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |:: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: 
                                                                                                                                                                                                                                                                                                                                                                                                    682 CKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHF 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   742 VVSAVERDLVVKGSL-LRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYL 800
                                                                                                               362 CNTKNCP-HGSALTFREEQCAA---YNHRTDLFKSFPGPMDWVPRYTGVAPRDQCKLTCQ 417
                                                                                                                                                                                                                                                                                                                                                          ANGIGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKS 681
                                                                                                                                                                                                                   CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTL---AVAWVPKYSGVSPRDKCKLICR 621
242 CQLIFGPDSSHCPQLPPPCAALWCFGHLNGHAMCQTKHSPWADGTPCGPAQACMGGRCLH 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pre 5.5.;
ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         507 RHNLNKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRS
                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1077 AA.
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Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
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Interpro; IPR000130; Zn_MTpeptdse.
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Genew; HGNC:13201; ADAMTS10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 PKEPREDKSSHPKDPRGP 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRPV-----PSTPRPP 606
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Q9H324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAMTS10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
AT10_HUMAN
                                                                                                                                                                                                                       565
                                                                                                                                                                                                                                                                                                                                                                     622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
   COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY),
SUBCELULALR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE: DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
FTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE. SIMILARITY: BELOWS TO PEPTIDASE FAMILY MIZB.
SIMILARITY: CONTAINS 1 ISP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD·328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LVILGSGQEVPQVGPSAAQTLRSFCTWQKGLNPPNDSDPDHFDTAILFTRQDLCGVSTCD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRAN 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
638428753167C7EF CRC64;
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ADAWIS-4.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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BREMS; AB042272; BAB16473.1; -...

BREMS; AB042273; BAB16473.1; -...

REMS; AB042273; BAB16475.1; -...

RICEPTO; IPR001590; Reprolysin.

RICEPTO; IPR000184; TSP1.

RICEPTO; IPR000184; TSP1.

RICEPTO; IPR000180; Zn_MTpeptdse.

RICEPTO; IPR00181; Reprolysin.

RYART; SM00209; TSP1, 1...

RYART; SM01209; TSP1, 1...

RYOSITE; PS00142; ADAM WEPRO; 1...

RYOSITE; PS00142; TSP1, 1...

RYOSITE; PS00142; TSP1, 1...

RYOSITE; PS00142; TSP1, 1...

RYOSITE; PS00142; TSP1, 1...

RYATOLASE; Metalloprotease; Zinc; Glycoprotein; Zymogen;

EXTRACELIULAR MALINE.

RYATOLER -...

RYATOLER -..

RYATOLER -...

RYATOLE
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88; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
TSP TYPE-1.
CYS-RICH.
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Matches 325; Conservative
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474
630 AA;
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SEQUENCE
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                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal lung;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                 origin.
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AT12_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSNR---CITNSIPAAEGTLCQTHTIDKGWCYKRVCVP-FGSRPEGVDGAWGPWTPWGDC 533
                                                                                                                                                                                                                                                                                                        LAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAE-PDSFAAVSLCGGLRGAFGYRGAE 133
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                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                              'Match 25.1%; Score 1296; DB 1; Length 1077; Local Similarity 35.4%; Pred. No. 9.4e-84; loss 335; Conservative 112; Mismatches 376; Indels 123;
                                                                                                                                                                                                                          (POTENTIAL)
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SIMILARITY)
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 5.
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N-LINKED (GLCNAC. . . ) (
N-LINKED (GLCNAC. . . ) (
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ZINC (CATALYTIC) (
DISINTEGRIN-LIKE.
CYS-RICH.
                                                                                                 ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
PF01421; F. PF01421; Reprolysh; 1. PF01562; Pep_M12B_propep; 1.; SM00209; TSP1; 5.
                                                                                                                                                                                                                                   118072
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATURATION PROCESS LEADIND THE: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND METALLOPROTEINAGE, DISINTEGRINAL REGION INCLUDING THE METALLOPROTEINAGE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND THE CTERMINAL PRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed exclusively in fetal lung. Is widely
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Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;
Tidentification, characterization, and intracellular processing of ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats.";
J. Balol. Chem. 276:17932-17940(2001).
-I- COFACTOR: BINDS 1 ZIMC ION (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    819
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                                                                                                 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-12 precursor (EC 3.42.-) (A disintegrin and
metalloproteinase with thrombospondin motifs 12) (ADAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 VLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTV-PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCTCTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPS
SIPFRGKEYKWKTYR-------GGGVK---ACSLTSLAEGFNFYTERAAAVVDGTPC
                                                                                                                                                                                                                                                                                           SPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFT--KPMHGYNFV
                                                                                                                                                                                                                                                                                                                                                                                                    VAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRY
                                                                                                 G-----YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLC
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 DAAHR--PVETQACG-EPC-PTWELSAWSPCSKSCGRGFQRRSLKC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPD--SFAAVSLCGGLRGA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PDINGRRYYWRGPEDSGDQGLIFQITAFQEDFYLHL
                                                                                                                                                                                                                    Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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; Mismatches 374; Indels 158;
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BY SIMILARITY.
ZINC (CATALYTIC)
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                                                                                         InterPro: IPR001762; Disintegrin.
InterPro: IPR002870; Pep_MI2B_propep.
InterPro: IPR001890; Reprolysin.
InterPro: IPR001894; TSP1.
InterPro: IPR000184; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF01562; Pep_MI2B_propep; 1.
SMART; SM00209; TSP1, 8.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                 DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                               (CATALYTIC)
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TYPE-1 3.
TYPE-1 4.
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TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 8.
POLY-GLU.
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N-LINKED
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; S
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                                                                 EMBL; AJ250725; CAC20419.1; -.
                                                                                                                                                                                                                             Repeat; Extracellular matrix.
                                                                           HGNC:14605; ADAMTS12
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MIM; 606184;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
N-proteinase) (PC I-NP) (Procollagen N-endopeptidase) (pNPI)
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FGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILR 186
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               ALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGAD-LEHYLLTL
                                                                  LATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDK
                                                                                                                                                                      SERLDAAADGTQCGEKKWCMAGKCI---TVGKKPESIPGGWGRWSPWSHCSRTCGAGVQS
                                                                                                                                                                                                                                                                                                                                                                   ARROCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLT
                                                                                                                                                                                                                                                                                                                                                                                 --YHWFPIF---NPAHPCELYCRPIDGQFSEKMLDAVIDGTPCFEGGNSRNVCINGICKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 AGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLF-TKPMHGYNFVVAIPAGASSIDIRQRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 MYFWQYGHWTECSVTCGTGIRRQTAHCIKKGRGMVKATFCDPETQPNGRQKKCHEKACPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPEYWDTAILFTRQDLCGA - - TTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL
                                                                                                                                                                                                          GHVFNMPHDNVK-VCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC
                                                                                                                                                                                                                                                                                                                                                                                                                      LAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLC--SPDSTSVCVQGKCIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 VGCDYEIDSNATEDRCGVCLGDGSSCQTVRKMFKQKEGSGYVDIGLIPKGARDIRVME--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKGLIGDDNYLALKNSQ-GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRP
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095450;
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ATS2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matix (By similarity).

-I-ALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI;
ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-PROCOLLAGEN PEPTIDASE ACTIVITY.

-I-TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON AND AND ARTA AND AT LOW LEVELS IN THYMUS AND BRAIN.

-I-DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-I DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

-I-PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBURIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).

--- DISEASE: Defects in ADAMTS2 are the cause of Ehlers-Danlos syndrome type VIC (EDS-VIC), a recessively inherited connectivetissue disorder characterized clinically by severe skin fragility and joint hypermobility and biochemically by the presence in skin of procollagen incompletely processed at the N-terminus.
--- SIMILARITY: CONTAINS 1 DISINITEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
--- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                    Colige A., Sieron A.L., Li S.W., Schwarze U., Petty E.,
Wertelecki W., Wilcox W., Krakow D., Cohn D.H., Reardon W.,
Byers P.H., Laplere C.M., Prockop D.J., Nusgens B.V.;
"Human Ehlers-Danlos syndrome type VII C and bovine dermatosparaxis
are caused by mutations in the procollagen I N-proteinase gene.",
Am. J. Hum. Genet. 65:308-317(1999).
-!- FUNCTION: Cleaves the propeptides of type I and II collagen prior
to fibril assembly. Does not act on type III collagen. May also
play a role in development that is independent of its role in
                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains at Ala-|-Gln.
                                                                        Vertebrata; Euteleostomi;
                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE
                                                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
(Procollagen I/II amino-propeptide processing enzyme).
ADAMIS2 OR PCINP OR PCPNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF00090; LSP_1; 4.
Pfam: PF01421; Reprolysin: 1.
Pfam: PF01421; Reprolysin: 1.
Pfam: PF01421; Reprolysin: 1.
PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS50022; TSP1; 4.
PROSITE: PS00142; TSP1; 1.
PROSITE: PS00142; ZINC_PROTEASE: FALSE_NEG.
PROSITE: PS001427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprc1ysin.
InterPro; IPR001884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                    MEDLINE-99347935; PubMed-10417273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001762; Disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJO03125; CAA05880.1; -. MEROPS; M12.301; -. Genew; HGNC:218; ADAMTS2.
                                                                   Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 604539; -
                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 225410;
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TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 4.

POLY ALA.

POLY ALA.

N-LINKED (GLCNAC. ...) (POTENTIAL).

HGENGHIMLIPDILKROSSUMA -> FREGAVAHACYPS

TLGGGGRWIA (IN ISOPORM SPNPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 AAFHRFHWSRCSQQELSRYLHS-*YDCLLDDPFAHDWP-ALPQ-LPGLHYSMNEQCRFDF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GGNEEEPGSHLFYNVIVFGRDLHLRLRPNARLVAPGAIMEWQGE--KGTIRVEPLLGSCL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSGDVN--AEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG-AHLLQR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 GPKV-IGNAALILRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 IMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LAFAGRIAG---GEEPEREVVVPIRLDPD-------INGRR-----YYW 42
Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
.lagen degradation; Extracellular matrix; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 -VETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 QIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 GVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 RPPTSPPLGGPQA---LDTG---ASLDSLDSLS-RALGVLEEHANSSRRRARRHAADDDY
                                                                          ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                        SITE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                             BECEEF25C23CAD2D CRC64;
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; Mismatches 404;
                                                                                                                                DISINTEGRIN-LIKE
TSP TYPE-1 1.
                                                                                                                                                                      CELL ATTACHMENT
                          Ehlers-Danlos syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1230;
                                                               ADAMTS-2
                                                                                                                                                           CYS-RICH
                                                                                                                                                                                      SPACER
                                                                                                                                                                                                                                                                                                                                                                                                             134722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 347; Conservative 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                        23.8%;
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Hydrolase; Metalloprot
Repeat; Collagen degra
Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                 567 121
1211 AA;
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                                                                                           ACT_SITE
METAL
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SEQUENCE
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.

-1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION HIT THE EXTRACELLULAR MATRIX.

-1- PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPE
                                                                                                                                                                                                                                                                                                                                                                               DNTTRSVHAKHCNDARPESRRACSRELCPGRWRAGPWSOCSVTCGNGTOERPVPC---- 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAM-TS 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 274:2555-25563(1999).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-!- TISSUE SPECIFICITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG,
                                                                                                                                                  732
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             CGGDNKSCKKVTGLFTK--PMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ
                                                                                                                                                                 -GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTP
                                                                                                                                                                                                                    770 TGKFILNEENDVDASSKTFIAMGVEWEYRDE-DGRETLQIMGPLHGTITVLVIPVGD-TR
                                                                                                                                                                                                                                                      PRVRYSFYLPKEP-----RED-----KSSHPKDPRG-----P
                                                                                                                                                                                                                                                                       828 VSLIYKYMIHEDSLNVDDNNVLEEDSVVYEWALKKWSPCSKPCGGGSQFTKYGCRRRLDH
                                                                                                                                                                                                                                                                                                                              888 KMVHRGFCAALSKPKAIRRACNPQECSQPVWVTGEWEPCSQTCGRTGMQVRSVRCIQPLH
                                                                                                                                                                                                                                                                                                                                                         QRTVPACDAAH----RPVETQACG-EPCP-TWELSAWSPCSKSCGRGFQRRSLKCVGHGG
---ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY
                                                RSCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDK
                                                                                                 CKLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKRRFDKCGV
                                                                                                                                                                                                                                                                                                      SVLHN---SVLSLSNQVEQ---PDDRPPARWVAGSWGPCSASCG-SGLQKRAVDCRGSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99395124; PubMed-10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, Novel Members of a
Zinc Metalloproteases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                -RTADDSFGICQEERPETARTCRLGPC 1028
                                                                                                                                                                                                                                                                                                                                                                                                         RLLARDQCNL -- HRKPQELDFCVLRPC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
ATS7_HUMAN
ID ATS7_HUMAN
AC Q9UKP4;
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            use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGSSDLR----RCFYSGDVNAEPD---SFAAVSLCGGLRGAFGYRGAEYVISPLPNASA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAAQRNSQGAHLLQRRGVP----GGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARPGHAQ-PHVVYKRQAPERLAQRGDSSAP-STCGV------QVYPELESRRERW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESRSRRRSGRAKRF----VSIPRYVETLVVADESMVKFHG-ADLEHYLLTLLATAARLYR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFTRQDLCGATT--CDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLCALAPGAPGPAPGRATEGRAALDIVHPVRVDAGGSFLSYELWPRALRKRDVSVRRD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YY----WRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAF--STEHLGVPLQGL 91
There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50092; TSP1; 1.
PROSITE; PS04Z7; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP TYPE-1 2.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MW; 6587044ED02FC104 CRC64;
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Mismatches 377; Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYSTEINE SWITCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY. ADAMTS-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.5%; Score 1212.5; 35.1%; Pred. No. 6.86
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CYS-RICH.
    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                         Pep_M12B_propep
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                                                                                                                                                                                                                                     InterPro; IPR002870; Pep_M12B_prop
InterPro; IPR001590; ReppolySin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMART; SM00209; TSP1; 2.
                                                                                                                                                                                                                InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00142; ZINC_PROTEASE; PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 35.1%; Pr
les 353; Conservative 116;
                                                                                                              EMBL; AF140675; AAD56358.1;
HSSP; P15167; 1ATL.
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                                                                                                                                                                            Genew; HGNC:223; ADAMTS7.
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CARBOHYD
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0UT-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (Procollagen I/II amino-propeptide processing enzyme) (Procollagen I/II amino-propeptide processing enzyme) (Procollagen I N-proteinase) (PC I-NP) (Procollagen N-endopeptidase) (PNPI).
GSGNDCEPV-GK--RPFIMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDDPAKDI 456
                                                                                                                                                        373 -NVKVCEEVFGKLRANHAMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP- 430
                                                                 431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWAD 489
                                                                                                       GTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPA 549
                                                                                                                    NGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSG 609
                                                                                                                                                                                  610 VSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP--DSTSVCVQGKCIKAGCDGNLGSKK 667
                                                                                                                                                                                                668 RFDKCGVCGGDNKSCKKVTGLFTKPMH-GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYL 726
                                                                                                                                                                                                                                    ALKNSQ-GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVL- 784
                                                                                                                                                                                                                                                                            ----SVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDD 837
                                                                                                                                                                                                                                                                                                                      SRGPGGGSRGGVPRPSTLHGRSRPGGVSPGSVTEPGSEPGPPAAASTSVS----- 845
                                                                                                                                                                                                                                                                                                                                          838 RPPARW---VA----GSWGPCSASCGSGLQKRAVDCRGS-----AGQRTVPACDAAHRP 884
                                                                                                                                                                                                                                                                                                                                                       "CDNA cloning and expression of bovine procollagen I N-proteinase: a new member of the superfamily of zinc-metalloproteinases with binding sites for cells and other matrix components."; Proc. Natl. Acad. Sci. U.S.A. 94:2374-2379(1997).
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colige A., Li S.W., Sieron A.L., Nusgens B.V., Prockop D.J.,
Lapiere C.M.;
                                                                                                                                                                                                                                                                                                                                                                                            885 VETQACGE-----PCPTWELSAWSPCSKSCGRG--FQRRSLKCVG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Skin;
MEDLINE-97225960; Pubmed-9122202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P79331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
1- SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV.
1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
1- TISSUE SPECIFICITY: ENEXMATIC ACTIVITY IS DETECTED AT HIGH LEVEL IN ALL TYPE I COLLAGEN-RICH TISSUES SUCH AS SKIN, BONES, TENDONS AND AORTH AND AT LOW LEVEL IN BAIN AND THYMUS. THE MANA LEVELS WERE DISPROPORTIONATELY HIGH IN HEART, LIVER, RETINA AND MUSCLE.
1- DOWAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
1- PTM: THE N-TERMINUS IS BLOCKED.
1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).

1- DISEASE: DEFECTS IN ADAMTS2 ARE THE CAUSE OF DERNATOSPARAXIS, A RECESSIVELY INHERITED DISORDER CHARACTERIZED BY SEVERE SKIN FRAGILITY AND BIOCHEMICALLY BY THE PRESENCE IN SKIN OF PROCOLLAGEN INOMPLEEFELY PROCESSED AT THE AMINO TENHUUG.

1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

1- SIMILARITY: CONTAINS I DISINTEGRIN-LIKE DOMAIN.

1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.

1- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                                        COLLAGEN PRIOR
                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains at Ala-; Gln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZNN_PROFEASE; FALSE_NEG.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprofease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Collagen degradation; Extracellular matrix; Heparin-binding.
                        Colige A., Beschin A., Samyn B., Goebels Y., Van Beeumen J.,
Nusgens B.V., Laplere C.M.;
Characterization and partial amino acid sequencing of a 107-kDa
procollagen I N-proteinase purified by affinity chromatography on
immobilized type XIV collagen.";
J. Blol. Chem. 270:16724-16730(1995).

-1- FUNCTION: CLEAVES THE PROPEPTIDES OF TYPE I AND II COLLAGEN PRIO
TO FIBRIL ASSEMBLY. DOES NOT ACT ON TYPE III COLLAGEN. MAY ALSO
PLAY A ROLE IN DEVELOPMENT THAT IS INDEPENDANT OF ITS ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC (CATALTIC) (BY SIMILARITY).
ZINC (CATALTIC) (BY SIMILARITY).
DISINTEGRIN LIKE.
TSP TYPE-1 1.
CYS-RICH.
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ZINC (CATALYTIC) (POTENTIAL).
BY SIMILARITY.
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InterPro; IPR000189; TSP1.
Fram; Pr000190; LSP_1.
Fram; Pr001090; LSP_1.
Fram; Pr01421; Reprojysin; 1.
Fram; Pr01451; Reprojysin; 1.
Fram; Pr01562; Pep_M12B_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
PubMed=7622483;
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                                                                                                                                                                                                                                                                                                                                COLLAGEN BIOSYNTHESIS
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ACT_SITE
METAL
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TSP TYPE-1 3.

TSP TYPE-1 4.

CELL ATTACHMENT SITE (POTENTIAL).

POLY-GLU.

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N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.1%; Score 1192; DB 1; Length 1205; Best Local Similarity 31.7%; Pred. No. 2.4e-76; Matches 329; Conservative 134; Mismatches 403; Indels 172;
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Search completed: April 29, 2003, 17:13:55 Job time: 25.7002 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 29, 2003, 17:10:24 ; Search time 21.9736 Seconds (without alignments) 4156.253 Million cell updates/sec

US-10-009-332-1 5164 1 MLLIGILTLAFAGRTAGGFE......DQCNLHRKPQELDFCVLRPC 950 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ŋ	Description	qene ADAMTS-1 prot	Ω			procollagen N-endo	protein C37C3.6a [		angiogenesis inhib					jararhagin C precu		meltrin alpha - mo	metalloproteinase	monocyte surface a	metalloproteinase	androgen-regulated	fibrolase (EC 3.4.	metalloproteinase	ecarin precursor -	trigramin precurso	fibrinolytic metal	fibrinolytic prote		vascular apoptosis	atrolysin C (EC 3.	
SUMMARIES			10	m	_	7	<#	10	S	~	0	so	'n	σ.	0	7	0	D.	0	<b>a</b>	ď	0	ശ	20	0	2	o.	0	<b>(</b> )	10
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ete.	Query	48.1	37.1	31.1	30.7	23.1	13.2	13.2		•		8.7	٠	6.7	6.5	6.4	6.3	6.2	6.1	0.9	5.9	5.9	5.8	•	٠	2.6		5.5	5.5	5.4
	Score	2482.5	1915	1604	1585	1192	681	681	559.5	510.5	493	450.5	411.5	344.5	337	329	323.5	319	313	308	307	304	300.5	297	292	290.5	289	286.5	284	280
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G02390	A43296	S41608	165967	S28258	JC5928	T00026	T18900	T26644	TSHUP1	A40558	A59414	JQ1301	T22836	S41607	S18968
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277.5 5.	273.5	265	265	257	256.5	255.5	253.5	251	248.5	245.5	244.5	243	234.5	234	233.5

## ALIGNMENTS

	RESULT T00017	1
	gene A	gene ADAMTS-1 protein - mouse C.Species: Mus musculus (house mouse)
	C; Date C; Acce	C.date: 22-Jan 1999 #Sequence_revision 22-Jan 1999 #text_change 21-Jui 2000 C.Accession: T00017
	R;Kunc Genomi	R;Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K. Genomics 46, 466–471, 1997
	A;Titl A:Refe	ie: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 g prence number: 214055; MUTD:98110583; PMID:9441751
	A; Acce	sston: T00017
	A; Mole	A;Scalus: preliminary; cranstated from GB/EMBL/DDBO A;Molecule type: DNA
_	A; Cros	A; Residues: 1.951 ANDA A; Cross-references: EMBL; AB001735; NID; 92809056; PIDN: BAA24501.1; PID; 92809057
	A; Experimen C; Genetics:	srimental source: strain 1298VJ etics:
	A; Gene A; Intr C; Supe	A;Gene: ADAMTS-1 A;Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2 C;Superfamily: thrombospondin type 1 repeat homology
	F;542-	F;542-598/Domain: thrombospondin type l repeat homology <thr3></thr3>
	Quer Best Matc	Query Match 48.1%; Score 2482.5; DB 2; Length 951; Best Local Similarity 48.0%; Pred. No. 2.8e-161; Matches 478; Conservative 158; Mismatches 249; Indels 111; Gaps 22;
	δy	1 MLLLGILTLAFAGRTAGG FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQ1 57
	Dp	20 LILLASITMILCARGAHGRPTEEDEELVLP-SIERAPGHDSTTTRIRL 66
	οy	58 TAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNA 109
	οgα	67 DAFGQQLHLKLQPDSGFLAPGFTLQTVGRSPGSEAQHLDPTGDLAHCFYSGTVNG 121
	δλ	110 EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRG 161
	qq	122 DPGSAAALSLCEGVRGAFYLQGEEFFIQPAPGVATERLAPAVPEEESSARPQFHILRRR- 180
	δλ	162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRR 206
<del>.</del> ,,,	qq	181RRGSGGAKCGYMDDETLPTSDSRPESGNTRNQWPVRDPTPQDAGKP 226
	QY	207SGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI 262
	qq	227 SGPGSIRKKRFVSSPRYVETMLVADQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSI 286
	ολ	263 NIVVVXVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC 322
	ΩĐ	287 SLVVVKILVIYEEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTAILFTRQDLC 346
	ΟŊ	323 GATTCDILGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEBVFG 382  :

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Cispecies: T47158
Riblum, H.; Bauersachs, S.; Mewes, H.W.; Well, B.; Wiemann, S.
Submitted to the Protein Sequence Database, March 2000
A;Reference number: 224379
A;Recession: T47158
A;Status: preliminary
A;Molecule type: man,A
A;Residues: 1-550 <AAA>
A;Residues: 1-550 <AAA>
A;Resperimental source: adult melanoma (MeWo cell line); clone DKFZp762C1110
A;Rote: DKFZp762C1110.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG
                                                                                        146 GGALLGVLQYRGAELHLQPLEGGTPNSA - - GGPGAHILRRK - - - SPASGQGPMCNV - - -
                                                                                                                                                                                                   240 HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL
                                                                                                                                                                                                                    WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLE
                                                                                                                                                                                                                                                                                                                                              360 AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::|||::|| | HGPLAQPLTLLQVLVAGNPQDTRLRYSFFVPRPTPSTPRDTPQD 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 SRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKD 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp762C1110.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.1%; Score 1604; DB 2; Best Local Similarity 49.7%; Pred. No. 1.2e-101; Matches 284; Conservative 106; Mismatches 142;
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C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C; Accession: 700355
R; Lshikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. 5, 169-176, 1998
A; Lshikawa, Freinon of the coding sequences of unidentified human genes. X. The complete A; Reference number: 214142; MUID:98403880; PMID:9734811
A; Accession: 700355
A; Molecule type: mRNA
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Experimental source: brain
                                                                                                        GSHTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNG 406
                                                                                                                                                                               GACVERHNINKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 558
                                                                                                                                                                                                                                                     RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL 618
                                                                                                                                                                                                                                                                                                                                                                                                NKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLN 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOKRAVDCRGSAGORTVPACDAAH - - RPVETQACGE - PCPTWELSAWSPCSKSCGRGFQR 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120
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                                  383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
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C;Superfamily: thrombospondin type 1 repeat homology
F;519-575/Domain: thrombospondin type 1 repeat homology <THR3>
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llarity 46.3%; Pred. No. 1.2e-122;
Conservative 123; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSLKCVGHGGRLLARDQCNLHRKPQE-LDFCVLRPC 950
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Best Local Simi
Matches 381;
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Matches 347; Conservative 128; Mismatches 338; Indels 132; Ga  101 CFYSGDVNAEDDSFAAVSLCGGLRGAFGYRGAEVVISPLPNASAPAAQRNSGGA			OY 654 CIKAGCDGNLGSKREPKCGVCGGDNKSCKKVTGLFTKP-MHGYNFVVAIPAGASSIDIR 712   :	QY 807DKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCS 852	<pre>procollagen N-endopeptidase (EC 3.4.24.14) I - bovine N.Alternate names: procollagen N-proteinase C;Species: Bos primigenius taurus (cattle) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999</pre>
•	189 623 248 683 308 743	QY         803 EPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASGGGKR         862           :	RESULT 4 121311 T21311 T21311 Hypothetical protein F25H8.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T21371; T24896 C; Accession: T21371; T24896 C; Accession: T21371; T24896 A; Reference number: Z19413 A; Reference number: Z19413 A; Recession: T21371 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	SP:F25H8.3	Aintrons: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1; 81 Query Match Best Local Similarity 36.7%; Pred. No. 1.2e-99;

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protein C37C3.6a [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C89114
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C: elegans: a platform for investigating bio A;Title: Genome sequence of the nematode C: elegans: a platform for investigating bio A;Title: Genome: A75000: MUID:99059613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/CA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Notecule type: DNA
A;Accession: C89114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1558 <STO>
A;Cross references: GB:chr_V; PIDN:AAC25867.1; PID:93294501; GSPDB:GN00023; CESP:C37C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASG 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 KSFREEQCEAFN----GYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVL 631
                                                                                                                                                                                                                                                                                                                               825
                                                                                                                                                                                                                   LSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPA--CDAAHR 883
632 APKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 P--MHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERD
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                               835 INVDDNNVLEDDSVGYEWALKKWSPCSKPCGGGSQFTKYGCRRLDHKMVHRGFCDSVSK
                                                                                                           VESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSV
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13.2%; Score 681; DB 2; Length 15
Best Local Similarity 33.7%; Pred. No. 3.8e-38;
Matches 162; Conservative 63; Mismatches 176; Indels
                                                                                                                                                 CNLHRKPQELDFCVLRPC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN-DARPEGRRACNRELC 969
           707
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A; Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3;
                                                                                                                                                                                                                                                                  Augusty-Greens Landon Lord Tangeron Caenor Anabortis elegans
C; Species: Caenor Caenor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 HYQGEVKSHGNMKAAISDCGALMGSIVMEDHFLVLQTLPK----RVHHLQKERHLVYKRS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRY-- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | :: | :: | :: | :: | : :: | : :: | : :: | : :: | : :: | :: | : :: | : :: | : :: | :: | :: | :: | :: | :: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: :: ::||:|:|
NNVHVLYQQDTLTPNLDIVIVRYEMWRTQPSALSTGVHKNGQAQSLLDAFCRYQAHMNPG 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| | || || || || || EMGHNMGMVHDGVQNQCNKGCCLMSAVNGAGKT-----TWSDCSVREFNAFLLQLDE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAP-AFSTEHLGVPLQGLTGGSSDLRRC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELGHVFNMPHDNVK-VCEEVFGKLRANHWMSPTLIQIDRANPWSACSAAIITDFL----D 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGHGDCLLDQPSKPISLPE----DLPGASYTLSQQCELAFGVGSK-PCP----YMQYCTK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGRGNCLRDASPGLISTNHLSDLRLPGQRFTADQQCSYFWGRDYKVEIPNGKAMDDICRI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 RHPLKNGN--LKMKFTAWNDTYHLNLRKNSRIVSPHIISVVRHGDDDVTTYAGLRDYEQC
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                                                                                                                                                                                                                                                   angiogenesis inhibitor homolog - Caenorhabditis elegans
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A; Map position: X
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                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein C37C3.6b - Caenorhabditis elegans
C5pecies: C5pecies
                                                        517 GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 KSFREEQCEAFN----GYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVL 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TDFRAEQCSKRNDEALDGNYHK-----WTP-YKG---KNKCELVCKPESGNFYYKW 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               750 LVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPRED-- 807
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                                                                                                                                                         950 C 950
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QY         272 LRDRDSGPKVTGGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC 327           1::	41 54 47 59 53	599 LAVAMVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSFDSTSVCVGKCLI		QY 824 SVLSLSNQVEQPDDRPPARWYAGSWGPCSASCGSGLQ-KRAVDCRGSAGQRIVPACDAAH 882	RESULT 10 T00260 hypothetical protein KIAA0605 - human C;Specials: Hono saplens (man) C;Specials: Hono saplens (man) C;Specials: Hono saplens C;Accession: T00260 C;Accession: T00260 R;Nagase, T.; Tshikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, DNA Res. 5, 31-39, 1998 A;Title: Prediction of the coding sequences of unidentified human genes. IX. The comp A;Reference number: Z14086; MUID:98290545; PMID:9628581	A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-951 < NAG> A; Cross-references: EMBL: AB011177; NID: g3043733; PIDN: BAA25531.1; PID: g3043734 A; Experimental source: brain C; Genetics: A; Note: KIAA0605 C; Superfamily: thrombospondin type 1 repeat homology F; 46-106/Domain: thrombospondin type 1 repeat homology	Query Match 9.5%; Score 493; DB 2; Length 951; Best Local Similarity 22.2%; Pred. No. 1.4e-25; Matches 171; Conservative 55; Mismatches 183; Indels 360; Gaps 27;
Qy         524PYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFR 580           bb         540 KGCPIQQCAVSGSITVQGQHRDCVNPAPNNGGKTCEGANIRGIVCGATSSNCLGFT 595           QY         581 EEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRA 622           l:         l:           Db         596 REEFCNKICSSIKYDPHKPDQQLTGEGFEHST	Oy         663	Qy         718 GLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRXS	Qy         804	ACCOMMENDATION THE STREET STRE	hypothetical protein T19D2.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T16892 R;Bentley, D R;B	NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CESP:T19D2 )/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 58 Score 510.5; DB 2; Length 860; Pred. No. 7.9e-27; )2; Mismatches 310; Indels 159; Gaps 40;	Qy 220 VETLVVADESMVKFHGADLEHYLLTLATAARLYRHPSILNPINIVVVKVLL 271

517 GSWAKWDPYGPCSRTCGGGVOLARRQCTNPTPANGGKYCEGVRYKYRSCNLEPCPS 572 	573 SASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN 623 	KSC 6		LEPLTVEVLSV-GKMTPPRVR :       :     : NOGLNVMVWNONGKSPSTT			386 FGHPGLDMELGPSQGQETNEVCEQAGGGACEGPPRGKGFRDRNVTGTPLTGDKDDEEVDT 445	813 816 446 HFASQEFFSANAISDQLLGAGSDLKDFTLNETVNSIFAOGPRSSIARSFFUDYFRINGS 605	84		r 34       YCDALTRPEPVHEFCAGRECOPR 62	98	9 6	VTRDIRCSEDEKLCDPNTRPVGEKNCTGPPCDRQWTVSD	902 WSPCSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRPC 950 	RESULT 11 T15976 hypothetical protein F08C6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T15976 A;Rentley, D. Submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid F08C6. A;Reference number: 218440 A;
Oy Db	oy Oy	Oy Db	Oy Db	Oy Dp	Oy Dp	0y	DD	Qy Dp	<i>&amp;</i> 원	ΟŸ	qq	Qy Dp	οy	qq	oy Op	RESULT T15976 T15976 T15976 C;Spec: C;Date: C;

47; 162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPR--- 218 267 VKVLLLRDRDSG----PKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDL- 321 57 ITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSD----LRRCFYSGDVNAEPD 112 61 IQAFNKKYNLSL---EXTLAKLLSSGVTVVKKNEKKGGSLDFGSTLDSCHYH---HYGEK 114 SFAAVSLCGGL------RGAFGYRGAEYVISPLPNASAPAAQRNSQ-GAHLLQRRG 161 :|:| ||: : : : | | : T---LAGEPKDFCGLDN-----VYIEESLYEDESAIFEDV------FVTGQRLTQ 215 ----YVETLVVADESMVKF----HG--AD--LEHYLLTLLATAARLYRHPSILNPINIVV 266 322 CGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVF 381 382 GKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGAS 441 Gaps 387 501 -----TGTFCGPSKWCQL 400 539 459 590 519 646 520 GSQLNRF------PQRACKVFCDVQQHYGSQRNYRFFGDNLPDGTSCGYD-- 563 678 623 679 ----NKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGK 734 YLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEP---LTVEVLSVGKMTP 791 792 PRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPP----ARWVA 845 664 665 WIEWNHCSVSC-----GRGSQARY-----RKCLSPHRILAFDCPGENKVT- 704 GSWGPCSASCGSG--LQKRAVD---CRGSAGQRTVPACDAAHRPVETQACGEPCPT---W 897 ----TCQNDGIW 803 540 RRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQC-----EAFNGY 624 YRKRNRAC-SITG----QCEGNEDETEVCSSESCPSV------LRVGNEWST 442 YTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK 502 GACVERHNLNK------GVQLA 591 NHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN---GTGYFY-VLAPKVVDGTLCSPDST 647 SVCVQGKCIKAGCDGNL------GSKKRFDKC-GVCGGD 564 RYCLDGECLALNCNNNALISRDQSCPTDTCPITDQSSSVYRQWGTWSLWTSCTATCGGG Query Match 8.7%; Score 450.5; DB 2; Length 957; Best Local Similarity 22.7%; Pred. No. 1.1e-22; Matches 227; Conservative 106; Mismatches 328; Indels 339; | : || || : || || : || || || || || SLWNEWSDCSRVCGKGLRSRSRSCFGSGCMGASSEQQFCN 843 EL-SAWSPCSKSCGRGFQRRSLKCVGHG--GRLLARDQCN 934 -----KSDTLF------113 175 219 388 382 735 846 757 868 804 g ò g δ g δy 원 ò QΥ qq òγ 셤 Qγ Dp óγ g Db Qγ δy g δ g ö qq οy g δ g δ q δý g

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A; Reference number: A44463; MUID: 93054601; PMID: 1385408
A; Accession: A44463
A; Molecule type: mRNA
A; Residues: 1-23, 'Q', 25-92,'G', 94-131,'G', 133-169,'Q', 171-571 < PA2>
A; Coost references: GB: X68251
A; Experimental source: venom gland
A; Coost reference inconsistent with the nucleotide translation
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIP:118104)
A; Note: sequence extracted from NCBI backbone (NCBIP:118104)
B; Pijimura, Y; Titani, K; Usami, Y; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.;
Biochemistry 30, 1957-1964, 1991
A; Reference number: A37958; MUID: 91129280; PMID:1993206
A; Reference number: A37958; MUID: 91129280; PMID:1993206
A; Recession: A37958; MUID: 91129280; PMID:1993206
A; Rocession: A37958; MUID: 91129280; PMID:1993206
A; Rocession: A37958; MUID: 91129280; PMID: 1993206
C; Comment: Inhibits collagen: and ADP-induced platelet aggregation.
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Keywords: hydrolase; metalloproteinase; venom; zinc
C; Superfamily: mouse meltrin homology circle
C; Superfamily: mouse meltrin homology circle
F; 362-444/Domain: disintegrin homology circle
F; 362-444/Domain: disintegrin homology circle
F; 295, 299, 305/Abinding site: zinc (His) #status predicted
F; 296/Active site: Glu #status predicted
R;Usami, Y.; Fujimura, Y.; Miura, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K Biochem. Biophys. Res. Commun. 201, 331-339, 1994
A;Title: A 28 kDa-protein with disintegrin-like structure (jararhagin-C) purified fro A;Reference number: JC2245; MUID:94256999; PMID:8198592
                                                                                                                                                               A; Molecule type: protein
A; Residues: 360-571 <USA>
A; Residues: 360-571 <USA>
A; Experimental source: venom
R; Paine, M.J; Desmond, H.P.; Theakston, R.D.; Crampton, J.M.
J; Biol. Chem. 267, 22869-22876, 1992
A; Title: Purification, cloning, and molecular characterization of a high molecular we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 DAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: || :| || :| || 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 AGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAFQEDF-YLHLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 RETYFIEPLKLPDSEAHA------VFKYENVE--KEDEAPKMCGVTQNWKSYEPIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 ADLEHYLLTLLATAARLYRHPSILNPI-NIVVVKVLL--LRDRDSGPKVT--GNAALTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DGLFSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH---- MMSPTLIQIDRANPWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GAEYVISP--LPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.7%; Score 344.5; DB 2; Best Local Similarity 22.7%; Pred. No. 1e-15; Matches 160; Conservative 88; Mismatches 256;
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                                                                                                             hypothetical protein F53B6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22545
R;White, S.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219578
A;Accession: T22545
A;Accession: T22545
A;Realus: preliminary; translated from GB/EMBL/DDBJ
A;Realus: preliminary; translated from GB/EMBL/DDBJ
A;Realus: preliminary
A;Residues: 1-1059 cwll.>
A;Residues: 1-1059 cwll.>
A;Residues: EMBL:281086; PIDN:CAB03121.1; GSPDB:GN00019; CESP:F53B6.2
A;Experimental source: clone F53B6
C;Genetics:
A;Gene: CESP:F53B6.2
A;Map Position: 1
A;Introns: 38/3; 92/3; 131/3; 169/1; 236/2; 282/3; 349/2; 376/2; 420/1; 576/3; 789/3; 84
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N;Alternate names: single chain botrocetin
N;Contains: aisintegrin-like 28K protein; hemorrhagic proteinase (EC 3.4.24.
N;Contains: aisintegrin-like 28K protein; hemorrhagic proteinase (EC 3.4.24.
C;Species: Bothrops jararaca (jararaca)
C;Species: Moust jararaca (jararaca)
A;Reference number: S24789
A;Reference number: S24789
A;Recssion: S24789
A;Residues: 1-571 cPAI>
A;Residues: 1-571 cPAI>
A;Residues: 1-571 cPAI>
A;Residues: 1-571 cPAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 411.5; DB 2; Length 1059; 25.7%; Pred. No. 5.7e-20; ive 53; Mismatches 128; Indels 143;
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Best Local Similarity
Matches 112; Conserv
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Db 379 CGTPERGONECCDAATCKLZSGSGGGHGDCCEGCKFSSGGTER 422  GY 517 GSWAKNDPYGECSTTGGGGYGLARDGCTNPTPANGGKTGCD	Oy 563  Db 496  Oy 609  Db 550  Db 550  Db 550  RESULT 15  S60251  C; Species: 16  C; Species:
	Qy         222 TLVVADESMYRFHGADLEHYLLTLIATAARLYRHPSILNPINIVVVKVLLIRDRDSGFKV 281           1 :

352, App 352, App

Sequence 3 Sequence 3

US-10-176-758-352 US-10-175-737-352 US-10-175-738-352 US-10-175-738-352 US-10-176-482-352 US-10-176-482-352 US-10-176-757-352 US-10-176-757-352 US-10-176-757-352 US-10-176-757-352 US-10-174-593-352 US-10-174-572-352 US-10-174-573-352 US-10-176-743-352 US-10-176-748-352 US-10-176-748-352 US-10-176-748-352 US-10-176-748-352 US-10-176-748-352 US-10-176-748-352 US-10-176-748-352 US-10-176-74-352 US-10-176-74-352

US-10-176-987-352 US-10-176-991-352 US-10-176-992-352

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April 29, 2003, 17:22:38 ; Search time 26 Seconds (without alignments) 2927.820 Million cell updates/sec
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1 MLLLGILTLAFAGRTAGGFE......DQCNLHRKPQELDFCVLRPC 950
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/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301932 seqs, 80129803 residues
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                                                                                                            - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## No. Score Match Length DB ID No. Score Match Length DB ID 2 408 42.9 823 9 US-10-163-316-2 3 45.3 16.3 10 US-09-965-631-4 5 17 1.8 608 10 US-09-965-631-2 5 17 1.8 608 10 US-09-965-631-2 5 17 1.8 608 10 US-09-965-631-2 5 17 1.8 727 9 US-10-105-929-13 5 240ence 2, Appli 6 17 1.8 727 9 US-10-105-929-13 5 Sequence 1, Appli 11 17 1.8 727 9 US-10-097-597-1 12 17 1.8 727 9 US-10-097-597-1 13 17 1.8 727 9 US-10-097-580-1 14 17 1.8 727 10 US-09-445-023A-1 15 17 1.8 727 9 US-10-097-580-1 16 17 1.8 967 12 US-10-105-929-2 17 1.8 727 9 US-10-097-580-1 18 17 1.8 967 12 US-10-105-929-2 18 18 17 1.8 967 12 US-10-105-929-2 19 18 17 1.8 967 12 US-10-105-929-2 19 18 18 18 551 12 US-10-105-929-1 2 Sequence 1, Appli 3 H4 1.5 518 10 US-09-359-10 5 Sequence 7, Appli 5 Sequence 1, Appli 6 H4 1.5 518 10 US-09-359-10 5 Sequence 1, Appli 7 14 1.5 518 10 US-09-352 5 Sequence 10, Appli 7 14 1.5 518 10 US-09-352 5 Sequence 10, Appli 7 14 1.5 518 10 US-09-352 5 Sequence 10, Appli 7 14 1.5 518 10 US-09-352 7 Sequence 10, Appli 7 14 1.5 518 10 US-09-352

260 NPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQ 319

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LKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVR 559
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                                                                                                                                                                                                                                               VKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLI
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SQUENCE 2. Application US/10163316
PUBLICATION NO: US20020197703A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 65552, A Human Matrix Met
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 823
                                                                                                                                                                                                                                                                                                                                                                                                                                 920 CVGHGGRLLARDQCNLHRRPQELDFCVLRPC 950
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100.0%; Pre
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ORGANISM: Homo sapiens
US-10-163-316-2
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408;
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                                                                                       LTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCS
                                                                                                                               VIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSAC
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                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09965631
Patent No. US20020115842A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. US20020115842A1e1 Hum
FILE REFERENCE: LEX-0241-USA
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
US-09-965-631-6
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LENGTH: 367
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US-09-965-631-6
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Conservative

Similarity

Best\_Loca Matches

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GENERAL INCREATION:

APPLICANT: MCCATTHY, Sean A.

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES

FILE REFERENCE: 07334-325001
CURRENT FILING DATE: 2010-03-09
PRIOR PAPLICATION NUMBER: US 69/128,709
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 14

SSET ID NO 8

FENTIOR BELLE FERENCE FERE
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Pred. No. 1.1e-07;
0; Mismatches 0;
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: US 60/058,108
PRIOR FILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR PILING DATE: 1999-09-01
PRIOR PILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
SPRIOR FILING DATE: 1999-09-01
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2

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; Patent No. US20020137142A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09803589
; Patent No. US20020112251A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AFTTAHELGHVFNMPHD 107
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-803-589-2
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Best Local Similarity
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US-10-105-929-13
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US-09-803-589-8
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                                                                                                                                                                                                                                                                                    APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Eth
TITLE OF INVENTION: NO. US20020115842Alel Human Proteases and Polynucleotides Encodin
FILE REFERENCE: LEX-0241-USA
CURRENT FILING DATE: 2001-09-27
PRIOR PELLING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
WUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 321
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Patent No. US20020112251A1

GENERAL INFORMATION:

APPLICANT: MCALTLY, Sean A.

APPLICANT: Holtzman, Douglas A.

APPLICANT: GOOGEATL, Andrew D.J.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: USES

FILLE REFERENCE: 07334-325001

CURRENT APPLICATION NUMBER: US 09/128,709

PRIOR PLILING DATE: 1998-08-04

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1998-08-04

PRIOR FILING DATE: 1998-08-06

PRIOR FILING DATE: 1998-08-06

PRIOR FILING DATE: 1998-08-06

PRIOR APPLICATION NUMBER: US 09/130,491

PRIOR APPLICATION NUMBER: US 06/054,666
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                                                        320 DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELG 364
                         320 DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELG 364
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100.0%; Pred. No. 4.4e-279;
.lve 0; Mismatches 0;
                                                                                                                                                                                                             ; Sequence 2, Application US/09965631; Patent No. US20020115842A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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US-09-965-631-2
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US-09-803-589-2
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APPLICANT: Ishioka, Kelko
APPLICANT: Ishioka, Kelko
APPLICANT: Ishioka, Kukako
APPLICANT: Ishioka, Yukako
APPLICANT: Matsushma, Kouji
APPLICANT: Matsushma, Kouji
APPLICANT: Matsushma, Kouji
APPLICANT: Matsushma, Kouji
APPLICANT: Muno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA
TITLE OF INVENTION: UNMBER: US/10/097,597
CURRENT APPLICATION NUMBER: US/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 9-160422
PRIOR APPLICATION NUMBER: US 9-160422
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Intoguchi, Eijii
APPLICANT: Incouch, Eijii
APPLICANT: Incouchi, Eijii
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Muman ADAMTS-1 protein, gene encoding the same, pharmaceutical
TITLE OF INVENTION: Human ADAMTS-1
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: 09745,023
PRIOR APPLICATION NUMBER: 09745,023
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 14
SOFTHARE: Patentin Version 3.0
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100.0%; Pred. No. 1.3e-07;
iive 0; Mismatches 0;
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APPLICANT: Hirose, Kunitaka
                           Inoguchi, Eiji
Hakozaki, Michinori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Matches 17; Conservative
     Kunitaka
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT CRGANISM: Mus sp. US-10-097-597-12
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US-10-097-580-1
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APPLICANT: Indouchi, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Mastushima, Kouji
APPLICANT: Mastushima, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
FILE REFERENCE: 057092
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/10/105,929
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR PLING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR PLING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR PLING DATE: EARLIER APPLICATION NUMBER: US 60/058,108
PRIOR PILING DATE: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 608
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10097597
Publication No. US20030022352A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 727
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Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-10-105-929-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-597-1
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US-10-097-597-12
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us-10-009-332-1.oli.rapb

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APPLICANT: Inoquchi, Authoria
APPLICANT: Inoquchi, Eiji
APPLICANT: Hakozaki, Michinori
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADI
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT PILICATION DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1997-06-03
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APPLICANT: Kimble, Judith E
APPLICANT: Kimble, Judith E
APPLICANT: Kimble, Judith E
TITLE OF INVENTION: Robert H
TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386
CURRENT APPLICATION NUMBER: US/09/321,987B
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR PRILING DATE: 1999-04-13
PRIOR PRILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.1
LENGTH: 950
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100.0%; Pred. No. 1.3e-07;
Live 0; Mismatches 0;
                                                  Sequence 12, Application US/09445023A
Patent No. US20020119167A1
GENERAL INFORMATION:
APPLICANT: HIFOSE, Kunitaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09321987B Patent No. US20020102210A1
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100.0%; Pre-
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US-10-105-929-2
; Sequence 2, Application US/10105929
; Patent No. US20020137142A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFWWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 727
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Matches 17; Conservative
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hes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Murine
US-09-321-987B-4
                              US-09-445-023A-12
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US-09-321-987B-4
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Sequence 1, Application US/09445023A

Patent No. US20020119167A1

SEQUENCE 1, NEORAMATION:

APPLICANT: HINOSE, Kunitaka

APPLICANT: Induchi, Elji

APPLICANT: Ishioka, Keiko

APPLICANT: Ishioka, Keiko

APPLICANT: Ishioka, Keiko

APPLICANT: Ishioka, Kouji

APPLICANT: Ishioka, Kouji

APPLICANT: Ishioka, Kouji

APPLICANT: Ishioka, Kouji

APPLICANT: Runo, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Runo, Kouji

APPLICANT: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS

CURRENT APPLICATION NUMBER: US/09/445,023A

CURRENT APPLICATION NUMBER: JP 9-160422

PRIOR PELING DATE: 1999-10-03

NUMBER OF SEQ ID NOS: 14

SSOFTHARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 727
                                                                                                             APPLICANT: Intose.

APPLICANT: Intose.

APPLICANT: Intose.

APPLICANT: Hakozaki, Michinori

APPLICANT: Hakozaki, Michinori

APPLICANT: Hakozaki, Michinori

APPLICANT: Shida, Yukako

APPLICANT: Shida, Yukako

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS

FILE REPRENCE: 2002-03-15

PRIOR PLILING DATE: 1999-12-03

PRIOR FILING DATE: 1997-06-03

PRIOR FILING DATE: 1997-06-03

PRIOR FILING DATE: 1997-06-03

SOFTWARE: PALENTIN NUMBER: JA

SEQ ID NO 12

LENGTH: 727

LENGTH: 727
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100.0%; Pred. No. 1.3e-07;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0; Indels
                      ; Sequence 12, Application US/10097580; Publication No. US20030032168A1; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                  APPLICANT: Hirose, Kunitaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Mus sp.
US-10-097-580-12
US-10-097-580-12
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US-09-445-023A-1
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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andraw D.
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: 09404/041001
CURRENT APPLICATION NUMBER: BALLER APPLICATION NUMBER: 09/130,491
FRIOR PELING DATE: 2002-03-25
FRIOR PELING DATE: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 05/058,108
FRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/054,961
FRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
FRIOR FILING DATE: EARLIER FILING DATE: 1997-09-06
FRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
FRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
FROOTWARE: FASTSO for Windows Version 3.0
SOFTWARE: FASTSO for Windows Version 3.0
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEC ID NOS: 16
SEC ID NOS: 16
SEC ID NOS: 17PEE: PRT
ORGANISM: Homo Sapiens
US-10-105-929-2
QUETY MATCH
BAST LOCAL SIMILATITY 100.0%; Pred. No. 1.7e-07;
MATCHES 17; CONSELVATIVE 0; Mismatches 0; Indels 0; Gaps
OY 356 AFTTAHELGHVFNWPHD 412
Db 396 AFTTAHELGHVFNWPHD 412
SEATCH COMPLETED APPLICATION: 17:25:35
JOB time: 31 secs
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drosophila drosophila homo sapien equus cabal manduca sex

equus cabal caenorhabdi caenorhabdi

homo sapien drosophila drosophila

caenorhabdi homo sapien

076840 044938 094944 099587 099587 099587 099587 099587 099587 099587 099587 099587 099587 099587 099587 099785

P90884 caenornace.
0991pl mus musculu
cardl homo saplen

Q9ugq1 Q9h8x0

drosophila caenorhabdi

Q8t458

9h8x0 homo saplen 09cx59 mus musculu 9glk7 oryctolagus

O9crc7 mus musculu 09g1k6 oryctolagus 09xsv8 bos taurus 08spm4 bos taurus

09g1k7

O8vhk4 mus musculu O9u631 drosophila

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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213 FVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLTRHPSILNPINIVVVKVLLL 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62:2002).

EMBL, AJ315733; CAC86014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 15 with thrombospondin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILNE-21856482; Pubmed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin; Protease.
SEQUENCE 950 AA; 103286 MW; 5DFBE18285CCCC3B CRC64;
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                                                                                                                                                                                                                                                                                                                                                            950 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 4043; Best Local Similarity 100.0%; Pred. No. 0; Matches 738; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                Q9W1Z6
Q8T458
Q8T458
Q99JF1
Q9UGQ1
Q9UGQ1
Q9CX59
Q9GLK7
Q9GCR7
Q9GCRC7
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Q22580
Q17591
O60345
095428
076840
044938
                              09GQR0
09VAV4
P82987
095N24
09U8G8
019204
096RW4
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Best Local Similarity
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663.5
581.5
579.5
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Q8TE58;
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Q8TE58
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Q91z56 mus musculu
Q19791 caenorhabdi
Q8sxb drosophila
Q8te60 homo sapien
Q8te57 homo sapien
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homo sapien
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3378.970 Million cell updates/sec
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                                                                                                                            1 FVSIPRYVETLVVADESMVK......DQCNLHRKPQELDFCVLRPC 738
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                                                                  April 29, 2003, 17:10:24; Search time 45.0027 Seconds
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08te60 h
08te57 h
09vf61 d
09w493 d
08te56 h
08te58 h
08tey8 h
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                            671580 seqs, 206047115 residues
                                                                                               US-10-009-332-1_COPY_213_950
4043
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Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Q91256
Q91256
Q85XB0
Q85XB0
Q8TE57
Q9VF61
Q9W493
Q8TE56
Q8WXS8
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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Gaps

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Indels

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homo sapien homo sapien homo sapien 096137 homo sapien 099154 oryctolagus

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REDLINE-94150718; Pubmed-7906398;

MEDLINE-94150718; Pubmed-7906398;

MISON R., Ainscough R., Anderson K., Baynes C., Berks M.,

MISON R., Ainscough R., Anderson K., Evellon R.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favellon A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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                                                                                                           245 CGSGLQKRAVDCRDSPGQQGASACDVDHRPLEKRACGEPCPTWELGNWSPCSKSCGRGFK 304
                            64
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                          YLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRV
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                            KCKLICRANGTGYFYVLAPKVVDGTLCTPDSTSVCVQGKCIKAGCDGNLGSKKKFDKCGV
                                                                               CGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGK
microry micros m
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Last annotation update)
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EMBL; Z69360; CAA93288.1; JOINED.
EMBL; Z69360; CAA93287.1; -.
EMBL; Z69361; CAA93287.1; -.
HSSP; P15167; 1DTH.
MEROPS; M12.135; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q19791 PRELIMINARY;
Q19791; Q27524;
Q1-00-1996 (TrEMBLrel. 01, C1
01-NOV-1998 (TrEMBLrel. 08, L5
01-DEC-2001 (TrEMBLrel. 19, L6
F25H8.3 protein.
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Submitted (FEB-1996)
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SEQUENCE FROM N.A.
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01-DEC-2001.(TrEMBLrel. 19, Last sequence update)
01-DRC-2001.(TrEMBLrel. 19, Last sequence update)
01-DRC-2002 (TrEMBLrel. 20, Last annotation update)
Similar to a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
193 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                       GVGSKPCPYMQYCTKLWCTGKAKGOMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNK
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ilarity 91.7%; Pred. No. 4.2e-147;
Conservative 11; Mismatches 17; Indels 0
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR00884; TSP1.
Pfam; PF00090; tsp_1; 2.
Integrin.
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SEQUENCE
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091256
11D 091256
07 01-D
07 01-D
07 01-D
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08 Mus.
08 Mus.
09 Mus.
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Gaps 67

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965 TDDRDNELLNGKF-LKTYPLKFVYAGVTMQYTGSSSVVEQVNTTYSWKLSRDLIVQIISL 1023
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| DVSPSKRQDTVLLSYSYTIDKPPDYBAEVEIYRWEMQAPSNCDSLCEGRSHRLPACISTT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN----HMM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::||:| | ||:::| |||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---TCDTLGMA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVERHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 VKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDN 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Submitted (APR-2002) to the EMEL/GenBank/DDBJ databases.

EMBL; AN094716; AAM1106911; -. SEQUENCE 1688 AA; 189867 MW; 48FBBDD4DEOCA4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| |: | || :||| ||: ||: |: |: || || ||:|::: |
457 LEVLIAVDNSMKQFHGEDLQPYILLILMSIVSSIFADASIGNSIRILLVRLISL-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | :: |::| | :| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLPGASYTLSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 KSCKKVTG-LFTKPMHGYN----FVVAIPAGASSIDIRQRGYKGLIGDDNYLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909 DTCHEVTGNLLVSNLLGLNDGNEPNKTLYYVTRIPKGASNIITQRGYP----DQNFIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 KNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQA--SRPILEPLTVEVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DKSSHPK-DPRGPSV---LHNSVLSLSNQVEQPDDRPPARWVAGSWGPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cch 28.5%; Score 1152; DB 5; 11 Similarity 34.5%; Pred. No. 7.6e-97; 281; Conservative 113; Mismatches 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 281; Conserv
                                                                                                               SEQUENCE FROM N.A.
                                                          NCBI_TaxID-7227;
                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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                                                                             17;
                                                                                                                                                       PKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLGMADVGT 125
                                                                                                                                                                                                                                                                                                                                                            MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEV--------FGKL 172
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                                                                                                                                                                                                                                                                               SRSMFCHHGACVRLAPESLTKIDGQWGDWRSWGECSRTGGGGVQKGLRDCDSPRPRNGGK 640
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFDKCGVCGGDNKSCKKVTGLFTKP-MHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYL 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSV 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932
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                                                                                                                                       99
                                                                                                                        YVETLVVADDESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG
                                                                                                                                                                                                                                                                                                                                                                                              RAN---HMMSPTLIQIDRANPWSACSAAIITDFLDSGHG--DCLLDQPSKPISLPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYN-----HSTNRLTLAVAWVPKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GK--LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|: : |::|||||| | : : ::| |||: :| :|| SLRAANGEFLLNGHFQVSLARQOIAFQDTVLEYSGSDAIIERINGTGPIRSDIYVHVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GS-HPPDISYEYMTAAVPNAVIRPISSALYLWRVTDTWTECDRACRGQQSQKLMCLDMST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | | : : | HRQS-----HDRNCQNVLKPKQATRMCNIDCSTRWITEDVSSCSAKCGSGQKRQRVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 RGSAGQRTVPA----CDAAHRPVETQACGEPCP--TWELSAWSPCSKSCG-RGFQRRSLK
                                                                             94;
                  Length 2165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
   Query Match 38.8%; Score 1567; DB 5; Best Local Similarity 39.6%; Pred. No. 4.8e-135; Matches 321; Conservative 113; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Æ
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PK----EPREDK-----SSHPKDPRGPSVLHNSVLSLSNQVEQ-
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE 1072 AA;
                                                                                                                                                                    1039 QEGCVLGRC 1047
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                              730 LDFCVLRPC 738
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKVTGLFTK - - PMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGH 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYL 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSID-WPGEFPFAGTTFEYQRSFNRPERLYAPGPTNETLVFEILMQGK--NPGIAWKYAL 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSK--PISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 GELGPRPIHGOWSAWSKWSECSRTCGGGVKFQERHCNNPKPQYGGIFCPGSSRIYQLCNI 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPCPSSASGKSFREEQCEAFN----GYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENFEFFFAMSGKVKDGTPCSPNKNDVCIDGVCELVGCDHELGSKAVSDACGVCKGDNSTC 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 PKVTGNAALTLRNFCAWQKKL-NKVSDKHPEYWDTAILFTRQDLCG--ATTCDTLGMADV 123
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   VETLVVADESMVKFHG-ADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GVGSKPCP---YMQYCTKLWC--TGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 GIMCDPKRSCSVIEDDGLPSAFITAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||:|| | ||:|| 465 IGNNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPKQAGQYKXPDKLPGQIYDADTQCKWQF
                                                                                                                                                                                                                                                                     of
                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                MEDLINE-2186482: PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otln C.;
Coloning, expression analysis, and structural characterization cseven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
EMBL; AJ311903; CAG83612.1; -.
SEQUENCE 1081 AA; 119655 MW; 0438BF645676461E CRC64;
                                                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                    Length 1081;
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35.0%; Pred. No. 2.7e-96;
tive 97; Mismatches 322; Indels
                                                                                                                Last sequence update)
Last annotation update)
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                                                                              1081
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                                                                              PRT;
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01-JUN-2002 (TrEMBLrel. 21, C;
01-JUN-2002 (TrEMBLrel. 21, L;
01-JUN-2002 (TrEMBLrel. 21, L;
ADAMTS18 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
860 PKVMNGTPPATKRPAYTWSIVQSECSVSCGGGYINVKAICLRDQNTQVNSSFCSAKTKPV 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 FGEKAKLÖMLDFKKDICKALWCHRIGRK----CETKFWPAAEGTICGHDMWCRGGQCVK
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                                                    625 DRP-----PARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPA-----CDAAHR
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type I motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, expression analysis, and structural characterization seven novel human ADAMTSS, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002)
EMBL, AJ315734; CAC86015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.2%; Score 1139.5; DB 4; Length 1072; Best Local Similarity 35.3%; Pred. No. 5.7e-96; Matches 281; Conservative 101; Mismatches 308; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1072 AA
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RC STRAIN-BERKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxter B.D., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,

RA Ballew R.M., Basu D., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Kravitz S., Kull D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mocherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mocherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          972 QP-APSSRQACNSQSCPPAWSAGPWAECSHTCGKGWRKRAVACKSTNPSARAQLLPDAVC 1030
                                        410 ANGTOYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKS 469
                                                               745 CTIHRGLYTKHHHTNQYYHMVTIPSGARSIRIYEMNV----STSYISVRNALRRYYLNG 799
                                                                                                                                                                                                                                           911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 AAHRPVETQAC-GEPC-PTWELSAWSPCSKSCGRGFQRRSLKCVGHG----GRLLARDQC 721
                                                                                                                                                                                                                                                                                                                                                                                                                    SQKCPRDS--VDFRAAQCAEHNSRRFRGRHYK------WKP-YTQVEDQDLCKLYCI 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                           624 DDRP-----PARWVAGSWGPCSASCGSGLQKRAVDC--RGSAGQRTVPA--CD
                                                                                                                                                                                                                                                                                                                                   CKKVTGLFTKPMH--GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNG
                                                                                                                                                                                                                    HEVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFY
                                                                                                                                                                                                                                                                                                        LPKEPREDKSSHPKDPRGPS-------QP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||: :|:|
1031 TSEPKPRMHEACLLORC 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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CG6107.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Na Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Nay Sier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Nay J.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Nanjliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 KV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---TCDTLGMA. 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.5%; Pred. No. 4.9e-94;
Matches 281; Conservative 111; Mismatches 260; Indels
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SEQUENCE 1229 AA; 138136 MW; C1293180AB19B700 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR002870; Pep_M12B_propep. InterPro; IPR001590; Reprolysin. InterPro; IPR000184; TSP1. InterPro; IPR000130; Zn_Wipeptdse. Pfam; PF01562; Pep_M12B_propep; 1. Pfam; PF01421; Reprolysin; 1. Pfam; PF01421; Reprolysin; 1.
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PROSITE; PSS0215; ADAM WERO; 2.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003709; AAF55199.1; -
FlyBase; FBgn0038340; CG6107.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Esburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Holt R.A., Sabburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandrall M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Robers T. H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Burtla R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M.,

Ra Berson K.Y. Benos P.V., Berman B.P., Bhandari D., Bollahakov S.,

RA Berson K.Y. Benos P.V., Berman B.P., Bhandari D., Bollahakov S.,

Borkova D., Botchen M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtls K.J., Cavley S., Dahlke C., Davneport L.B., Dayles P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrac C., Ferrac S., Fleischmann W.,

RA Bratis N.L., Harvey D., Halman T.J., Hernandez J.R., Rouck J.,

RA Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum A.,

RA Jalail M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Basso P., Leif Y., Levitsky A.A., Li J., Li Z., Ling T., Li X.,

Rabson D.R., Nelson K.A., Moy M., Nurshy D.M., Nelson D.L.,

RA Briskas R., Jectifer M., Venter E., Wang X.,

Rand S., Wasatnan D.A., Wathstoon S., Santh T.,

Randson D.R., Wasatnan D.A., Wathstoon S., Santh T.,

Randson D.R., Wasatnan D.A., Wathstoon S., Santh R.,

Randson D.R., Wasatnan D.A., Wathstoon S., Santh R.,

Randson D.R., Wasatnan D.A., Wathstoon S., Cheeler F., Shen H.,

Randson D.R., Wasatnan D.A., Wathstoon S., Santh S.,

Randson S., John W., Wolder S., Wolley K.C., Wu D., Yury S., Smith H.O.,

Randson D.R., Wasatnan D.A., Wathstook G.M., Weissenbach J.C.,

Randson D.R., Wasatnan D.A., Wath
                                                                                                                                                                                                                                                                                                                   1011 SAACGELGTREKTYACVQTFTNMQRSNIVDMSYCKLKFDVAYHEECREGC--WVLSEWST 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                            639
                                                            : | : | | : | | 911 LDVSPSKRQDTVLLSYSYTIDKPPDYEAEVEIYRWEWQAPSNCDSLCEGRSHRLPACIST 970
                                                                                                                                                                                                                                                                  640 SASCGS-GLQKRAVDC--RGSAGQRT----VPACDAAHRPVETQACGEPCPTWELSAWSP
                                                                                                                                               ------DKSSHPK-DPRGPSV---LHNSVLSLSNQVEQPDDRPPARWVAGSWGPC
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Last sequence update)
Last annotation update)
                                                                                                                                                                                971 TQGVKVAPQFCDKSAMPKIDDRACNTDCRLNLTVTSISE-----
                                                                                                                                                                                                                                                                                                                                                                                                              CSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKP 727
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Drosophila melanogaster (Fruit fly).
                                 574 VGKMTPPR-----VRYSFYLPKEPRE-
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NCBI_TaxID=7227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETQACG-EPCPT-WELSAWSPCSKSCGR-GF----QRRSLKCVGHGGRLLARDQCNLHR 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 VRVKYRSCNLEPCPSSASGKSFREEQCEAFN--GYNHSTNRLTLAVAWVPKYSGVSPRDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DRDSGPK -- VTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKV-CEEVFGKLRANHMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 ARGGCRLQFNLTIDSEVGACSAPH-EFCSTLWC--KVNGE--CVTHMRPTAPGTLCGRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 GGDNKSCKKVTGLFTKPM----HGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 QG--KYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 LSQQCELAFG-----VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGK
                                                                                                                                                                                                                                                                                                                                                                                                               Indels 120;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.6%; Score 1117; DB 5; Length 1054; Best Local Similarity 35.0%; Pred. No. 6.6e-94; Matches 276; Conservative 116; Mismatches 276; Indels 120,
                                                                   R Flybase; PERO129791; CG4096.
R InterPro; IPR002870; Pep_M12B_propep.
R InterPro; IPR001590; Reprolysin.
R InterPro; IPR000884; TSP1.
R InterPro; IPR000130; Zn_WPeptdse.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
R Pfam; PF00090; TSP1; 2.
R SMART; SM00209; TSP1; 2.
R PROSITE; PS50092; TSP1; 1.
R PROSITE; PS50192; TSP1; 1.
R PROSITE; PS00142; ZINL_PROTEASE; UNKNOWN_1.
R PROSITE; PS01042; ZINL_PROTEASE; UNKNOWN_1.
R PROSITE; PS01042; ZINL_PROTEASE; UNKNOWN_1.
Science 287:2185-2195(2000).
                   EMBL; AE003435; AAF46065.1;
HSSP; P15167; 1ATL.
                                                             MEROPS; M12.231;
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776 --IHYEYTVPVNRTAENQSEPEKPQDSLFIWTHSGWEGCSVQCGGGERRTIVSCTRIVNK 833
                                                                 580 PRVRYSFYLPKEPREDKSSHPKDPR------GPSV------LHNS
                                                                                                                                                            613 VLSLSNQVEQPDDRPP-----ARWVAGSWGPCSASCGSGLQKRAVDC----R
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954 K-----CDASTRPRAEEAC 967
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Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 LSIGHHGERSLESFCHWQNEEYGGARYLGNNQVPGGKDDPPLVDAAVFVTRTDFCVHKDE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 ANHAMSPTLIQIDRANP----WSACSAAIITDFLDSGHGDCLL---DQPSKPISLPEDLP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GASYTLSQQCELAFGVGSKPCPYMQY - - CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCE 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCG 464
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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26.1%; Score 1057; DB 4; Length 1095;
Best Local Similarity 32.6%; Pred. No. 2.5e-88;
Matches 261; Conservative 109; Mismatches 290; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-2185482; PubMed-11867212; Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.,

"Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).

EMBL: AJ315735; CAC86016.1; -.

Integrin; Protease.

SEQUENCE 1095 AA: 121099 MW; A5C6540484754D5D CRC64;
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
17, with thrombospondin domains.
                                                                                                                                                                             1095 AA
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                                                                                                                                                                          PRELIMINARY;
                                       1037 KPAEMEPC 1044
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            726 KPQELDFC 733
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                                                                 656 GSAGQRTVPACDAAHRPVETQAC-GEPC-PTWELSAWSPCSKSCGRGFQRRSLKCVGHGG 713
                                                                                                67 PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 125
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834 TITLVNDSDCPQASRPEPQVRRCNLHPCQSRWVAGPWSPCSATCEKGFQHREVTCVYQLQ
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adsintegrin-like and metalloprotease with thrombospondin type 1
ADAMTS14.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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MEDLINE-21638061; PubMed=11779638;

MEDLINE-21638061; PubMed=11779638;

Bolz H., Ramirez A., von Brederlow B., Kubisch C.;

Transcrentation of ADAMTS14, a novel member of the ADAMTS

metalloproteinase family.";

Biochim. Biophys. Acta 1522:221-225(2001).

E Biochim. Biophys. Acta 1522:221-225(2001).

R EMBL; AF358666; AAL40229.1;

R InterPro; IPR001890; Pep_MIZB_propep.

R InterPro; IPR001890; Reprolysin.

R InterPro; IPR001884; TSP1.

R Pfam; PF00152; Pep_MIZB_propep; 1.

Pfam; PF001562; Pep_MIZB_propep; 1.

R Pfam; PF00160; LSP1; 4.

R SMART; SM00209; TSP1; 4.

R PROSITE; PS50015; TSP1; 1.
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MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD---NVKVCEEVFGKLRANHMMSPTL 182
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IEVLLVVDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESLGVHINIALVRLIMVGYRQSL
                                    PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT
                                                                 SLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLTRQDF-GPSGMQ--GYAPVTG
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TESSUB-FERAL LONG;
MEDILE-21856482: Pubwed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUN-2002 (TrEMBLrel. 21, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Metalloprotease-disintegrin protease.
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Collide A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,
Collide A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,
Li S.W., Prockop D.J., Laplere C.M., Nusgens B.V.;
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High Homology with ADAMTS-2 and ADAMTS-3.";
J. Blol. Chem. 277:5756-5766(2002).
EMBL, AR366351; AAL79814.1; -
SEQUENCE 1159 AA; 127336 MW; A5B130149BF7FF34 CRC64;
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NCBI_TaxID=9606;
                                                                 QAAFHRFHWSRCSKLELSRYLPS - - YDCLLDDPFDPAWPQPPELPGINYSMDEQCRFDFG
                                            242 VGSKPC---PYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
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Best Local Similarity 31.8°
Matches 266; Conservative
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                                                                                                                                                                                     321 SLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLIRQDF-----GPSGYAPVTG 374
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  seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
EMBL, AJ345098; CAC87943.1; -.
                                                                                            Length 1223;
                                                                                                                Indels
                                                                     1223 AA; 133925 MW; D585B6593977ED15 CRC64;
                                                                                         25.2%; Score 1020; DB 4;
31.6%; Pred. No. 7.6e-85;
.lve 96; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGPCSASCGSGLQKRAVDCR------
                                                                                                            Matches 264; Conservative
                                                                                                  Local Similarity
Lopez-Otin
"Cloning, e
                                                                     SEQUENCE
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1207 AA.

PRT;

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Q8TE59 ID Q8TE59

RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
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Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cal S., Cobaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cal S., Cobaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cal S., Cal S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
25.0%; Score 1012; DB 4; Length 1207;
Best Local Similarity 31.9%; Pred. No. 4.1e-84;
Matches 259; Conservative 117; Mismatches 295; Indels 140;
                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
Last sequence update)
Last annotation update)
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"Structure of von Willebrand Factor-cleaving Protease (ADAMTS13), a
The structure of von Willebrand Factor-cleaving Protease (ADAMTS13), a
The structure of the
                                                     DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHPPDAQPGLYYSANEQC 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 VERHNINK-HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPIPANGGKYCEGVRVKYR 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL 133 POTENTIAL.
CHAIN 75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE.
SEQUENCE 1427 AA; 153632 MW; EBIBC3AABC1A4442 CRC64;
                              649 KRAVDCRGSAGQRTVPACD----AAHRPVETQAC-GEPCPT-WELSAWSPCSKSCGRGFQ 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
                                                                                                                                                                                                                                                                                                                                                                                               ADANTS13.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,
Fujikawa K.;
                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Von Willebrand factor-cleaving protease precursor.
                                                                                                                                                                                                                                                                     A.
                                                                                                                                           1058 HRTVRCTN-----PRKKCVLSTRPREAEDC 1082
                                                                                                                                                                                                                                                                   1427
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                                                                                                                                                                                                                                                                     PRELIMINARY;
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PubMed-11557746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675 TQACG-EPCPT-WELSAWSPCSKSCGRGFQRRSLKCVGHGGRLL-----ARDQCNLHRKP 727
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                                                                                                                                   480 DA---LCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRFFCCDGRM 536
                                                                                                                                                                                                              GSKKRFDKCGVCGGDNKSCKKVTGLFT--KPMHGYNFVVAIPAGASSIDIRQRGYKGLIG 509
                                                                                                                                                                                                                                                                                                                              DDNYLALKNSQGKYLLNGHFVVS--AVERDLVVKGSL-LRYSGTGTAVESLQASR---PI 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681
                                             432 MCNTQACEKTQ -- LEFMSQQCARTDGQPLRSSPGGASFYH-------WGAAVPHSQG 479
                                                                                                    398 VSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP----DST-SVCVQGKCIKAGCDGNL 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                       537 DSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTVTP-NLTSVYI--ANHRPLF-
SCNLEPCPSSASGKSFREEQCEAFNG------YNHSTNRLTLAVAW---VPKYSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Goad D.L., Goad M.E.;
"Molecular cloning of lapine aggrecanase-2 (ADAMTS-11) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chondrocytes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317415; AAG33062.1; -. HSSP; Q9PW35; 1BUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29193 MW; 97A1CA80B33452FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AA
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Pfam; PF00400; tsp.1; 1.
Pfam; SW00209; Tsp1; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
ROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Incerpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSP1.
Interpro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEWBLrel. 16, Cr
01-MAR-2001 (TrEWBLrel. 16, La
01-JUN-2002 (TrEMBLrel. 21, La
Aggrecanase-2 (Fragment).
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Search completed: April 29, 2003, 17:18:02 Job time : 54.0027 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2003, 17:10:24 ; Search time 9.08922 Seconds (without alignments) 3367.676 Million cell updates/sec Run on:

1 FVSIPRYVETLVVADESMVK........DQCNLHRKPQELDFCVLRPC 738 US-10-009-332-1\_COPY\_213\_950 4043 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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238	236.5	220.5	220 219	219 208.5	208.5
34 35	36	20 G	41	4 4 3 3	4 4 5

## ALIGNMENTS

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"Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene.";
J. Biol. Chem. 272:556-562(1997).
                                                                 30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Progesterone-regulated genes in the ovulation process: ADAMTS-1 and cathepsin L proteases.";
Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
-!- FUNCTION: CLEAVES AGGECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                  Kuno K., Lizasa H., Ohno S., Matsushima K.; "The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene encoding an ADAM family protein with TSP motifs."; Genomics 46:466-471(1997).
                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20243757; Pubmed=10781075;
Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99303657; PubMed=10373500;
Kuno K., Terashina Y., Matsushina K.;
"ADAMTS-1 is an active metalloproteinase associated with the
extracellular matrix.";
J. Biol. Chem. 274:18821-18826(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJUSE 20389568; PubMed=10930576;
Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M.,
Ohno H., Matsushima K.;
"ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan.";
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-97150761; Pubmed-8995297;
Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.
                                     968 AA.
                                     PRT;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-129/SvJ;
MEDLINE-98110583; Pubmed-9441751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett. 478:241-245(2000)
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, AND INDUCTION.
                                                  054768;
                                 ATS1_MOUSE
P97857; 054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION.
RESULT 1
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                                                                                                                                                                                                                                                                                                          DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

SIMILARITY: BELONGS TO PEPTIDAGE FAMILY M12B.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SAMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 7.
                                                                               CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-1-LEU-1692 STE, WITHIN THE CHONROLITH SULEARE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
                                                                                                                                                                                                                                          INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA CELLS OF PREOVULATORY FOLLICLES.
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA, MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMRAT; SMUZACE; LOEI, C.
PROSITE: PSSO121: DISINTEGRIN_1; FALSE_NEG.
PROSITE: PSSO0427; DISINTEGRIN_1; FALSE_NEG.
PROSITE: PSSO0427; ZINC_PROTEASE; 1.
Hydrolase; Mctaloportease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Heparin-binding.

The strength of the str
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N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                                                                                                                                                                                               INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC (CATALYTIC) (BY SIMILARITY).
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N -> S (IN REF. 2).
T -> S (IN REF. 2).
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TSP TYPE-1 2.
TSP TYPE-1 3.
POLY-ARG.
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EMBL; D67076; BAA11088.1; ALT_FRAME.
MEROPS; M1.10249; M1.2245; M1.10249.249; M1.10249.249; InterPro; IPR001762; Disintegrin.
InterPro; IPR001870; Pep_M12B_propep.
InterPro; IPR001890; Pep_M12B_propep.
InterPro; IPR0001890; Reprolysin.
InterPro; IPR0001890; Reprolysin.
InterPro; IPR0001890; Reprolysin.
InterPro; IPR000180; ZPB1; 3.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 3.
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09UHIS, 09UBG0, 09UHBS1; 09P2RC, 09NSJ8;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
with thrombospondin motifs 11 (ADAM-TS 1) (ADAM-TS1) (METH-1).
ADAMTS1 OR METH1 OR KIAAA1346.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                          40;
Length 968;
                          176; Indels
 55.8%; Score 2257; DB 1; 53.6%; Pred. No. 1.2e-156; ive 130; Mismatches 176;
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                          Conservative 130;
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                 Similarity
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      Query Match
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A Park H.-S., Toyloda A., Ishli K., Totcki Y., Choi D.-K., Soeda E.,

A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

A Menzel U., Delabbar J., Kumpf K., Lehmann R., Parterson D.,

Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Rosenthal A., Kump A., Schillhabel M., Schudy A., Zimmermann W.,

A Shintani A., Sasaki T., Nagamine K., Mitsuyama S.,

A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,

Scharfe M., Schoen O., Desario A., Reichell J., Kauer G., Bloecker H.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

Lehrach H., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation -
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCION: CLEAVES AGGRECAN, A CARTILAGE PROTECGITCAN, AND MAY BE INVOLVED IN ITS TURNOVER (BY SIMILARITY). HAS ANGIOGENIC INHIBITOR ACTIVITY. ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAX A CRITICAL ROLE IN FOLLICULAR RUPFURE.
-! CATALTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLO-!-LEU-1939
SITE, WITHIN THE CHONBOTIN SULFATE ATTACHMENT DOMAIN.
-! COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-! SUBSELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matrix (By similarity).
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                     the
                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-20181126; PubMed-10718198; Nagase T., Kikuno R., Ishikawa K. I., Hirosawa M., Ohara O.; Prediction of the coding sequences of unidentified human genes.XVI The complete sequences of 150 new cDNA clones from brain which code
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                                                                                                                         Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S., Lombardo M., Iruela-Arispe M.L.; "BETH-1, a human ortholog of ADATS-1, and METH-2 are members of family of proteins with anglo-inhibitory activity."; J. Biol. Chem. 274:23349-23357(1999).
                     of
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SEQUENCE FROW N.A.
TISSUE-Endothelial cells;
TISSUE-Endothelial cells;
MEDLINE-20247184; Pubmed=10785405;
Glienke J., Schmitt A.O., P. Hilarsky C., Hinzmann B., Weiss B., Rosenthal A., Thierauch K.H.;
Rosenthal Gene expression by endothelial cells in distinct
                     21
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C., Pritchard M.A., Estivill X., Arbones M.L.;
Ing, characterization and mapping on human chromosome
                              orthologue of murine Adamts-1."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 267:2820-2830(2000).
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                                                                                                          MEDLINE-99367466; PubMed-10438512;
                                                                           SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro."; Res. 7:65-73(2000).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
P -> A (IN REF. 4 AND 5).
C -> H (IN REF. 1).
S -> N (IN REF. 1).
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
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Matches 403; Conservative 131; Mismatches 172; Indels
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Pfam; PF00090; tsp_1; 6.
Pfam; PF01421; Reprolysin; 2.
Pfam; PF01562; Pep_M12B_propep; 2.
SMARY; SM00209; TSP1; 3.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
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TSP TYPE-1 2.
TSP TYPE-1 3.
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CYS-RICH.
                                                                           or send an email to license@isb-sib.ch)
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EMBL; AF60152; AAD48080.1; ALT_INIT.
EMBL; AF207564; AAF23772.1; --
EMBL; AF001697; BAA92584.1; ALT_INIT.
EMBL; AP001697; BAA95502.1; --
EMBL; AL162080; CAB82413.1; --
                                                                                                                                                                                                                                                        MIM; 605174; -...
InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
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CARBOHYD
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SEQUENCE OF 18-967 FROW N.A.
STRAIN-Sprague-Dawley; TISSUE-Liver;
STRAIN-Sprague-Dawley; TISSUE-Liver;
STRAIN-Sprague-Dawley; TISSUE-Liver;
Diamantis I., Luethi M., Hoesli M., Reichen J.;
Diamantis I., Luethi M., Hoesli M., Reichen J.;
Cloning of the rat ADAMYS-I gene and its down regulation in endothelial cells in cirrhotic rats.";
Liver 20:165-172(2000).
Liver 20:165-172(2000).
LIVER 20:165-172(2000).
STRILAGE NOTECON, CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY STMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER SIMILARITY).
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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
ADAWTS-1 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAW-TS 1) (ADAM-TS 1).
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241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                           357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF
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                                    493 GEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTD-R
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Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens
Little S.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Induction of a disintegrin and metalloprotease with the thrombospondin type I motif (ADAMTS)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).
                             SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1683-GLU-|-LEU-1684 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...) (POTENTIAL)
                                        matrix (By similarity).
INDUCTION: DOWN-REGULATED IN ENDOTHELIAL CELLS DERIVED FROM
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BY SIMILARITY.
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KFRSSQ -> RSRGSL (IN RE
V -> A (IN REF. 2).
R -> P (IN REF. 2).
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L -> TR (IN REF. 2).
T -> G (IN REF. 2).
T -> G (IN REF. 2).
TMLV -> NLLK (IN REF. 2
                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
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I -> V (IN REF. 2)...
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BY SIMILARITY.
ADAMTS-1.
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TSP TYPE-1 3.
POLY-ARG.
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CYS-RICH.
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Pfam; PF01562; Pep_M12B_propep; 2.
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607
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967 AA;
                                                            CIRRHOTIC LIVER
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PubMed=10610729;

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                                       RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                   ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                 181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                                              GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                  KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                            PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 9) (ADAM-TS 8) (METH-2).
ADAMTS8.
                                                                                                                                                             FTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER 536
                                                                                                                                                                                                                                                                                   DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPK--EPRE 594
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                                                                                                                                                                                                                                                                                                                                                       ----FNAIPTFS------EWVIEEWGECSKTCGSGWQRRVVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
    Length 967;
                  Indels
Query Match
55.7%; Score 2251; DB 1; Best Local Similarity 53.5%; Pred. No. 3.3e-156; Matches 400; Conservative 131; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           905 AA.
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                       229 FVSEARFVETLLVADASMAAFYGTDLONHILTVMSMAARIYKHPSIRNSVNLVVVKVLIV 288
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Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.,
"ADAM-TS8, a novel metalloprotease of the ADAM-TS family located
mouse chromosome 9 and human chromosome 11.";
Genomics 62:312-315(1999).
-1- FUNCTION: HAS ANT-ANGIOGENIC PROPERTIES (BY SIMILARITY).
-1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracell
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                       SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (CATALYTIC) (BY S.
ZINC (CATALYTIC) (BY S.
DISINTEGRIN LIKE.
TSP TYPE-1 1.
CYS-RICH.
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PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glyc
Repeat; Extracellular matrix; Heparin-binding.
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TSP TYPE-1 2.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000084; TSP1.
InterPro; IPR000084; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 2.
Pfam; PF00421; Reprolysin; 1.
SMART; SM00209; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS500142; ZINC_PROTEASE; 1.
PROSITE; PS500142; ADAM_MEPRO; 1.
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FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES

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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMYS-8 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 NGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSC 470
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                              237
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MADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMS 179
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-20079168; PubMed=10610729;
Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;
"ADAW-TS8, a novel metalloprotease of the ADAM-TS family located mouse chromosome 9 and human chromosome 11.";
Genomics 62:312-315(1999).
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"METH-1, a human ortholog of ADAMTS-1, and METH-2 are members family of proteins with angio-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
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MEDLINE-99367466; PubMed-10438512;
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                                                                                         -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLUIAR MATRIX.
-!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).
                                                 TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWEN EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
         -i- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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R InterPro; IPR001762; Disintegrin.
R InterPro; IPR0018019 Pep_M12B_propep.
R InterPro; IPR001809; Pep_M12B_propep.
R InterPro; IPR001809; Pep_M12B_propep.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR001030; Zn_MTpeptdse.
R Ffam; PF01562; Pep_M12B_propep; 1.
R Ffam; PF01562; Pep_M12B_propep; 1.
R FAM: SMART; SM00109; TST1; 2.
R ROSITE; PS50012; ZINC_PROTEASE; 1.
R ROSITE; PS500427; DISINTEGRN 1; FALSE_NEG.
RW Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; KW Repeat; Extracellular_matrix; Heparin-binding.
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SIMILARITY).
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                                      matrix (By similarity).
                                                                                                                                                        -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i-SIMILARITY: CONTAINS 1 DISINITEGRIN-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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BY SIMILARITY.
ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
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1larity 49.6%; Pred. No. 1.1e-130;
Conservative 133; Mismatches 185;
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N-LINKED (GLCNAC.
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DISINTEGRIN-LIKE.
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EMBL; AF175283; AAF25806.1; -.
HSSP; P34179; 11AG.
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MEDLINE=20181126; PubMed=10718198;

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16-0CT-2001 (Rel. 40, Created)
15-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWNS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 9) (ADAW-TS 9) (ADAM-TS 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                         RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLG
                                 PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG--ASYTLSQQCE
                                                                                                                                                     238 LAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLCLKGAC
                                                                                                                                                                    293 VERHNINKHR--VDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY
                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CPL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAVDCRGSAGQRIVPACDAAHRPVETQAC-GEPCP 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1629 AA
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AC 09P2N4, H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                           MALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

IISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.

EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, LUNG, PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECTED IN COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN OR
Nagase T., Kikuno R., Ishikawa K. I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:65-73(2000).
-! COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-! SUBCELLURAR LOCATION: Secreted. Associated with the extracellular
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PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Pep_MI2B_propep.
InterPro; IPR001890; Reprolysin.
InterPro; IPR001894; TSP1.
InterPro; IPR001894; TSP1.
InterPro; IPR001894; TSP1.
InterPro; IPR001891; Zm, MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS0427; IDSINTEGRIN_1; FALSE_NEG.
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ADAMTS-9.
DISINTEGRIN-LIKE.
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                                                                                                                                                                                                                           :99
(BY SIMILARITY).
                                                                                                                                                                                                      Length 1629;
                                                                                                                                                                                                  Query Match 44.0%; Score 1779; DB 1; Length 11 Best Local Similarity 45.1%; Pred. No. 1.4e-121; Matches 354; Conservative 115; Mismatches 250; Indels
                                                                                                                                                                -> L (IN REF. 1).
C1C4CEFF58B8941F CRC64;
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                      (BY
(BY
 (CATALYTIC)
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                      ZINC
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"The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";
J. Biol. Chem. 275:2791-2794 (2000).
J. Biol. Chem. 275:2791-2794 (2000).
INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. COULD ALSO BE A ONE CRITICAL FACTOR IN THE EXACERBATION OF NEUROBEGENERATION IN ALZHEINER'S DISEASE.
-!- CAPALYTIC, ACTIVITY: Cleaves aggrecan at the 392-Glu-(-Ala-393).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-:- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-:- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-:- ISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED AT VERY LOW LEVEL IN PLACENTA AND SKELETAL MUSCLES.
-:- INDOCTION: BY INTERLEUKIN-1.
-:- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-:- THIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-:- THIGHT INTERACTION FOR IS CLEAVED BY A FURIN BIODPEPTIDASE.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIZB.
-:- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
                                                                                                                                                ATS4_HUMAN STANDARD; PRT; 837 AA.
075173, Gyun83;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0UN-2002 (Rel. 41, Last annotation update)
15-0T-200 (Rel. 41, Last annotation update)
MDAWIS-4 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS 4) (ADAM-TS 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-99286303; PubMed-10356395;
Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M.,
Tortorella M.D., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
Liu R.-O., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
Nagase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K.,
Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
Trzaskos J.M., Arner E.C.,
"Purification and cloning of aggrecanase-1: a member of the ADAMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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MEDLINE-20400518; PubMed-10827174;
Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross
Burn T.C., Arner E.C.;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sawaji Y., Nagase H., Saklatvala J., Clark A.R.;
"ADAWTS-4 genomic locus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa K.-I., Nagase T., Suyama M., Miyajima
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98403880; PubMed=9734811;
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                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                         SEFPC 1053
734 VLRFC 738
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SEQUENCE 1
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGVGSKPCPYM-QYCTKLWCIGKAKGOMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
TSP TYPE-1.
CYS RICH.
SPACER.
POLY ALA.
N'LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · · · ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
CAUTION: HAS SOMETIMES BEEN REFERRED TO AS ADAMTS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5DF9C9AC137DF41F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1761; DB 1;
Pred. No. 1.3e-120;
l; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> T (IN REF. 1).
-> Q (IN REF. 3).
-> R (IN REF. 3).
                                                                                                                                                                                                                      InterPro: IPR001762; Disintegrin.
InterPro: IPR001590; Reprolysin.
InterPro: IPR001690; Reprolysin.
InterPro: IPR000190; Rap.
InterPro: IPR000190; LSP_1:
InterPro: IPR000190; LSP_1: 1.
Pfam: PF001020; LSP_1: 1.
PMART; SM00209; TSP1: 1.
PROSITE: PS00142; ZINC_PROTEASE; 1.
PROSITE: PS50092: TSP1: 1.
PROSITE: PS50092: TSP1: 1.
PROSITE: PS000427: DISINTEGRIN_1; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.6%; Sco.
53.1%; Pred
                                                                                                                                           EMBL; AB014588; BAA31663.1; -. EMBL; AF148213; AAD41494.1; -. EMBL; AY044847; AAL02262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90224 MW;
                                                                                                                                                                                    MEROPS; M12.221; -.
Genew; HGNC:220; ADAMTS4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              682
837 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                             MIM; 603876;
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METAL
ACT_SITE
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METAL
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SEQUENCE
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CARBOHYD
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MEDLINE-20289799; PubMed=10830953;
MEDLINE-20289799; PubMed=10830953;
MEDLINE-20289799; PubMed=10830953;
MEDLINE-20289799; PubMed=10830953;
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Makasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Schlarfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Scharfe M., Schoen O., Desario A., Reichelt J., Rauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrneyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UNAO; Q9UKP2;

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last sequence update)

ADAMTS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase

With thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TSS) (Aggrecanase-2)

ADAMTSS OR ADAMTS11.
                                                                                                                                                                                                                                                                                                                                                  534 VERDLVVKGSL-LRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEP 592
299 NKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                   357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTL---AVAWVPKYSGVSPRDKCKLICRANGT
                                                                                                                                                                                                 Abbaszade I., Liu R.-O., Yang F., Rosenfeld S.A., Ross O.H., Link J.R., Ellis D.M., Tortorella M.D., Pratta M.A., Hollis J.M., Wynn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K., Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H., Ito Y., Newton R.C., Magolda R.L., Trzaskos J.M., Hollis G.F., Arner E.C., Burn T.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of ADAMIS11, an aggrecanase from the ADAMIS family.";
J. Biol. Chem. 274:23443-23450(1999).
                                              513 QDFNIPQAGGWGPWGPWGDCSRICGGGVQFSSRDCIRPVPRNGGKYCEGRRTRFRSCNTE
                                                                                                                                                                            414 GYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKV
                                                                                                                                                                                                                                                                  TGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 AA.
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"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=99367476; PubMed=10438522;
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TISSUE-Fetal brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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Query Match
Best Local 8
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CARBOHYD
                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                        ARTHRITIC PATIENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                         zinc metalloproteases.";
J. Biol. Chem. 274:2555-25563(1999).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN MATHRITC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANTATION PERIOD.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                      matrix (By similarity).
TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA BUT ALSO IN OTHER TISSUES, SUCH AS HEART AND BRAIN, AND ALSO CERVIX, UTERUS, BLADDER, ESOPHAGUS, RIB CARTILAGE, CHONDROBLASTOMA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
                                                                                                                                                                                                                               COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MINI 605007; --

MINI 6
                   Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
*ADAM-TS5_ ADAM-TS6, and ADAM-TS7, novel members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISINTEGRIN-LIKE.
TSP TYBE-1 1.
CYS-RICH.
SPACER.
SPACER.
POLY-ALA.
POLY-ARA.
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    MEDLINE=99395124; PubMed=10464288
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
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                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                               Length 930;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                         138 A -> G (IN REF. 2).
614 R -> H (IN REF. 3).
692 P -> L (IN REF. 2).
101715 MW; B64281502F28193B CRC64;
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
A -> G IN REF. 2).
R -> H (IN REF. 3).
P -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                         43.2%; Score 1745; DB 1;
48.7%; Pred. No. 2.1e-119;
Live 98; Mismatches 219;
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728
802
807
138
614
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ADAMTS4.
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MEDILE-993514; Pubmed-10464288;
MEDILE-93514; Pubmed-10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
J. Biol. Chem. 274:2555-3616199;
J. Biol. Chem. 274:2555-25563(1999).
INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN, IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANTATION PERIOD.
TOTAL CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-1-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 3. 4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS5) (Aggrecanase-2) (ADAM-TS) (Implantin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGCDNKSCKKV 473
                                                                                                                        121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRANHMMS 179
                                                           61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
               299 NKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCNLE
                                                                                                                                                                                                                                                                                                                                                                                              :| | | :||: || |||| : | :||:| || |||||: :
482 SGSFKKFRYGYSDVVTIPAGRTHILVRQQGGSGL--KSIYLALKLADGSYALNGEYTLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                      180 PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELA
                                                                                                                                                                                                                     186 PVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGKDYDADRQCQLT
                                                                                                                                                                                                                                                   240 FGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
                                                                                                                                                                                                                                                                      357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTL---AVAWVPKYSGVSPRDKCKLICRANGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 IGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 VERDLVVKGSL-LRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEP
FVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                930 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 REDKSSHPKDPRGP 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- PSTPRPP 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATS5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAMTS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                              MATING (BY SMILLAILY).

TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

SIMILARITY: BELOWGS TO PEPTIDASE FAMILY MIZB.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                   COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Brain;
MEDLINE-20415831; Pubmed-10961658;
Satoh K., Suzuki N., Yokota H.;
"ADAWTS-4 (a disintegrin and metalloproteinase with thrombospondin motifs) is transcriptionally induced in beta-amyloid treated rat
                                                                                                                                                                                   COSCI. Lett. 289:177-180(2000).
FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEGCLYCAN, AND MAY INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN "ARTHRITIC DISEASES.
CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
63A428753167C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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SIMILARITY).
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PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS500142; ZNUC_PROFIESE; 1.
PROSITE: PS004427; DISINTEGRIN_1; FALSE_NEG.
Hydrolage: Metalloprotease; Zinc; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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ADAMTS-4.
ZINC (CATALYTIC) (BY
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ZINC (CATALYTIC) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1730.5; DB 1
Pred. No. 1.5e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (DISINTEGRIN-LIKE. TSP TYPE-1. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB042272; BAB16474.1; -.
EMBL; AB042271; BAB16473.1; -
EMBL; AB042273; BAB16475.1; -
InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001639; Reprolysin.
InterPro; IPR000189; Zn_MTpeptdse.
Pfam; PF004021; Reprolysin; 1.
SWART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPACER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
474
630 AA;
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METAL
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DVGTMCDFKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPT 181
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P58397;
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                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified morprofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                   matrix (By similarity).

DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-
IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR
UNDECTABLE LEVEL THEREAFTER.

DOMAIN: THE SPACER DOWAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. ..) (POTENTIAL)
(GLCNAC. ..) (POTENTIAL)
(GLCNAC. ..) (POTENTIAL)
                                                                                                              THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY) . SIMILARITY) .
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CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARIA BY SIMILARIY.
ZINC (CATALYTIC) (BY SIMILARIZINC (CATALYTIC) (BY SIMILARIZINC (CATALYTIC)
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                                                                                                                          SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.7%; Score 1728; DB 1;
47.5%; Pred. No. 3.7e-118;
iive 104; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISINTEGRIN-LIKE TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 104; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPACER.
TSP TYPE-1 2.
                                                                                                                                                                                                                                                                                                              MEROPS; M12.423; M12.423; MGD; MGT:1346221; Adamts5.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001876; Pep_M12B_propep.
InterPro; IPR001894; TSP1.
InterPro; IPR0001884; TSP1.
InterPro; IPR000130; LSP1.
Pfam; PF00090; tsp_1; 2.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; MTPPP
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POLY-ARG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
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PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Extracellular
                                                                                                                                                                                                                                                                                                            MEROPS; M12.225; -.
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Matches 328;
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ACT_SITE
METAL
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CHAIN
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            셤
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origin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
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--- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fetal lung;
MEDLINE-21264577; PubMed-11279086;
MEDLINE-21264577; PubMed-11279086;
Cal S., Arguelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Arguelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Arguelles J.M., Fernandez P.L., Lopez-Otin C.;
Cal S., Arguelles J. Structural and intracellular processing of ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats.";
J. Biol. Chem. 276:17932-17940(2001).
I. COPROTOR: BINDS 1 ZING (BY SIMILARITY).
I. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648
                                                                                                                                                                                                                                                                                                   PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416
                                                                                                                                                                                                                                                                                                                                                                                  YVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536
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                                                                                                                                                                  PEYSYCPGMDYCARLWCAVVRQGQMYCLTKKLPAVEGTPCGKGRYCLQGKCVDKTKKKYY 562
                                                                                                                                                                                                                   NINKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                                                                                                                           677
                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-
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SIMILARITY).

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

PTM: SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND

TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE

THE CAPACHOROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND

THE CAPACHOROTEINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1

DOMAINS.
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R InterPro; IPR001290; RepP.M12B_propep.
R InterPro; IPR001290; Reprolysin.
R InterPro; IPR001290; Reprolysin.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
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R Pfam; PF001421; Reprolysin; 1.
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ZINC (CATALYTIC) (BY SIMILARITY)
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                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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ADAMTS-12.
DISINTEGRIN-LIKE.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
4DAMTS-10 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVK-VCEEVFGKLRANHM 177
                                                                                                                                                                                                                                                                                                                           342 ISKERWVETLVVADTKMIEYHGSENVESYILTIMNMYTGLFHNPSIGNAIHIVVVRLILL 301
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                  2 VSIPRYVETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
Length 1593;
                                                                                                                      Indels 129;
      DB 1;
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cch 29.3%; Score 1184.5; DE similarity 34.4%; Pred. No. 2.6e-78 279; Conservative 122; Mismatches 28
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                                                                                                                                                                                                                                                                                                           matrix (By similarity).
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                                                                                                                                                               thrombospondin type I repeats.";
Submitted (JuN-1999) to the EMBL/GenBank/DDBJ databases.
-I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                 member of the ADAM-TS family containing multiple
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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Genew, HGC.13201; ADAMTS10.
Genew, HGC.13201; Disintegrin.
InterPro; IPR001876; Disintegrin.
InterPro; IPR001890; Reprolysin.
InterPro; IPR0001890; Reprolysin.
InterPro; IPR000180; Zn_MTpeptdse.
Fram; PR01421; Reprolysin; 1.
FR051TE; PS00129; TSP1; 5.
FR051TE; PS00129; TSP1; 2.
FR051TE; PS00142; INC_PR0TEASE; 1.
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TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
N-LINKED (GLCNAC. ..) (F.
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-1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
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                          Mammalla; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                    "ADAM-TS10: a novel
     Eukaryota; Metazoa;
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es 291; Conserv
                                                                                                               SEQUENCE FROM N.A.
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                                                                                                              284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | : : | | | | : : : | 835 VAPHYCSAHSKLPKRQRACNTEPCPPDWVVGNWSLCSRSCDAGVRSRSVVCQRRVSAAEE 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEQ-----PDDRPPA-----RWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTV 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 KALDDSACPQPRPPVLEACHGPTCPPEWAALDWSECTPSCGPGLRHRVVLCKSADHRATL 954
                                                                                                                                                       224
                                        RDRDSGPKVTGNAALTLRNFCAWQKKL-----NKVSDKHPEYWDTALLFTRQDLC--G 111
                                                                                                                                                                        225 LPGASYTLSQOCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEG
                                                                                                                                                                                                                                                                        285 KL----CLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGG
                                                                                                                                                                                                                                                                                       341 KYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNG-----YNHSTNRLTLAVAWVP
                                                                                                                                                                                                                                                                                                                                                 KKRFDKCGVCGGDNKSCKKVTGLFT--KPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEV
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       ---KLRANHMMSPTLIQIDRANP--WSACSAAIITDFLDSGHGDCLLDQPSK-PISLPED
                                                                                                                                                                                                                                                                                                                                                                                        394 KYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGS
                                                                                                 112 ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
ADAWIN-7 precursor (EC 3.4.24.-) (A disintegrin and in thrombospondin motifs 7) (ADAW-TS7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997 AA.
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ID ATS7_HUMAN
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Conservative

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238 VSKEKWVETLVVADAKMVEYHGQPQVESYVLTIMNMVAGLFHDPSIGNPIHITIVRLVLL 297
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                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the PMBL outstation the Burpapen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                matrix (By similarity).
TISSUE SPECIFICITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELFAL MUSCLE, KIDNEY, PANCREAS.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                          extracellular
                                                   Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, Novel Members of a New Family of Zinc Metalloproteases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50092; TSP1; 1.
PROSITE; PS0427; DISINFGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (CATALTITE) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALTITE) (BY SIMILARITY).
ZINC (CATALTITE) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
SPACER.
TSP TYPE-1 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (POTENTIAL)
. .) (POTENTIAL)
. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.1%; Score 1094; DB 1; Length 9: 37.5%; Pred. No. 5.8e-72; .ive 90; Mismatches 301; Indels
                                                                                         3iol. Chem. 274.25555-25563(1999).
COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ADAMTS-7.
CYSTEINE SWITCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000884; TSF1...
InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF01522; Pep_M12B_propep; 1.
Pfam; PR01522; Pep_M12B_propep; 1.
PR0SITE; PS00142; ZINC_PROFERSE; 1.
PROSITE; PS00142; ZINC_PROFERSE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
                                         MEDLINE=99395124; PubMed=10464288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997 AA;
  NCBI_TaxID=9606;
                                                                                                                                                                                                               SIMILARITY).
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ACT_SITE
METAL
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CARBOHYD
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CHAIN
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0TN-2002 (Rel. 41, Last annotation update)
15-JUN-2022 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
N-proteinase) (PC I-NP) (Procollagen N-endopeptidase) (pNPI)
(Procollagen I/II amino-propeptide processing enzyme).
                                   EDEEEDLKITHHADNTLKSFCKWQKSINMKGDAHPLHHDTAILLTRKDLCAAMNRPCETL 357
                                                                                                                  236
                                                                                                                                                                                                         ELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER 295
                                                                                                                                                                                                                                                                                                    HNLNKHRYDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNL 355
                                                                                                                                                                                                                                                                                                                                                                                                             589
                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 EPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGY 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 641 AKKLRDAVVDGTPCTQVRASRDLCINGICKNVGCDFEIDSGAMEDRCGVCHGNGSTCHTV 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685
                                                                                        119 GMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD-NVKVCEEVFGKLRANHM 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 FYVLAPKVVDGTLCSP--DSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKV 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 TGLFTKPMH-GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ-GKYLLNGHFVV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 YSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARW---VA----GSW 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 HGRSRPGGVSPGSVTEPGSEPGPPAAASTSVS-----PSLKWPNLVAAVHRGGW 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 SAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVL-----SVGKMTPPRVR 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G--QAPLGLGGWRRHLVLMGPRLPTQLLFQESNPGVHYEY-TIHREAGGHDEVPPPVFSW 919
61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATT--CDTL
                                                                                                                                                                               MSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP-ISLPEDLPGASYTLSQQC
                                                                                                                                                                                                                                                                                                                                                                                 637 GPCSASCGSGLQKRAVDCRGS-----PGQRTVPACDAAHRPVETQACGE----PCPTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE
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MEDLINE-99347935; PubMed-10417273;
Colige A., Sieron A.L., Li S.-W., Schwarze U., Petty E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1211 AA.
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095450;
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27;

76; Gaps

VSIPRYVETLVVADESMVKFHG-ADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60

:: :: :: ::

Matches 280; Conservative

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Similarity

Local

Fri May

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                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI; ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-PROCOLLAGEN PEPTIASE ACTIVITY.

TISSUE SPECIFICITY: EXPERSESED AT HIGH LEVEL IN SKIN, BONE, TENDON AND AORTA AND AT LOW LEVELS IN THYMUS AND BRAIN.

BOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-I DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXPRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: Defects in ADAWTS2 are the cause of Ehlers-Danlos syndrome type VIIC (EDS-VIIC), a recessively inherited connectivetissue disorder characterized clinically by severe skin fragility and joint hypermobility and blochemically by the presence in skin of procollagen incompletely processed at the N-terminus. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISTRYEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                               COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO SUBUNIT: MAY UPPE XIV (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Collagen degradation; Extracellular matrix; Heparin-binding; Alternative splicing; Ehlers-Danlos syndrome.

SIGNAL 1 29 POTENTIAL.

PROPEP 30 253 BY SIMILARITY.

CHAIN 254 1211 ADAMTS-2.
                                                                                                                                                            CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00142; ZINC_PROTEASE; FALSE_NEG. PS00427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pep_M12B_propep.
Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR0000884; TSP1.
Interpro; IPR0001030; Zn_MTpeptdse.
Pfam; PF00090; tsp. 1; 4.
Pfam; PF01421; Reprolysin; 1.
Pram; PF01562; Pep_MA2B_propep; 1.
SMART; SM00209; TSP1; 4.
PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_prc
InterPro; IPR001590; Reprolysin.
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Genew; HGNC:218; ADAMTS2.
                                                                                                                                                   collagen biosynthesis
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1211
408
409
                                                                                                                                                                                                    Ala-I-Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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MIM; 225410;
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PROSITE; 1
PROSITE; 1
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35;
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TLGGOGRWIA (IN ISOFORM SPNPI).
MISSING (IN ISOFORM SPNPI).
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                                                                                                                                                                                                                                                                                                                                                              497
                                                                                                                                                                                                                                                                                                        67 PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 125
                                                                                                                                                                                                                                                                                                                       SLIEIGNPSQSLENVCRWAYLQQKPDTGHDEYHDHAIFLTRQDF-GPSGMQ--GYAPVTG 384
                                                                                                                                                                                                                                                                                                                                                MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQ 184
                                                                                                                                                                                                                                                                              8 VETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
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                                                                                                                                                                                                                                                                                                                                                                                                     242 VGSKPCPYMQY---CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                405 KLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 GGDNKSCKKVTGLFTK--PMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 SCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDKC
                                                                                                             (POTENTIAL).
                                                                                                                                           (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                    Best Local Similarity 34.2%; Pred. No. 1.7e-70;
Matches 276; Conservative 110; Mismatches 300; Indels 120;
                                                                                                              (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                           DB 1; Length 1211;
                    CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                     BECEEF25C23CAD2D CRC64;
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                                                                                                                                                                                                                  26.6%; Score 1075; DB 1; Pred. No. 1.7e-70;
                                                                                                    (GLCNAC
                                     TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
POLY-ALA.
POLY-GLU.
TYPE-1 1.
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          CYS-RICH
                               SPACER
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188
112
251
949
993
1031
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722
693
851
911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Magase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Trediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 4.141-180(1997).

Code for large proteins in vitro.";
DNATION: Cleaves the properides of type II collagen prior to
fibril assembly. Does not act on types I and III collagens.
Coproror: Subcenturants Locarion: Secreted. Associated with the extracellular matrix (By similarity).
Coproror: Specific Try: Found in cartilage and skin.
Coproror: Tissue Specific DOMAIN AND THE TSP TYPE-I DOMAINS ARE IMPORTANT
Coproror.
Coproro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               ATS3_HUMAN STANDARD; PRT; 1205 AA.
015072; 09BX28;
16-0CT-2001 (Rel. 40, Created)
15-JUN -2002 (Rel. 41, Last sequence update)
15-JUN -2002 (Rel. 41, Last annotation update)
ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS3) (Procollagen II amino_propeptide processing enzyme) (Procollagen II N-proteinase) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-227 FROM N.A.
SEQUENCE OF 1-227 FROM N.A.
MEDLINE-21402912; PubMed-11408482;
Fernandes R.J., Hirohata S., Engle J.M., Colige A., Cohn D.H.,
Eyre D.R., Apte S.S.;
"Procollagen II amino propeptide processing by ADAMTS-3. Insights on
    661 RIVPACDAAH----RPVETQACG-EPCP-TWELSAWSPCSKSCGRGFQRRSLKCVGHGGR 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-!- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
                                                                                                                                1003 RTADDSFGICQEERPETARTCRLGPC 1028
                                                                                          715 LLARDQCNL -- HRKPQELDFCVLRPC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
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InterPro; IPR001762; Disintegrin.
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Genew; HGNC:219; ADAMTS3.
MIM; 605011; -.
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67 PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLIERGNPSRSLENVCRWASQQQRSDLNHSEHHDHAIFLTRQDFGPA---GMQGYAPVTG 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 MCHPVRSCTLNHEDGFSSAFVVAHETGHVLGMEHDGQGNRCGDETAMGS-----VMAPLV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 FGVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERH 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 PCPSSASGKSFREEQCEAFNG---YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGT
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                            SIMILARITY).
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BY SIMILARITY.
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N-LINKED (GLCNAC. ..)
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N-LINKED (GLCNAC. ..)
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(BY
                                                           Pfam; PF00090; tsp_1; 4.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMART: SM02020; TSP1; 4.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS001427; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS00427; DISINIEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycopi
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N-LINKED (GLCNAC.
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ZINC (CATALYTIC)
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TSP TYPE-1 1.
CYS-RICH.
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TSP TYPE-1 3.
TSP TYPE-1 4.
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     Pep_M12B_propep.
Reprolysin.
InterPro; IPR002870; Pep_M12B_prop
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSPI.
InterPro; IPR000130; Zn_MTpeptdse.
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36;

Db 715 VKGTFTRTRRKIGYLKMFDIPPGARHY
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Search completed: April 29, 2003, 17:14:25 Job time : 26.0892 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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2054640 seqs, 14551402878 residues IDENTITY\_NUC Gapox 1.0 Scoring table: Searched:

4109280 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

em\_htgo\_other:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htg\_hum:\* em\_htg\_mus: gb\_ba:\*
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			•			SUMMARIES	
Result			* Query				
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ACCESSION VERSION KEYWORDS		gen AJ3 AJ3 ADA	5733 5733 5733	1 GI:1 qene; d	- R	5 grin; metalloproteas	; thrombo
SOURCE	X.	hum	lan.	Sue			
		Euk	Eukaryota; Mammalia:	; E		Chordata; Craniata; Ve. Primates: Catarrhini;	Vertebrata; Euteleostomi; ; Hominidae; Homo.
REFERENCE	ENCE	7					
AUT	AUTHORS	Cal	, s,	Obaya, A.	 	Llamazares, M., Garabay	a,C., Quesada,V. and

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<b>HSA315733</b>	
COCUS	HSA315733 2853 bp mRNA linear FRI 01-MAR-2002
DEFINITION	Homo sapiens mRNA for metalloprotease disintegrin 15 (ADAMTS15
	gene).
ACCESSION	AJ315733
VERSION	AJ315733.1 GI:19171175
KEYWORDS	ADAMTS15 gene; disintegrin; metalloprotease; thrombospondin.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	T.
AUTHORS	Cal,S., Obaya,A.J., Llamazares,M., Garabaya,C., Quesada,V. and
	Lopez-Otin, C.

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Submitted (26-JUN-2001) Cal S., Biochemistry and Molecular Biology,
University of Oviedo, Campus del Cristo, Asturias. 33006, SPAIN
Location/Qualifiers
Cloning, expression analysis, and structural characterization o
seven novel human ADAMTSs, a family of metalloproteinases with
disintegrin and thrombospondin-1 domains
Gene 283 (1-2), 49-62 (2002)
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οy	1561	AAAIGGGAICCCIATGGCCCCTGCTCGCGCACATGTGGTGGGGGGGGGG	ζζ D	2641	GCCCATC
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Qy	1741	GAGGAGCAGTGTGAGGCTTTCAACGGCTACACCACAGCACCAACCGGCTCACTCTCGCC	Qy	2821	GAGCTGC
οy	1801	GTGGCATGGCTGCCCAAGTACTCCGGCGTGTCTCCCCGGGAAGTGCAAGCTCATCTGC 1860	RESU AX31	RESULT 2	
QQ	1801		LOCUS	JS	
oy op	1861	CCAGCCAATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGACGGCACGCTG 1920 	ACCESSI VERSION KEYWORD	ACCESSION VERSION KEYWORDS	
QY Db	1921	TGCTCTCCTGACTCCACCTCCGTCTGTCCAAGGCAAGTGCATCAAGGCTGGCT	SOURCE ORGA	URCE ORGANISM	humar Homo Eukar Mammë
δλ	1981	GGGAACCTGGGCTCCAAGAAGACATTCGACAAGTGTGGGGGTGTGTGGGGGACAATAAG	REFE AU	REFERENCE AUTHORS	1 Plown
Dp	1981		II	TITLE	Novel Novel
Oy Db	2041	AGCTGCAAGAAGGTGACTGGACTCTTCACCAAGCCCATGCATG	FEATUR	FURES	a)
P O	2101	GCCATCCCGCAGGCGCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAAGGCTGATC 2160 	BASE	BASE COUNT	
VQ	2161	GGGGATGACAACTACCTGGCTCTGAAGAACAGCCAAGGCAAGTACCTGCTCAACGGCAT	no a	Query Ma	Match
qq	2161		Ma	Best Loc Matches	est Local Simi atches 2847;
Qy Db	2221	TTCGTGGTGTTCGGCGGTGGAGCGGGACCTGGTGGAAGGCCAGTCTGCTGCGGTACAGC 2280 	Qy Db	1 76	ATGCTTT        ATGCTTC
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Qy Dp	2341	GTGGAGGTCCTCTCCGTGGGGAAGATGACACCGCCCGGGTCCGCTACTCCTTCTATCTG 2400	Qy Db	121	TACTGGC           TACTGGC
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Qy Dp	2521	GCACGCTGGGTGGCAGCTGGGGCCGTGCTCCGCGAGCTGCGGCAGTGGCCTGCAG 2580	Qy	301	16C11C1
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1arity 99.5%; Pred. No. 0;
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TATGT       TATGT GCACA GCACA GCACA	CGGCGG CGGCGG GTGTCT 	ACCGCCAT 	GCCATCCTC	CCCTCATCCAGATC
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and 52xaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and 52xaki, Y. L. Fujiyama, A., Taylor, T.D., Hong-Seog, P., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

L. Submitted (01-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC):

1.72. Suchiro-chou, Tsurumi, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoridgsc:iken.go.jp, URL:http://hgp.gsc:riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

On Mar 7, 2002 this sequence version replaced gi:11559301.
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Homo sapiens genomic DNA, chromosome 11q, clone:PPll-121M22,
complete sequence.
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RS Birren, B. Linton, L. Nusbaun, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Bastlen, V., Beda, F., Callangelo, M., Collins, S., Cangouslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Cooke, P., DeArcalano, K., Daiza, S., Callymore, A., Cooke, P., DeArcalano, K., Daiza, S., Callymore, A., Cooke, P., DeArcalano, K., Daiza, S., Callymore, A., Cooke, P., DeArcalano, K., Deard, G., Gago, D., Galagan, J., Gardya, S., Glode, S., Goyette, M., Gaham, L., Karatas, M., Karan, J., C., Illev, I., Johnson, R., Moccarth, M., Graham, L., Alborton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lancares, R., Madchars, T., Lakocque, K., Lanazares, R., Landers, T., Lancares, R., Maranda, C., Managa, V., Morran, C., Luu, G., Looke, R., Macdonald, P., Marquis, N., Mellin, J., Wenera, L., Milnova, T., Miranda, C., Managa, V., Morran, C., Howalin, J., Menera, L., Milnova, T., Miranda, C., Monnell, P., O'Nell, D., Ollyar, T. M., Ollyar, J., Peterson, T., O'Donnell, P., O'Nell, D., Ollyar, T. M., Ollyar, J., Severy, P., Spencer, B., Stangermonn, N. Schjanovich, N., Severy, P., Spencer, B., Stangermonn, V., Stolyanovich, N., Severy, P., Spencer, B., Stangermonn, V., Stolyanovich, N., Severy, P., Spencer, B., Stangermonn, V., Stolyanovich, N., Severy, P., Spencer, B., Stangermonn, V., Zalnoun, J., Zimmer, A. and Zody, M., Yi, Wymai, D., Ye, W.J., U., Direct, Submission

AL Submitted (O'S-MAR-2000) Whitehead Institute/AMT center for Genome Research, 320 Challes Street, Cambridge, MA 02141, USA

Direct, Submission

AL Submitted (O'S-Mar-2000) Whitehead Institute/AMT center for Genome Research, 320 Challes Street, Cambridge, MA 02141, USA

Anderson, S., Baldwin, J., Barna, M., Bartier, G., Ganpoplanov, A., Cartie, M., Parketta, P., Fitzhuch, M., Gage, D., Ganpoplanov, A., Castle, A., Cooke, P., DeArellanow, M., Bartier, G., Gardyna, S., Garder, M., Merchan, C., Cartie, M., Parketta, M., Thun, J., Lakoque, K., Lamazares, R., Landers, R., Parketta, M., Marchan, M.,
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Chemistry: Dye-terminator Big Dye; 100% of reads
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                                                                                                                                     1 (bases 1 to 172905)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-211H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L7808
Center clone name: 211_H_6
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                                                                                                                                                                                                                                 Unpublished
                                             ORGANISM
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                   SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTTCTATTCTGGGGACGTGAACGCCGACCCGACTCGTTCGCTGTGAGCCTGTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 134295 CAGGAGGACTTTTACCTACACCTGACGCGGATGCTCAGTTCTTGGCTCCGGCCTTCTCC 134354
                                                                                                                                                                                                                                                                                                                                                                                                          DD 134355 ACTGAGCATCTGGGCGTCCCCTCCAGGGGCTCACCGGGGGCTCTTCAGACCTGCGAGCC 134414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 134175 CCAGAGGGGGGGGGGGGGGGTCGTTCCCATCCGACTGGACCGGACATTAACGGCCGCCGCTAC,134234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 134475 GGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGCCC 134534.

      QY
      901 AAAGTGACAGCACCCCGAGTACTGGGACACTGCCATCCTCTCACCAGGAGGAC 960

      DD
      135015 AAAGTGACTACAGGACCCCGAGTACTGGGACACTGCCATCCTCTCACCAGGAGTG 135074

                                                                                                                                                            Db 134235 IACTGGCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTCAGATCACAGCATTT 134294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 134775 GAGACGTGGTGGTCGCGGACGAGTCAATGGTCAAGTTCCACGGCGCGGACCTGGAACAT 134834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 134835 TATCTGCTGACGCTGCTAGCGGCGCGCGACTCTACCGCCATCCTCAAC 134894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 134955 GTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTGAAC 135014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCTAGCGCCCCGGCGCGCGCAGCGCAACAGCCAGGGCGCACACCTTCTCCAGCGCGGG 480
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61 CCAGAGCGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTGAAC 900
                                                                                                                        121 TACTGGCGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTCAGATCACAGCATTT 180
                                                                                                                                                                                                                                                                                                                                                                       ACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACGGGGGCTCTTCAGACCTGCGACGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGAGGACTITTACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTTCTCC
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                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 161899 bases at least Q40 consensus quality: 167402 bases at least Q40 consensus quality: 167402 bases at least Q30 Consensus quality: 169801 bases at least Q20 Insert size: 177000; agarose-fp Insert size: 171405; sum-of-contigs Quality coverage: 4.1 in Q20 bases; sum-of-contigs Quality coverage: 4.2 in Q20 bases; sum-of-contigs
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41: contig of 10580 bp in length
gap of 100 hp
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/clone="RP11-211H6"
/clone_11b="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
15050. .23535
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/note="assembly_fragment"
2737. .4052
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23636. .30261
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/note="assembly_fragment
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/db_xref="taxon:9606"
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122. .1343
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58888: C
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgCITTIGCTGGGCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCTTTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                             Length 172905;
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                                                                                                                                                                                                                                                                                                                1502 others
                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 957.2; DB 2;
illarity 98.2%; Pred. No. 3.8e-161;
Conservative 0; Mismatches 18;
                                                                                                                                                                                83803. 98393 ...
/note="assembly_fragment"
98494. .117356
/note="assembly_fragment"
117457. .140589
/note="assembly_fragment"
140690. .172905
/note="assembly_fragment"
a 41333 c 39516 g 46194 t
                                                                             41042. 54893
/note="assembly_tragment"
54994. 68888
/note="assembly_tragment"
68989. 83702
                                                30362. .40941
/note="assembly_fragment"
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/note~"assembly_fragment
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Db 98460 ATGCTTCTGCTGGGCCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCCCTGAG 98519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98638 TICAGGAGGACTITIACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTTCT 98697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 ACTACTGGGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTCAGATCACAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAG-AGCGGGAGGTA-GTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AIGCTTTTGCTGGGCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCTTTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Game of the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAGGAGGACTTTTACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGGCTCTTCAGACCTGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCTTCTATTCTGGGGACGTGAACGCCGAGCCGGACTCGTTCGCTGTGTGAGCCTGT
consists of 7 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 170692,
                                                                                                                                                    contig of 1856 bp in length
contig of 5109 bp in length
contig of 5109 bp in length
gap of unknown length
contig of 13924 bp in length
contig of 13956 bp in length
gap of unknown length
contig of 14317 bp in length
gap of unknown length
gap of unknown length
contig of 60517 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI human BAC library 11"
1. 1856
/note="assembly_name:Contig25"
1957. .7065
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/life. .21089
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21190. .34145
/note="assembly_name:Contig28"
34.246. .48562
/note="assembly_name:Contig28"
/note="assembly_name:Contig29"
/note="assembly_name:Contig29"
/note="assembly_name:Contig29"
/note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                                                                                        109279: gap of unknown length 170682: contig of 61403 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 893; DB 2; 1
Pred. No. 1.1e-149;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48663. .109179
/note="assembly_name:Contig30"
109280. .170682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a 39732 c 39514 g 46884 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-121M22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     .09179: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.3%;
Best Local Similarity 96.0%;
Matches 948; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                              21089:
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34245:
48562:
48662:
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1957
7066
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC023429 170682 bp DNA linear HTG 10-APR-2001
Homo sapiens chromosome 11 clone RP11-121M22, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea 1 to 170682)
Abola, A. P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Man, J., Kopp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefers, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                  901 AAAGTGAGTGACAAGCACCCCGAGTACTGGGACACTGCCATCCTCTTCACCAGGAC 960
                                                                                                          840
                                                                                                                             GTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTGAAC 900
                                                                                                                                                                                                                  Submitted (14-FEB-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Stanford DNA Sequencing and Technology Development
                  TATCTGCTGACGCTGCTGGCAACGGCGCGCGCGACTCTACCGCCATCCTCAAC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Vector: Milmpl8; X02513
Chemistry: Dye-primer; 128 of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165770 bases at least Q40
Consensus quality: 16770 bases at least Q40
Consensus quality: 167918 bases at least Q20
Insert size: 172423; agarose-fp
Insert size: 17082; sum-of-contigs
Quality coverage: 9.0x in Q20 bases; sum-of-contigs.
*NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 170682)
Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J. Viv,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apr 10, 2001 this sequence version replaced gi:13562078,
                                                                                                       CCCATCAACATCGTTGTGGTCAAGGTGCTTGTTTAGAGATCGTGACTCCGGGCCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC023429.19 GI:13569974
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
HOMO Sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                        78623 AGTIGATCIGCCGTCACTIGCACC 78598
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                                                                                                                                                                                                                                                                                                                                                                           961 CTGTGTGGAGCCACCACCTGTGACAC 986
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JOURNAL
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AUTHORS
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Burren,B., Nusbaum,C. and Lander,E.
In Unpublished

L Unpublished

L Onbublished

L Dasses I to 182656)

Burren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Bryen,A., Camarata,J., Campoplano,A., Chagaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cook,P., Dearellano,K., Dearen,K., Diaz,JJS., Dodge,S., Faro,S., Ferreira,P., Fitzlandy,W., Gage,D., Galagan,J., Gandyna,S., Glide,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Maradas,A., Kalls,C., LaRocque,K., Johnson,R., Johnes,C., Kamat,A., Karadas,A., Kells,C., LaRocque,K., Liu,G., Lamazares,R., Landers,T., Leboczky,J., Levine,R., Liu,G.,
418
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                                                 98877.
                                                                                          478 . ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           778 .
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                                                                                                                                                                                                                      98997
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                                                                                                                                                                                                                                                             598
                                                                                                                                                                                                                                                                                  98998 GGAACCCCGCCATCCTACGGCCCTGGACCTTACAAGCCGCGGCGGGGGGCTTCGGGG
                                                                                                                                                                                                                                                                                                                                                                  GGGGTGTTCCGGGGGCCTTCCGGAGACCCCACCTCTCGCTGCGGGGTGGCCTCGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCCCATCAACATCGTTGTGGTCAAGGTGCTTCTTAGAGATCGTGACTCCGGGCCCA
            GCGGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGC
                                                                                               CCAATGCTAGCGCGCCGCGCGCGCAGCGCAACAGCCCAGGGCCGCACCTTCTCCAGCGCC
                                                                                                                                                                                                                    98938 GGGTGTTCCGGGGGCCTTCCGGAGACCCCACCTCTCGCTGCGGGGTGGCCTCGGGCT
                                                                                                                                                                                                                                                                                                                                               AGAGTCGTAGCCGGCGCAGGTCTGGGCGCGCCCAAGCGTTTCGTGTCTATCCCGCGGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTATCTGCTGACGCTGGCAACGGCGCGCGCGCTCTACCGCCATCCCAGCATCCTCA
                                                                                                                                                                                                                                                             539 GGAACCCCGCCATCCTACGGGCCCTGGACCCTTACAAGCCGCGGCGGCGGGGCTTCGGGG
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AC101990.2 GI:22381363
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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            329
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MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McRernan,K., McPheeters,R., Meldim,J., Menca,L., Mindova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Rapeack,M., Riley,R., Rise,C., Rogov,P., Raymond,C., Retta,R., Peterson,K., Sentos,R., Schauer,S., Schubback,R., Senman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Travers,M., Travis,N., Talamas,J., Tesfaye,S., Theodore,J., Tophan,K., Travers,M., Travis,N., Wyman,D., Ye,W.,J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M., J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M., Jouchassion S., Barna,N., Bastlen,V., Boussinted (23 Nov-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 50 Charles Street, Cambridge, MA 02141, USA 50 Charles Street, Cambridge, MA 02141, USA 50 Charg,J., Chazaro,B., Chepelly,L., Goukhaller,B., Lock,P., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Goode,P., Goode,P., Landers,T., Johnson,R., Hardey,R., Maclean,C., Macdonald,P., Major,J., Matthews,C., Kamat,A., Murphy,T., Naylor,J., Nayyen,C., Nicol,R., Norbu,C., Norman,C., Nuroll,C., Romen,C., Romens,L., Nuroll,D., Oliver,J., Peterson,R., Murphy,T., Naylor,J., Nayyen,C., Nicol,R., Norbu,C., Norman,C., Romens,J., Romens,J., Romens,J., Naylor,J., Nayyen,C., Nicol,R., Norbu,C., Norman,C., Nuroll,D., Oliver,J., Peterson,R., Roman,J., Roylor,J., Nayyen,C., Romens,J., Roylor,J., Naylor,J., Naylor,J.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 21, 2002 this sequence version replaced g1:17060766. All repeats were identified using RepeatWasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
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Center clone name: 11732

Sequencing vector: Plasmid: n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 178030 bases at least Q40

Consensus quality: 179964 bases at least Q30

Consensus quality: 180647 bases at least Q20

Insert size: 172000; agarose-fp

Insert size: 181156; sum-of-contigs
Quality coverage: 8.1 in Q20 bases; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
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362 461: gap of 100 bp
462 1538: contig of 1077 bp in length
1539 1638: gap of 100 bp
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39782

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100 bp
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180 bp
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1888865; gap of
1888865;
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8 a 41160 c 39770 g 48758 t
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3397: cc
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4947: con.
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6893: con+*
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Query Match 27.3%; Score 779.8; DB 2; Best Local Similarity 87.1%; Pred. No. 1.6e-129; Matches 856; Conservative 0; Mismatches 127;

AP003459 28000 bp DNA linesr PRI 08-MAR-2002 Homo sapiens genomic DNA, chromosome l1q, clone:RPl1-211H5, complete sequence.

DEFINITION

RESULT 8 AP003459 LOCUS

0

Gaps

Length 182656;

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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 27.3%; Score 778.8; DB 9; Length 28000; Best Local Similarity 98.5%; Pred. No. 3.3e-129; Matches 786; Conservative 0; Mismatches 12; Indels 0; Gaps
                                                                                                           Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3510 GCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGGCTGATCGGGGATGACAACTAC
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Rabaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaratunge, H.C., Blankenburg, K., Bonnin, D., Barbaratunge, H.C., Blankenburg, K., Bonnin, D., Bunder, S., Briteva, M., Brown, R., Brown, M., Bryant, N. Barbarata, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bunder, C. Burrel, P., Burkett, C., Burrell, K.L., Byrd, M.C., Carron, T.F., Carler, M., Cavaco, S., Chokolary, J., Charkova, D., Chen, G., Chen, R., Caper, M., Dathorne, S.R., David, R., Dellandy, C., Day, Carroll, L., Dederich, D. A., Delandy, K.R., Delgado, O., Denn, A.L., Ding, Y., Ding, M., Parler, C., Edgar, D., Edgar, D., Edgard, C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edgards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edgards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edgards, C.C., Elbaj, C., Harris, M., Garola, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunerathe, P., Hale, S., Hanilton, K., Gorrell, J.H., Guevara, W., Gunerathe, P., Hale, S., Hanilton, K., Jacobson, B., Jia, Y., Johnson, R., Jollylet, S., Joudah, S., Marinda, M., Marey, M., Rei, J., Massey, E., Mahniney, E., McLedd, M. P., Meador, M., Mail, S., Savery, G., Miner, G., Miner, G., Mitchell, T., Mohabbar, K., Morgan, M., Norger, M., Rojas, A., Parlans, E., Pull, L., Oulles, M., Ruis, S., Savery, G., Scotte, M., Svatek, A., Tabor, Y., Tankerisa, K., Tanesy, J., Taylor, C., Taylor, T., Telffed, B., Thomas, M., Tanesy, J., Taylor, C., Taylor, T., Telffed, B., Thomas, M., Williams, G., Williams, G., Wallillams, G., Wallillan, M., Wal
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinde;
                                                                                                                                                                                                                                                                                                            4050 GAGACACAGAGCCTGCGGGGAGCCCTGCCCACCTGGGAGCTCAGCGCCTGGTCACCCTGC
                                                                                    GAGACACAAGCCTGCGGGGAGCCCTGCCCCACCTGGGAGCTCAGCGCCTGGTCACCCTGC
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***, 49 unordered pieces.

AC126507
AC126507.1 GI:21700463
HTG; HTGS PHASEL.
Rattus norvegicus.
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REFERENCE AUTHORS

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                                            Worley,K.C.
Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178764)
                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                           Center project name: GZFU
Center clone name: GH230-254N12
Center clone name: CH230-254N12
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 124573 bases at least Q40
Consensus quality: 131850 bases at least Q30
Consensus quality: 137700 bases at least Q30
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    CAGGAGGACTTTACCTACACCTGACGCGGATGCTCAGTTCTTGGCTCCCGCCTTCTCC
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    CAGCAGGACTTTTATCTACACCTGACGCCAGATGCCCAGTTCCTGGCTCCCGCCTTTGCT
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                                                                              DD 101448 ATGCTTCTACTGGGCATCTCAATCCTGGCTTTGCCTGGCGACCTGCTAGCAGCTCGAG 101507
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                                                                                                                       CCAGAGGGGGGGGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC 120
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Score 775.8; DB 2;
Pred. No. 8.2e-129;
0; Mismatches 127;
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 27.2%;
87.0%;
   Query Match 27.2
Best Local Similarity 87.0
Matches 852; Conservative
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orgyrcligddnylalknsqckyllaghevvssybrdlvykgsvlrysgctanveslo
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snovrdpdnrpparnyagsvgcgsgldkravdcrdspgqggasacdvuhrple
kracgepcptwelgnwspcskscgrgfkrrplkcvghggrllarddlrrpqeldf
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Contact: MGC help desk
Email: capabbr-remail.nih.gov
Final: capabbr-remail.nih.gov
Tissue Procurement: dilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (JLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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ROD 07-AUG-2002
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<1. .1024
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/product="Similar to a disintegrin and metalloproteinase
with thrombospondin motifs 1 (ADAMTS-1)"
/protein_id="AAH09667.1"
/db_xref="GI:16307156"
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3927)
                    Mus musculus, Similar to a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1), clone IMAGE:3491991, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:3491991"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone=llb="NCL_GGAP_Lu29"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (29-JUN-2001) National Institutes of Health, Mammalian
Submitted (29-JUN-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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ilarity 85.4%; Pred. No. 2.1e-128;
Conservative 0; Mismatches 148; I
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/db_xref="taxon:10090"
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PAT 31-JAN-2002

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2 2670 bp DNA metalloprotease and gene of the same.

Novel metalloprotease E55282 E55282.1 GI:18629795

DEFINITION ACCESSION VERSION

RESULT 11 E55282

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PN JP 2001008687-A/18
PN JP 2001008687-A/18
PP 16-JAN-2001
PF 25-JUN-1999 JP 1999180973
PR PI NOBORU YAMAJI KOICHI NISHIMURA, MIHO SASAMATA
PC C12N15/09, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC C12N9/64, C12O1/37,
PC C12N15/00, C12N5/00
CC LOOK CC LOOK CONTRACT LOCATION/Qualifiers
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2670)
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/organism='Homo sapiens
Location/Qualifiers
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Pred. No. 6.6e-109;
0; Mismatches 885;
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Novel metalloprotease and gene of the sr
Patent: JP 2001008687-A 18 16-JAN-2001;
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llarity 59.2%;
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1804 GCATGG			2005	2044	2125	2185 GATGGG	2245	2305	2365	2401 CCCAAA         2425 CCTAAT	RESULT 12 E58655 LOCUS E586	ACCESSION E586 VERSION E586 KEYWORDS UP 2	Σ	AUTHORS Yama TITLE NOVE	COMMENT OS PN PD PD	P P P P P P P P P P P P P P P P P P P	CCC CC FH
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751 CGACTCTACCGCCATCCCAGCATCCTCAACCCCATCAACATGTGGTCAAGGTGCTG 810 ' ) 11	CTTCTTAGAGATCGTGACTCCGGGCCCAAGGTCACCGGCAATGCGGCCTGACGTGCGC.	B71 AACTTCTGTGCCTGGCAGAAGAAGCTGACAGGGGGGAGAGGGGGGGG	931 GACACTGCCATCCTCTTCACCAGGCAGGACCTGTGTGGAGCCACCACCTGTGACACC 987	988 CTGGGCATGGCTGATGTGGGACCATGTGTGACCCCAAGAGAAGCTGCTGTCATTGAG 1047 "IIII	1048 GACGATGGGCTTCCATCAGCCTTCACCACGGGCCAGGGGCCACGTGTTCAACATG 1107:	1108 CCCCATGACAATGTGAAAGTCTGTGAGGAGGTGTTTGGGAAGCTCCGAGCCAACCACG 1167.	1168 ATGTCCCGACCCTCATCCAGATCGACCGTGCCACCCTGGTCAGCCTGCTGCT 1227	1228 ATCATCACCAACTTCCTGGACAGGGGCACGGTGACTGCCTCCTGGACCAACCCAGCAAG 1287	1288 CCCATCTCCCTGCCCGAGGATCTGCCGGGCGCCAGCTACACCCTGAGCCAGCAG 1341	1342 TGCGAGCTGGCTTTTGGCGTGGGCTCCAAGCCCTGTCCTTACATGCAGTAC 1392 	1393 TGCACCAACTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTGCCAGACCCGC 1449	1450 CACTTCCCCTGGGCCGATGGCAGCTGTGGCGAGGCAAGCTCTGCTCAAAGGGGC 1509 .   1	1510 TGCGTGGAGAGACACACCTCAACAAGGACAGGGTGGATGCTTCCTGGGCCAAA 1563	1564 TGGGATCCCTATGGCCCCTGCTGCGCACATGTGGTGGGGGCGTGCAGCTGGCCAGGAGG 1623 ·	1624 CAGTGCACCACCCCCGCCACCCTGCCAACGGGGGAGTACTGCGAGGGGGTGAGTGA	1684 TACCGATCCTGCAACCTGGAGCCTGCCCCAGCTCCGGAAAGAGCTTCCGGGAG 1743 	1744 GAGCAGTGTGAGGCTTCAACGGGTACAACCACAGCGCCCAACCGGCTCACTCGCCGTG 1803 
oy D	9 8	Qy Dp	oy Op	o o	Oy Dp	oy op	oy Db	Qy Dp	Qy Db	Oy Dp	oy op	oy Dp	Oy Dp	Qy Dp	Oy Dp	Oy Dp	Oy Dp

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linear PAT 31-JAN-2002
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mall, N., Nishimura, K. and Sasamata, M. mall, N. Nishimura, R. and Sasamata, M. vel metallic protease tent: 19 2001017183-A 3 23-JAN-2001; MANOUCHI PHARNACEUT CO LTD Homo sapiens (human)
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23-JAN-2001
09-JUL-1999 JP 1999196584
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LAINIS/09/COYK16/40,CIZNI/15,CIZNI/19,CIZNI/Zi,CIZNS/10, PC
N9/50,CIZDI/37,
CIZNI5/00,CIZNS/00
GGTGCCCAAGTACTCCGGCGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGCCGA 1863
                                                                                             GAAGGTGACTGGACTCTTCACCAAGCCCATGCATGCTACAATTTCGTGGTGGCC 2103
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TRLPGSAGELALHLSAFGKGFVLRLAPDDSFLAPERKIERLGGSGRATGGERGLRGCF
TRLPGSAGELALHLSAFGKGFVLRLAPDDSFLAPERKIERLGGSGRATGGERGLRGCF
FSGTVNGGPPEBLAAVSLCRGLSGSFLLDGEEFTIP 19PQGAGGSLAQPHRLQRWGPAGAR
PLPRGPEWEWFETGGORGERGHOEDSFEESQEFEAEGASEPPPLGATSRFKFFVSE
ARFVETLLVADASMAAFYGADLQNHILTLMSVAARIYKHPSIKNSINLMVVKVLIVED
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VADIGTICDPNKSCSVIEDEGLQAAHTLAHELGHVLSMPHDDSKPCTRLFGPMGKHHV
MAPLEYHLLOYTLPWSPCSAMYLTELLDGGHGPCLLDARGAALPLPTGTLEDERMALYQLD
QQCRIFGPDFRHCPNTSAQDVCAQLWCHTDGAEPLCHTKNGSLPWADGTPGGPGHLC
SEGSCLPEEDVERPKPVVDGGWAPWGPWGECSRTCGGCVQFSHRECKDPEPQNGGRYC
LGRRAKYQSCHTEECPPDGKSFREQQCEKYNAYNTDMDGNLLQWVFKYAGVSPRDRC
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Vazquez,F., HastIngs,G., Ortega,M.-A., Lane,T.F., Lombardo,M., P. Oikemus,S. and Iruela-Arispe,M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3711)

1 (bases 1 to 3711)

1 (bases 2 to 3711)

1 (bases 3 to 3711)

1 (bases 3 to 3711)

1 (bases 4 to 3711)

1 (bases 5 to 3711)

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1 (bases 7 to 3711)

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9 (bases 
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Submitted (16-APR-1998) Pathology, Beth Israel Deaconess Medical
Center, 99, Brookline Avenue, Boston, MA 02214, USA
Location/Qualifiers
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Homo sapiens METH2 protein (METH2) mRNA, complete cds.
AF060153.1 GI:5725507
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/protein_id="AAD48081.1"
/db_xref="G1:5725508"
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/gene="METH2"
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KLECRARGRSEFKVFEAKVIDGTLCGPETLAICVRGGCVKAGCDHVVDSPRKLDKCGV
CGGKGNSCRRVSGSLTPTNYGYNDTYTPAGATNIDVKORSHGVQNGNYLALKTAD
GQYLLNGNILASAIEQDILVKGTILKYSGSIATLERLGSFRPLPEPLIVQLLVVPGEV
PPPKVKYTFFVPNDVDFSMQSSKERATTNIIQPLLHAQWYLGDWSECSSTGGAGWQRR
TVECRDPSGQASATCNKALKPEDAKPCESQLCPL"
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                                                                                                                                                                          Length 3711;
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                                                                                                                                                                          Score 666; DB 9; Length 37:
Pred. No. 6.2e-109;
0; Mismatches 885; Indels
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1168 ATGTCCCCGACCCTCATCCAGATCGACCGTGCCAACCCCTGGTCAGCCTGCAGTGCTGCC 1227
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                                                                                            2002 GCCCTGCCCTCCCCACAGGCCTCCCGGGCCGCATGGCCCTGTACCAGCTGGACCAGCAG
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ROD 02-FEB-1999
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Mus musculus colon adenocarcinoma cell_line:murine colon 26 cDNA to
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Submitted (28-SEP-1995) Kouji Kuno, Cancer Research Institute,
Kanazawa University, Pharmacology; Takara-machi 13-1, Kanazawa,
Ishikawa 920, Japan (Tel:0762-62-8151(ex.5454), Fax:0762-60-7704)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Murliae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuno, K., Kanada, N., Nakashima, E., Fujiki, F., Ichimura, F. and Matsushima, K.
Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene
J. Biol. Chem. 272 (1), 556-562 (1997)
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Kuno,K., Kanada,N., Nakashima,E., Fujiki,F., Ichimura,F. and Matsushima,K.
Maleular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin mptifs as an inflammation associated gene
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/cell_line="murine colon 26"
/cell_type="colon adenocarcinoma"
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/db_xref="G1:1813340"
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/translation="MGDVORARSRGSLSAHMILLILASITMILCARGAHGRPTEEDE
ELVLPSLERAPGHDSTTTRLIDAFGQQLHLKLQPDSGFLAPGFTLQTVGRSPGSEAQ
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PAVPBEESSARPQFHILRRRRRGSGGAKCGVMDDETLPTSDSRPESONTRNGWPVRDP
TPQDAGKFPSGFSIRKKFRCSGGAKCGVMDDETLPTSDSRPESONTRNGWPVRDP
TPQDAGKFPSGFSIRKKFRCSGGAKCGVMDDETLLPTSDSRPESONTRNGWPVRDP
TPQDAGKFPSGFSIRKKFFYSSPRYVEEMLANADOSMAPFHGSGLKYTLLLFESYARFF
YKHPSIRNSISLANGKTCDTLGMAADVGTVCDPSRSCSYLEDDGLAGAFTTAHEEGHYFN
MPHDDAKHGASLNGVSGGSHTMAAMJOGTVCDPSRSCSAYWTSFLDGAAFTTAHEGHYFN
MPHDAKHGASLNGVSGGSHTMAAMJOGTVCDPSRGSKGCPNGGGGGANUFGCCAM PREADGTSGCEGKKVVSGKVNKTDMKHFATPVHGSWGPWGDGSRTGGGGUVQT
MRECDNPVFKNGGKYCEGKRVFYRSCNIEDCPDNNGKTFREEQCEANNEFSKASFGNE
PTVEWTPKRAGVSPKONKTNCTSCNIEDCPDNNGKTFREEQCEANNEFSKASFGNE
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AGCDRIIDSKKKFDKCGVGGGGGTGYFPVLQPKVVDGTPCSPDGTSVCVGGCVVK
RACCNTARRADGTYLLNGWFTLSTLEDGDLTYKGTVLTRSSSSSAALERIRSS
SPLKEPLTIQVLWVGHALRADGTYLLNGWFTLSTLEDGDLTYKGTVLTRSSSSSAALERIRSS
SPLKEPLTIQVLWVGHALRADGTYLLNGWFTLSTRAIPTFSEWYIEWGEGSKTCGSG
GWQRRVVQCRDINGHPASECAKEVKPASTRPCADLPCPHWQVGDWSPCSKTCGSG 870 1442 • ATCTCCCTGCCCGAGGATCTGCCGGGCGCCAGCTACACCTGAGCCAGCAGTGCGAGCTG 1350 GTCAAGTTCCACGGCGCGCGCACTGGAACATTATCTGCTGACGCTGCTGGCAACGGCGGCG 750 930 CATGACAATGTGAAAAGTCTGTGAGGAGGTGTTTGGGAAGCTCCGAGCCAACCACATGATG 1170 AAGCGTTTCGTGTCTATCCCGCGGTACGTGGACGCTGGTGGTCGCGGACGACGACTCAATG 690 Gaps CTTCTTAGAGATCGTGACTCCGGGCCCAAGGTCACCGGCAATGCGGCCCTGACGCTGCGC AACTTCTGTGCCTGGCAGAAGAAGCTGAACAAAGTGAGAGCACCCCGAGTACTGG TCCCCGACCCTCATCCAGATCGACCGTGCCAACCCCTGGTCAGCCTGCAGTGCTGCCATC CGACTCTACCGCCATCCCAGCATCCTCAACCCCATCAACATCGTTGTGGTCAAGGTGCTG GACACTGCCATCCTCTTCACCAGGCAGGACCTGTGGAGCCACCACCTGTGACACCCTG ATCACCGACTTCCTGGACAGCGGGCACGGTGACTGCCTGGACCAACCCAGCAAGCCC Length 4180; 12; Indels 22.3%; Score 636; DB 10; Similarity 60.7%; Pred. No. 1.3e-103; 8; Conservative 0; Mismatches 700; 905 t Б 1146 1051 c ಥ 1078 Query Match Best Local Simi Matches 1098; BASE COUNT ORIGIN 1143 1203 1323 1383 1443 1503 1563 1623 1171 631 691 751 811 871 1051 1111 1231 1743 1803 931 991 1291 ð q ò 8 g g a g 9 g ò ç ò ò ò QQ ò g ά qq ò g ò g ò

GCTTTTGGCGTGGGCTCCAAGCCCTGTCCTTACATGCAGTAC---TGCACCAAGCTGTGG 1407

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2879 1467 1527 1581 2102 1641 1701 2222 1761 2279 1821 1881 2399 1941 2001 2519 2061 2121 2181 2699 2241 2759 2301 2361 2939 CTCAACAAGCACAG-----GGTGGATGGTTCCTGGGCCAAATGGGATCCCTATGGCCCC TGCTCGCGCACATGTGGTGGGGGCGTGCAGGAGGAGGAGTGCACCAACCCCACC CCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAGGGTGAAATACCGATCCTGCAACCTG GAGCCCTGCCCCAGCTCAGCCTCCGGAAAGAGCTTCCGGGAGGAGCAGTGTGAGGCTTTC TICIATETECTEGCACCCAAGGTGGTGGACGCCACGCTGTGCTCTCCTGACTCCACCTCC GGCACCAGCTGTGGCGAGGGCAAGCTCTGCCTCAAAGGGGCCTGCGTGGAGAGACAAC TGCTCAAGAACCTGTGGTGGTGGAGTTCAATACACAATGAGAATGTGACAACCCAGTC AACGGCTACAACCACAGCACCAACCGGCTCACTCTCGCCGTGGCATGGGTGCCCAAGTAC TCCGGCGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGCCGAGCCAATGGCACTGGCTAC GCCGGCGTCTCGCCAAAGGACAGGTGCAAGCTCACCTGTGAAAGCCAAAGGCATTGGCTAC CGGGACCTGGTGGTGAAGGGCAGTCTGCTGCGGTACAGCGGCACGGGCACAGCGGTGGAG TGCACCGGGAAGGCCAAGGGACAGATGGTGTCCCAGACCCGCCACTTCCCVTGGGCCGAT TTTTTCGTCTTACAGCCCAAGGTTGTAGATGGCACTCCCTGTAGTCCAGACTCTACCTCT GTCTGTGTCCAAGGCAAGTGCATCAAGGCTGGCTGTGATGGGAACCTGGGCTCCAAGAAG AGATTCGACAAGTGTGGGGTGTGTGTGGGGGAGACAATAAGAGCTGCAAGAAGGTGACTGGA CTCTTCACCAAGCCCATGCATGCTACAATTTCGTGGTGGCCATCCCCGCAGGCGCCTCA ATAGTCACTAGTACAAGACCTGGGTATCATGACATTGTCACAATTCCTGCTGGAGCCACC AGCATCGACATCCGCCAGCGCGGTTACAAAGGCCTGATCGGGGATGACAACTACCTGGCT CTGAAGAACAGCCAAGGCAAGTACCTGCTCAACGGGCATTTCGTGGTGTCGCGGTGGAG AGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTGACCGTGGAGGTCCTCTCCGTGGGG AGAATICCGCAGCTTTAGTCCACTCAAAGAACCCTTAACCATCCAGGTTCTTATGGTAGGC AAGATGACACCGCCCGGGTCCGCTACTCCTTCTATCTGCCCAAAGAGCCTCGGGAGGAC 2431 AAGTCCTCTC 2043 2103 1822 2400 1863 1408 1923 1468 1983 1528 1582 1642 2163 1702 2223 1762 2280 2340 1882 1942 2460 2002 2520 2062 2580 2122 2640 2182 2700 2242 2760 2302 2820 2362 2880 2422 Db Dp g ò g οy g à οy δ òγ g οŽ a οy Q δ g οy qq δy q ò οp Qγ g δ g g δ ò 셤 à QQ ð

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GLKHYLLTLFSVAARLYKHPSTRNSYSLVVVKILVIHDEOKGPEVTSNAALTLRNFCN
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CSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAKPGYHD
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GEWSSCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS"
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LWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTDRKHFDTPFHGSWGMW(
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                                                                                                       complete cds
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Glienke, J., Schmitt. A., Pilarsky, C., Hinzmann, B., Weiss, B.,
Rosenthall, A. and Thierauch, K.H.
Direct Submission
Submitted (19-NOV-1999) Experimental Oncology, Schering AG,
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Pred. No. 8.7e-103;
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/db_xref="taxon:9606"
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                              TGCCTCAAAGGGGCCTGCGTGGAGACACACACACAAACTCAAAAG-----CACAGGGTGGAT 1548
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Search completed: May 1, 2003, 22:35:26 Job time : 10450 secs

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May 1, 2003, 19:20:41; Search time 606 Seconds (without alignments) 10602.230 Million cell updates/sec Run on:

US-10-009-332-2 2853 1 atgettttgetgggeateet......gegteetgaggeegtgetga 2853 Title: Perfect score: Sequence:

Scoring table:

2185239 seqs, 1125999159 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched:

4370478 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ (			SUMMARIES		
Result.	Score	Query	Query Match Length DB	DB	ID	Description	
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## ALIGNMENTS

RESULT 1 AAH41003

Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; ss. Human metalloprotease MDTS6 cDNA. AAH41003 standard; cDNA; 2853 BP. 23-AUG-2001 (first entry) Homo sapiens AAH41003; 

10-NOV-2000; 2000WO-JP07917. WO200134785-A1. 17-MAY-2001.

(YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST. 11-NOV-1999; 99JP-0321740. 16-MAY-2000; 2000JP-0144020.

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This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint; diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents obtain an encoding the metalloprotease termed MDTS6.
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ò	61	CCAGAGCGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC	120
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ó	121	TACTGGCGGGTCCCGAGGACTCCGGGGATCAGGACTCATTTTTCAGATCACATTT	180
QQ	121	TACTGCCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTCAGATCAGGATTT	180
οy	181	CAGGAGGACTITITACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTTCTCC	240
qq	181	CAGGAGGACTTTTACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTTCTCC	240
ò	241	ACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGCTCTTCAGACCTGCGACGC	300
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ογ	301	TGCTTCTATTCTGGGGACGTGAACGCCGAGCCGGACTCGTTCGCTGCTGTGAGCCTGTGC	360
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ολ	361	GGGGGGTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGCCC	420
QQ	361	GGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGCCC	420
ý,	421	AATGCTAGCGCCGCGCGCGCGCACACACCCAGGCGCGCACCTTCTCCAGCGCCCG	480
q	421	AATGCTAGCGCGCGGCGGCGCAGCGCAACAGCCCAGGGCGCACACCTTCTCCAGCGCCGG	480
ογ	481	GGTGTTCCGGGCCGCCCTTCCGGAGACCCCACCTCTCGCTGCGGGGGGGG	540
qq	481	GGTGTTCCGGGCGCGCCTTCCGGAGCCCCACCTCTCGCTGCGGGTGGCCTCGGGCTGG	540
γò	541	AACCCCGCCATCCTACGGGCCCTGGACCCTTACAAGCCGCGGGGGGGG	600
g	541	AACCCCGCCATCCTACGGGCCCTGGACCCTTACAAGCCGCGGGGGGGG	009
ογ	601	AGTCGTAGCCGGCGCAGGTCTGGGCGCCCCAAGCGTTTCGTGTCTATCCCGCGGTACGTG	099
qq	601	AGTCGTAGCCGGCGCGCGCGCCCAAGCGTTTCGTGTCTATCCCGCGCGTACGTG	099
οy	661	GAGACGCTGGTCGCGGACGAGTCAATGGTCCAAGGTTCCACGGCGCGGACCTGGAACAT	720
q	661	GAGACGCTGGTGGTCGCGGACGACGACGATCAAGTTCCACGGCGCGCGGACCTGGAACAT	720

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                                                                                                                                                                                                                                                                                                                                            Human; novel human protein; NHP; protease; biological disorder; obesity;;
high blood pressure; arthritis; connective tissue disorder; infertility;
gene therapy; enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patterns
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                 CCCAAAGAGCCTCGGGAGGACAAGTCCTCTCATCCCAAGGACCCCCGGGGACCCTCTGTC
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gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid encoding a human protease, for screening libraries and assessing ge
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                                                                                                                                                                                                                                                                         GAGCTGGACTTCTGCGTCCTGAGGCCGTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 40-41; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                     AAD35571 standard; cDNA; 3446
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                                                                                                                                                                                                                                                                                                                                                                                                 Human protease cDNA #4.
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AAD35571

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tissue disorders and
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Pred. No. 0;
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 connective
therapy.
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blood pressure, arthritis,
They are also used in gene
                                                                   Query Match 99.8
Best Local Similarity 99.9
Matches 2849; Conservative
                                          612
                                         Sequence 3446 BP;
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	Qy         2281         GGCACGGGCACAGCGGTGGA           Db         2677         GGCACGGCACAGCGGTGGA           Qy         2341         GGCACGGCACAGCGGTGGA           Qy         2341         GTGAGGTCCTCTCCGTGGG           Qy         2401         CCCAAAGGTCCTCTCGTGGGAGA           Qy         2401         CCCAAAGAGCTCCTCGGGAGGA           Qy         2461         TTGCACAAGAGCCTCGGGAGGA           Qy         2461         TTGCACAAGAGCCTCGGGAGGA           Qy         2461         TTGCACAAAGAGCCTCCGGAGGA           Qy         2451         TTGCACAAAGAGCCTCCTCAG           Qy         2451         TTGCACAAACAGCGTCCTCAG           Qy         2521         GCACGCTGGGTGGCTCCTCAG           Qy         2521         GCACGCTGGGTGGCTGCCTCAGG	2917 GCACG 2581 AAGCG 2977 AAGCG 2977 AAGCG 2641 GCCCA 3037 GCCCA 2701 GCCTG 3097 GCCTG 3157 GTGGG 2761 GTGGG 2761 GTGGG 2761 GTGGG 2761 GTGGG 2761 GTGGG 2821 GAGCT 3217 GAGCT	RESULT 4 AAS97182 ID AAS97182 standard; CDNA; XX AC AAS97182; XX DT 26-FEB-2002 (first entry XX DF Human metalloprotease par XX W Human; protease; PCR prim KW vasotropic; antimigraine; KW hypertensive; hypotensive KW anorectic; antimiframmato KW metalloprotease; serine p KW lung; prostrate; cervical KW lung; prostrate; cervical
C 1020 C 1416 C 1080 C 1476 G 1140 C 1200 C 1596	1260 1656 1320 1716 1380 1776 1440		C 2196 C 1860 C 2256 G 1920 G 2316 T 1980 T 2376 G 2440 G 2436
	TGGTCAGCCTGCAGTGCTGCATCATCACCGACTTCCTGGACAGCGGGCACGGT	CGCCACTTCCCCTGGGCCGATGGCAGCTGTGGCGAGGGCAAGCTCTGCCTC	CAGTGTGAGGCTTTCAACGCCTACAACCACAGCACCAACCGGCTCACTCGCC TGGGTGCCCAAGTACTCCGGGGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGC 1111111111111111111111111111111111
TGACCCTGGGCATGGCT TGACCCTGGGCATGGCT TGACCCTGGGCATGGCTT TITITITITITITITITITITITITITITITITITI	TGCTGCCATCACCGACC TGCTGCCATCATCACCGACC TGCTGCCATCTCCCTGC THILLIHIHIHIHIHI TAGCAAGCCATCTCCCTGC THILLIHIHIHIHIHIHIHI TAGCAAGCTGCTTTTGGCC TTGCGAGCTGCTTTTGGCC TGTGTGTGCACCGGGAAGC	36CCGATGGCCACGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	CACCGGCTACAACCACAGC CTCCGGCGTGTCCCCGGG CTTCTATGTGTCTCCCCGGG CTTCTATGTGTTGCTGCCAGC CTTTTTTTTTT
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961 95 1357 97 1021 99 1417 99 1141 99 1537	9y 1201 9b 1597 9y 1261 9b 1657 9y 1321 9b 1717	1441 1837 1501 1897 1957 1621 2017 2017 1681	Db 2137 Qy 1801 Qy 1861 Db 2257 Qy 1921 Db 2317 Qy 1981 Db 2377

imer; cytostatic; immunomodulator, cardiant; e; analgesic; endocrine; nootropic; tranquiliser; ve; neuroleptic; neuroprotective; anabolic; tory; aspartyl protease; cysteine protease; protease; cancer; heemstopoletic; breast; colon; al; brain; ovarian; bladder; kidney; pain; cardiovascular disease; neuronal disease; 2280 2676 2340 2736 2400 2796 2460 2520 2916 2580 2976 2640 2700 3096 2760 3156 TIGCTGGCCCGGGACCAGTGCACCGCAAGCCCCAG 2820 2616 2856 AGCTCTCCAACCAGGTGGACCAGCCGGACGACGAGGCCCCCT AGCTGGGGGCCGTCCGCGAGCTGGGGCAGTGGCCTGCAG CCAAGCATCGACATCCGCCAGCGCGTTACAAAGGGCTGATC AAGAGCTGCGGCGGGGATTTCAGAGGCGCTCACTCAAGTGT 3AGAGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTGACC ACAAGTCCTCTCATCCCAAGGACCCCCGGGGACCCTCTGTC GGGGCTCCGCCGGGCAGCGCACGGTCCCTGTGTGATGCA CACAAGCCTGCGGGAGCCCTGCCCCACCTGGGAGCTCAGC AGAGCTGCGGCCGGGGATTTCAGAGGCGCTCACTCAAGTGT AAAAGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTGACC 3GGAAGATGACACCGCCCGGGTCCGCTACTCTTTTTG artial DNA sequence #11. PERGECCETECTER 2853 TITTITITITI BP. 2937 3

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/Potension; hypertension; psychotic disorder; disorder; inflammatory disorder; ss.
   attention disorder
disorder;
dysfunction; mood
                     hypotension;
             disorder; hy
a, metabolic
migraine; sexual
                                  dyskinesia;
                 coquition
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Homo sapiens.

WO200183782-A2

08-NOV-2001

04-MAY-2001; 2001WO-US14431

04-MAY-2000; 2000US-201879P.

(SUGE-) SUGEN INC.

G, Caenepeel S; Manning Sudarsanam S, ď Plowman GD, Whyte Payne V;

WPI; 2002-041502/05 P-PSDB; AAU72899

Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory *:* disorders

Claim 30; Figure 1P; 232pp; English.

The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering (S) (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or hardner protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases. (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders and dyskinesias), metabolic disorders and inflammatory disorders and dyskinesias), metabolic disorders and inflammatory disorders such as those above. Assyl155 represent human protease coding sequences and primers of the invention.

Sequence 2937 BP; 531 A; 958 C; 936 G; 512 T; 0 other;

300; ...**.** ý, TACTGGCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTTCAGATCACAGCATTT 180 CCAGAGCGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC 120 255 CAGGAGGACTITIACCIACACCTGACGCCGGATGCTCAGTICTTGGCTCCCGCCTTCTCC 315 375 ATGCTTTTGCTGGGCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCTTTGAG 60 9; Gaps ACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGCTCTTCAGACCTGCGACGC 98.6%; Score 2814.4; DB 24; Length 2937; llarity 99.5%; Pred. No. 0; Conservative 0; Mismatches 6; Indels 9; ( Local Similarity les 2847; Conserv Query Match Best Loca Matches 9/ Н 61 136 121 196 181 256 241 316 q Q ò ò g ŏ ö g ò g

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TGCTTCTATTCTGGGGACGTGAACGCCGACCCGACTCGTTCGCTGTGAGCCTGTGG

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1035 1020 1095 1080 AACCCCTGGTCAGCCTGCAGTGCTGCCATCATCACCGACTTCCTGGACAGCGGGCACGGT 1260 CACGAGCTGGGCCACGTGTTCAACATGCCCCATGACAATGTGAAAGTCTGTGAGGAGGTG 1140 TTTGGGAAGCTCCGAGCCAACCACATGATGTCCCCGACCCTCATCCAGATCGACCGTGCC 1200 1440 420 495 480 555 540 615 900 675 999 735 720 795 780 855 840 900 975 960 376 TGCTTCTATTCTGGGGACGTGAACGCCGAGCCGGACTCGTTCGCTGCTGTGAGCCTGTGG CCCATCAACATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCCCAAG CCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCAGCCTTCACCACTGCC GGGGGGCTCCGGGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGCCC AATGCTAGCGCCGGCGGCGCAACAACAACAAGCCAACAACCTTCTCCAGCGCCGG GGTGTTCCGGGGGCCTTCCGGAGACCCCACCTCTCGCTGCGGGGTGGC;;;;CGGGCTGG GAGACGCTGGTGGTCGCGGACGAGTCAATGGTCAAGTTCCACGGCGCGGGACCTGGAACAT TATCTGCTGACGCTGCTGCCAACGCCGCGCGCGACTCTACCGCCATCCCAGCATCCTCAAC AAAGTGAGTGACAAGCACCCCGAGTACTGGGACACTGCCATCCTCTTCACCAGGAGGAC CTGTGTGGAGCCACCACCTGTGACACCCTGGGCATGGCTGATGTGGGTACCATGTGTGAC 1456 TACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTGTGT GACTGCCTCCTGGACCAACCCAGCAAGCCCATCTCCCTGCCCGAGGATCTGCCGGGCGCC AGCTACACCCTGAGCCAGCAGTGCGAGCTGGCTTTTGGCGTGGGCTCCAAGCCGTGTCCT TACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTGTC 361 196 916 421 496 1036 1021 9601 1156 1216 481 541 661 721 781 856 841 916 901 961 1081 1141 1276 1261 1336 1321 1381 1201 Qγ g οy g οy g ò g δ g g g Db ò Qγ Db δ ò οy g οy q Qγ Dp Ω g ò Op δy g δy qq ò g δy g

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AGGCCCCCTGCACGCTGGCTGGCAGCTGGGGGCCGTGCTCCGCGAGCTGCGGCAGT
             CTCAAGTGTGGGCCACGGAGGCCGGCTGCTGGCCCGGGACCAGTGCAACTTGCACCGC
                                                 GGCCTGCAGAAGCGGGGGGTGGACTGCCGGGGTCCGGGCAGGGCACGGTCCCTGCC
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                                                                                                                                                                                                                                                                  protease PRTS-11 cDNA sequence.
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22-JUN-2000; 2000US-213955P.
29-JUN-2000; 2000US-215396P.
07-JUL-2000; 2000US-216821P.
14-JUL-2000; 2000US-218946P.
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P-PSDB; AAU74751.
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Walia NK, Yao M
Azimzai Y, Lu Y
Kallick DA;
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                      CAGACCCGCCACTTCCCCTGGGCCGATGGCACCTGTGGCGAGGGCAAGCTCTGCCTC 1575
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Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer; cardiovascular; atherosclerosis; autoimmune disorder; dermatitis; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; cell proliferative disorder; developmental disorder; epilepsy; buchenne muscular dystrophy; epithelial disorder; neurological disorder; reproductive disorder; endometriosis; ss.
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useful (e.g. in the diagnosis, treatment and prevention of gastrointestinal gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders

Page 168; 177pp; English

The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and Improcardial infarction, autoimmune/inflammatory e.g. acquired immunodeficlency syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g. cancer, developmental e.g. Duchenne and Becker miscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and allabeimer's disease and reproductive e.g. infertility and endommetriosis disorders. Numerous other examples of each disorder are given in the specification. The present nucleic acid sequence encodes the human protease PRTS-11 protein of the invention.

BP; 529 A; 958 C; 931 G; 512 T; 0 other; Sequence 2930

ج**و** ج 240 180 480 009 134 CCAGAGCGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC 120 194 254 314 300 374 360 434 420 554 540 614 494 GAGACGCTGGTGGTGGGGGGGGGGTCAATGGTCCAAGTTCCACGGCGCGGACCTGGAACAT 720 Gaps 9 ATGCTTTTGCTGGGCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCTTTGAG ACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGGCTCTTCAGACCTGCGACGC GGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCTGCCC AATGCTAGCGCCGCCGCCGCCAGCGCAACAGCCAGGGCGCACCTTCTCCAGCGCCGG GGTGTTCCGGGGGGCCTTCCGGAGACCCCTCTCGCTGCGGGGTGGCCTCGGGCTGG CAGGAGGACTTTTACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTTCTCC AGTCGTAGCCGGCGCGCGCGCGCGCGTTTCGTGTCTATCCCGCGGGTACGTG Score 2812.8; DB 24; Length 2930; Pred. No. 0; . 9 7; 0; Mismatches 98.6%; 99.5%; st\_Local Similarity 99.5 tches 2843; Conservative 75 135 255 375 9 121 195 181 241 315 301 361 435 421 495 481 555 541 615 601 675 661 Query ò g ŏ d 9 9 9 9 g QY Db òγ q qq Ω g ò q ò δ g 셤 ò

1080 1200 1154 1454 1500 854 900 GTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTGAAC CACGAGCTGGGCCACGTGTTCAACATGCCCCATGACAATGTGAAAAGTCTGTGAGGAGGTG GAGACGCTGGTGGTCGACGACGACGACGTCAAGTTCCACGCCGCGCGACCTGGAACAT CCCATCAACATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCCCCAAG CTGTGTGGAGCCACCACCTGTGACACCCTGGGCATGGCTGATGTGGGTACCATGTGTGAC CCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCAGCCTTCACCACTGCC TITGGGAAGCTCCGAGCCAACCACATGATGTCCCCGACCCTCATCCAGATCGACCGTGCC GACTCCTCCTGGACCAACCCAGCAAGCCCATCTCCCTGCCCGAGGATCTGCCGGGCGCC TATCTGCTGACGCTGCTGCAACGGCGGCGACTCTACCGCCATCCCAGCATCCTCAAC AACCCCTGGTCAGCCTGCAGTGCTGCCATCACCGACTTCCTGGACAGTGGGCACGGT AGCTACACCCTGAGCCAGTGCGAGCTGGCTTTTGGCGTGGGCTCCAAGCCCTGTCCT TACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTGTGC GACTGCCTCCTGGACCAACCCAGCAAGCCCATCTCCCTGCCCGAGGATCTGCCGGGCGCC AAAGGGCCTGCGTGGAGAGACACAACCTCAACAAGCACAGGGTGGATGGTTCCTGGGCC AGGCAGTGCACCACCCCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAGGGTG AAATACCGATCCTGCAACCTGGAGCCCTGCCCCAGCTCAGCCTCCGGAAAGAGCTTCCGG GAGGAGCAGTGTGAGGCTTTCAACGCCTACAACCACCACCAACCGGCTCACTCTCGCC 1035 1095 735 721 795 781 855 841 915 901 975 196 1021 1081 1155 1141 1215 1275 1261 1321 1395 1455 1575 1335 1381 1441 1515 1501 1561 1621 1695 1681 1755 1741 1201 Qγ g δy D ŏ g ă qq δλ qq οy QQ Db qq qq Dp δ δ ò ò g õ ò pp ò g qq δ ò q Qy g g δ ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding novel members of a disintegrin, metalloproteinse and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
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                                                                                       a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; noctropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosupp.essive; Allzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury; ss.
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                                                         Rat; ADAWIS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain;
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Rat metalloproteinase ADAMTS-5 cDNA.
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1; novel human protein; NHP; protease; biological disorder; obesity; blood pressure; arthritis; connective tissue disorder; infertility; therapy; enzyme; gene; ss.
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llarity 99.5%; Pred. No. 1.4e-216; 
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The present sequence encodes human metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimar's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                             1021 CCCAAGAGAAGCIGCTCIGTCATIGAGGACGATGGGCTTCCATCAGCCTTCACCACTGCC 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury; ss.
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P-PSDB; AAB21261.
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Score 1045.2; DB 21; Length 1143; Pred. No. 1.1e-207;

36.6%; 96.6%;

1101 CAAGTACTCCGGCGTGTCCCCGTGACAAGTGTAAGCTCATC

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Matches 1085;
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                                                                                                                                        Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a cDNA encoding novel human protein (NHP), human protease. NHPs share structural similarity with animal protease particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertilit They are also used in gene therapy.
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Pred. No. 3.8e-189;
); Mismatches 2;
                                                                                                                                                                                                                                                                      "Human protease #1"
                                                                                                                                                                                                                             Location/Qualifiers
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99.8%;
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Best Local Similarity 99.8
Matches 957; Conservative
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/*tag=
                                                                                                             Human protease cDNA #1
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P-PSDB; AAE22540.
                          AAD35568 standard;
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                                              ACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGCTCTTCAGACCTGCGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uman; MDTS4; ADAM-type metalloprotease; drug screening;
Disintegrin And Metalloprotease; cancer; arthritis; probe;
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                                                                                                                                                                        The invention relates to the novel human ADAM (A Disintegrin And Metalloprotease) type metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 apenes, the recombinant production of MDTS4 and MDTS4, and antibody specific for MDTS4 or MDTS5, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present sequence represents a human ADAM-type metalloprotease-related DNA sequence, used in an exemplification as a probe for screening human cDNA libraries in order to isolate MDTS4 cDNA.
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                                                                                                                as an anti-cancer
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                                                                                                               its preparation
                                                                                                                                                      Japanese
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59.2%;
                                                                                                                                                     Example 1; Page 11-12; 22pp;
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                                   99JP-0196584
                                                                                                                A new metal protease and it
anti-arthritic therapeutic
                                                             (YAMA ) YAMANOUCHI PHARM
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                                                                                     WPI; 2001-275950/29
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Matches 1355; Conserv
                                   09-JUL-1999;
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                                                                                      GACACTGCCATCCTCTACCAGGCAGGACCTGTGTGG - - - AGCCACCACCTGTGACACC
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antiarthritic;
                                                                 AACCTGGGCTCCAAGAAGAGATTCGACAAGTGTGGGGGTGTGTGGGGGGAGACAATAAGAGC
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/note= "a disintegrin and metalloprotease (ADAM)
type metal protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ADAM type metal protease MDTS3 encoding cDNA SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; a disintegrin and metalloprotease type metal
MDTS2; MDTS3; ADAM type metal protease; cytostatic;
cancer; arthritis; arthrosis deformans; ss.
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Gaps 11;
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                                                                                                                                The present sequence encodes a disintegrin and metalloprotease (ADAM); type metal protease designated MDTS3, isolated from human. MDTS proteins have cytostatic and antiarthritic activities. They can be used as a drug for cancers, arthritis and arthrosis deformans.
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                                                                                                                                                                                                    Sequence 2670 BP; 511 A; 853 C; 867 G; 439 T; 0 other;
                                                                           use.
                                                                                                                                                                                                                            Query Match 23.3%; Score 666; DB 22; 1
Best Local Similarity 59.2%; Pred. No. 7.2e-129;
Matches 1355; Conservative 0; Mismatches 885;
                                                                          for
                                                                          metal protease gene, arthrosis deformans
                                                                                                                Example 3; Page 27-28; 31pp; Japanese.
            LTD
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            (YAMA ) YAMANOUCHI PHARM
                                                                         New metal protease and cancers, arthritis and
                                   WPI; 2001-285362/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial venous malformation; immune deficiency; ss.
1984 AACCTGGGCTCCAAGAAGAGATTCGACAAGTGTGGGGGTGTGTGGGGGAGACAATAAGAGC
                                                                                                                                                                                                                                   2284 ACGGGCACAGGGGTGGAGAGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTGACCGTG
                                  ATCCCCGCAGGCGCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGGCTGATCGGG
                                                                                                                                                                                                                                                                                                         GATGACAACTACCTGGCTCTGAAGAACAGCCAAGGCAAGTACCTGCTCAACGGGCATTTC
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
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P-PSDB; AAY49502.
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AAZ32000 and AAZ32001 encode, and AAY49501 and AAX49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 have been found to be potent inhibitors of anglogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to anglogenesis including abnormal wound healing, inflammation, rheumatiod arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotharpy or conditions, both chronic and disagnosis. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAZ32081 represent sequences given in the exemplification of the present
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Pred. No. 7.3e-129;
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Human; METH2; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb angiogenesis; obsier-Webber syndrome; plaque neovascularisation; telanglectasia; haemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control; ss.
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The present sequence is the coding sequence of human METH2 (ME for metalloprotease and TH for thrombospondin). METH2 can be used for inhibiting and pogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rhewardcoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic sears, nonunion fractures, scleroderma, trachona, vascular adhesions, myocardial angiogenesis, sclonary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, osler-Mebber syndrome, plaque neovascularisation, telangiectasia; haemophilac joints, angiofilorema, filbromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis, METH2 can also bequed in birth control. METH2 can also be used in diagnostic methods for the
                                                                                                                                                                                                                                                                                                                    METH1 and METH2 polynuclectides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                          Jonak ZL, Trulli SH;
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                              HUMAN GENOME SCI INC.
SMITHKLINE BEECHAM CORP.
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INUELA-ARISPE L.
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Fornwald JA, Terrett JA
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11; 157 CTCATTITICAGATCACAGCATTICAGGAGGACTITIACCTACACCTGACGCCGGAIGCT 216 217 CAGTICTIGGCICCGCCTICICCACIGAGCAICIGGGCGICCCCCCCCAGGGGCTCACC 276 277 GGGGGCTCTTCAGACCTGCGACGCTGCTTCTATTCTGGGGACGTGAACGCCGAGCCGGAC 336 GGGGGCGAGCGGGGCTGCTGTTTTTTCGGCACCGTGAATGGGGAGCCCGAG 336 TCGTTCGCTGCTGTGAGCCTGTGCGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCC 396 GAGTICACCATCCAGCGCAGGGGGGGGGGCTCCCTGGCTCAGCGCACCGCCTGCAG 456 517 CGCTGCGGGTG-GCCTCGGGCTGGAACCCCGCCATCCTACGGGCCCTGGACCCTTACAA 575 Gaps 48; Length 3008; Indels 23.3%; Score 666; DB 22; 1 59.2%; Pred. No. 7.3e-129; Live 0; Mismatches 885; Query Match 23.3 Best Local Similarity 59.2 Matches 1355; Conservative 277 337 397 457 337 397 ŏ g ŏ a ò g ò g ò 요 ŏ g ò

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                            TACCGATCCTGCAACCTGGAGCCCTGCCCCAGCTCAGCCTCCGGAAAGAGCTTCCGGGAG 1743
                                              1717 TACCAGTCATGCCACACGGAGGAATGCCCC-----CCTGACGGGAAAAGCTTCAGGGAG 1770
                                                                  GAGCAGTGTGAGGCTTTCAACGGCTACAACCACAGCACCAACCGGCTCACTCTCGCCGTG 1803
                                                                                                       GCATGGGTGCCCAAGTACTCCGGGCGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGCCGA 1863
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                                                                                                                                                                                  Human, METH1, METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
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metalloprotease thrombospondin (METH) proteins METH1 and METH2
metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of
anglogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to anglogenesis including abnormal
wound healing, inflammation, rheumatoid arthritis, psoriasis,
cancer and other disorders related to anglogenesis including abnormal
cancer and other disorders related to anglogenesis including abnormal
cancer and other disorders, and arthritis, psoriasis,
candometrial bleeding disorders, and arthritis, psoriasis,
macula degeneration, haemanglomas, and arthrial-venous malformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
or mobilisation (chemotaxis) of immune cells. The etalology of these
cancer or some autoimmune disorders may be genetic, somatic, such as
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat infiammatory
conditions, both chronic and acute conditions. The products can also
used for detection and diagnosis. AA323202 to AA323080, and AA449503 to
the activation of the present
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
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Matches 1098; Conserv
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28-AUG-1998;
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                GCCTCGATGCTCTCCAGCTTAGACCATAGCCAGCCCTGGTCACCTTGCAGTGCCTACATG 1742
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cancer therapy; benign through points, angroyence therapy; benign through cancer therapy; benign through call and dealing; endometriosis; rheumatoid arthritis; psoriasis; wound healing; endometriosis; scaleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb angiogenesis; Osler-Webber syndrome; wound granulation; plaque neovascularisation; telangiectasia; haemophiliac joint; EST; angiofibroma; fibromuscular dysplasia; expressed sequence tag; Crohn's disease; atherosclerosis; birth control; ss.
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The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, requing cancer, benign tumours, an ocular angiogenic disease, rehumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, heamophiliac joints, angiofibroma, therowical dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also
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Best Local Similarity 60.7%; Pred. No. 1.3e-122;
Matches 1098; Conservative 0; Mismatches 700; Indels 12; Gaps
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                                                                                                                                                       METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
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                                                           ZL,
                                                           Jonak
                                                         SM,
                                                                                                                                                                                                                                     Claim 7; Pages 543-546; 768pp; English.
                                                           Ruben
                                                         Hastings GA,
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Fornwald JA, Terrett JA;
  FORNWALD J A.
(FORN/) FORNWALD J A (TERR/) TERRETT J A.
                                                                                                                  4PI; 2001-025136/03
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

May 1, 2003, 19:29:16; Search time 103 Seconds (without alignments) 8494.649 Million cell updates/sec Run on:

US-10-009-332-2 2853 1 atgcttttgctgggcatcct......gcgtcctgaggccgtgctga 2853 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 441362 seqs, 153338381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodatcal/lina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodatcal/lina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodatcal/lina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodatcal/lina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodatcal/lina/PGTUS\_COMB.seq:\*
6: /cgn2\_6/ptodatcal/lina/Packfiles1.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	;	sednence I, Appil	Sequence 1, Appli	28	7	8	-	14,	٦,	14,	12,	7,7	10,	5,	9	ς,	.16,	7	ų	δ	ω,	ģ	m	Sequence 5, Appli	4,	9	Sequence 23, Appl	24,
SUMMAKIES	ΙD		US-US-TSO-43T-T	US-09-392-184-1	US-09-484-970B-58	US-09-392-184-7	US-09-369-364A-8	US-09-122-126B-1	US-09-122-126B-14	US-09-369-364A-1	US-09-369-364A-14	US-09-369-364A-12	US-09-130-491-7	US-09-369-364A-10	US-09-392-184-5	US-09-369-364A-6	US-09-369-364A-3	US-09-369-364A-16	US-09-491-522-2	US-09-491-522-1	US-09-491-522-9	US-09-491-522-8	US-09-392-184-6	US-09-930-872-3	US-09-930-872-5	US-09-369-364A-4	US-09-491-522-6	US-09-392-184-23	US-09-392-184-24
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US-09-369-364A-18 US-09-930-872-1	US-09-369-364A-20 US-08-985-526-2	US-08-985-526-4 US-09-276-531-117	US-08-808-982-1	US-09-306-902A-1 US-08-706-216-5	US-09-152-060-23	US-09-392-184-12	US-08-592-500-1	US-08-195-006-1	PCT-US94-07644A-1	US-08-715-554-1	US-08-583-118-1	US-08-232-463-14	US-07-642-734C-3
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## ALIGNMENTS

	9
RESULT 1 US-09-130-491-1 US-09-130-491-1 Sequence 1, Application US/09130491 ; Sequence 1, Application US/09130491 ; Patent No. 6416974 ; GENERAL INFORMATION: APPLICANT: HOLYZEMEN, Douglas A. APPLICANT: GOOGGETI, Andrew D.J. TITLE OF INVENTION: TANGO-71, TANGO-74, TANGO-76, AND TANGO-83 FILE REFERENCE: 09404/041001 CURRENT APPLICATION NUMBER: US/09/130,491 CURRENT RILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: US 60/054,961 EARLIER APPLICATION NUMBER: US 60/054,961 EARLIER PILING DATE: 1997-09-05 NUMBER OF SEQ ID NOS: 16 NUMBER OF SEQ ID NOS: 16 SEQ ID NO 1 LENGTH: 4676 SEQ ID NO 1 LENGTH: APPLICATION: (460)(3360)	Ouery Match  22.0%; Score 628.2; DB 4; Length 4676;  Best Local Similarity 57.1%; Pred. No. 1.1e-127;  Matches 1305; Conservative 0; Mismatches 913; Indels 69; Gaps  QY 175 GCATTCAGGAGGATCTACACCTGAGGCGGAGGAGCTCATTTTGGCCCGGC 234

530 1056 590	627 1176 657	1236 717 <sup>.</sup> 1296	777 1356	837 1416	897 1476 ·	957 1536	1017	1077 <sup>· ·</sup> 1656	1137 1716	1197 1776	1257 1836	1317 . 1896	1377 1956	1434 2016	1494 2076	1548
CCAGCGCGGGGTGTTCCGGGCGGCCTTCCGGAGACCCCACCTCTCGCTGCGGGGTGGC	CTTCGGGGAAGTCGTAGCCGGCGCACTCTCGGCGCC	GGACAGCCCACAGGGACTGGAAGCATAAGAAAGAAGGGATTTGTGTCCAGTCAGCGCTAT GTGGAGACGCTGGTGGTCGCGGACGAGCTAATGGTCAAGGTTCCACGGCGCGGACCTGGAA [	CATTATCTGCTGACGCTGCTGGCACGCGCGCGCACCTACCGCCATCCTCCTCCTCTCTCT	AACCCCATCAACATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCCC	AAGGTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTG	AACAAAGTGAGTGACAAGCACCCGAGTACTGGGACACTGCCATCCTCTTCACCAGGCAG   11	GACCTGTGTGGAGCCACCACTGTGACACCCTGGGCATGGCTGATGTGGGTACCATGTGT	GACCCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCACCTTCACCACT	GCCCACGAGCTGGGCCACGTGTTCAACATGCCCCATGACAATGTGAAAGTCTGTGAGGAG	GTGTTTGGGAAGCTCCGAGCCAACCACATGATGTCCCCGACCCTCATCCAGATCGCTGT	GCCAACCCTGGTCAGCTGCAGTGCTCATCACGACTTCCTGGACAGGGGCAC	GGTGACTGCCTCCTGGACCAACCCAGCAAGCCCATCTCCCTGCCCGAGGATCTGCCGGGC	GCCAGCTACACCCTGAGCCAGCAGTGCGAGCTGTTTGGCGTGGGCTCCAAGCCCTGT	CCTTACATGCAGTAC TGCACCAAGCTGTGGTGCACGGGAAGGCCAAGGGACAGATG	GTGTGCCAGACCCGCCACTTCCCCTGGGCCCGATGGCACCAGCTGTGGCGAGGGCAAGGTC [	TGCCTCAAAGGGGCCTGCGTGGAGAGACAACCTCAACAAGCACAGGGTGGAT
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AAGCICATCIGCCGAGCCAATGGCACTGGCTACTICTATGTGCTGGCACCCAAGGTGGTG
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Patent No. 6395899
GENERAL INFORMATION:
APPLICANT: Robison, Kaith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING FITLE OF INVENTION: PROTEASE HOMOLOGS
FILE REFERENCE: 5800-55
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                                                                                                       PEATURE:

NAME/KEX: misc_feature

LOCATION: (1)...(4888)

OTHER INFORMATION: reprolysin (ADAM family of metalloprotease)

NAME/KEX: misc_feature

LOCATION: (1)...(4888)

OTHER INFORMATION: n = A,T,C or G

US-09-392-184-1
                                                                                                                                                                                                                                Length 4858;
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Pred. No. 1.3e-125;
0; Mismatches 912;
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                                          FastSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/09/392,184
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.05
SEQ ID NO 1
LENGTH: 4858
                                                                                                                                                                                                                             Query Match
21.7%;
Best Local Similarity 57.1%;
Matches 1306; Conservative 0
                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 007074.1
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APPLICANT: JONEWICH, WAYNE
PAPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 58
LENGTH: 3706
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; Sequence 58, Application US/09484970B
; Patent No. 6426186
; CENERAL INFORMATION:
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Matches 1077; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(3126); OTHER INFORMATION: reprolysin (ADAM family of metalloprotease) US-09-392-184-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEASE HOMOLOGS
FILE REFERENCE: 5800-55
CURRENT APPLICATION NUMBER: US/09/392,184
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ IN NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2361 GAAGATGACACCGCCCCGGGTCCGCTACTCCTTCT 2395
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ORGANISM: Homo sapiens
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Pred. No. 7.8e-120;
0; Mismatches 905;
                                                         APPLICANT: Apte, Suneel
APPLICANT: Apte, Suneel
APPLICANT: Hirohata, Tilna L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding 21r
FILE REPERENCE: 264734007/10-39-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 8
Sequence 8, Application US/09369364A Patent No. 6391610
                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus ADAMTS-8
FEATURE:
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Best Local Similarity 57.3%;
Matches 1335; Conservative (
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NAME/KEY: misc_feature
COCATION: (3636)
CTHEN INFORMATION: n = T
US-09-369-364A-8
                          Patent No. 6391610
GENERAL INFORMATION:
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FITLE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEO ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
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Pred. No. 3.8e-110;
0; Mismatches 746;
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Matches 1043; Conservative
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APPLICANT: Apte, Suneel
APPLICANT: HITCHER, Tina L.
APPLICANT: HITCHER, Satchi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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19.1%; Score 545.8; DB 4;
Best Local Similarity 57.7%; Pred. No. 8.2e-110;
Matches 1042; Conservative 0; Mismatches 747;
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                                                                                                                    AGATTATCGGAACCTTCAATAAAAAAGCAAGGGTTATACTGACGTTGTGAGGATCCCTG
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                                                                                                                        APPLICANT: Apte, Suneal
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satohata, Satohat
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                                                                                                               Length 5804;
                                                                                                                                   Indels
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                                                                                                              Score 411.2; DB 4
Pred. No. 1.7e-80;
0; Mismatches 785
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54.48;
                                                                                                                          Similarity 54.4
11; Conservative
                LOCATION: (3)..(5648)
NAME/KEY: misc_feature
LOCATION: (1406)
OTHER INFORMATION: n=T
NAME/KEY: misc_feature
LOCATION: (1563)
OTHER INFORMATION: n=T
US-09-369-364A-12
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FEATURE:
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Sequence 7, Application US/09130491
Patent.No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-11, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
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                                                         ACAACCTCAACAAGCACAGGGTGGATGGTTCCTGGGCCAAATGGGATCCCTATGGCCCCT
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; LOCATION: (3)..(737)
US-09-369-364A-10
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US-09-369-364A-10
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                                                                                                                                                                                                                         Length 2114;
                                                                                                                                                                                                                      Score 318; DB 4; I
Pred. No. 2.4e-60;
0; Mismatches 470;
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.8%;
Matches 705; Conservative
                                                                                                                        TYPE: DNA ORGANISM: Rattus rattus
                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (3)...(1445)
US-09-130-491-7
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                                                                                                                                                                 TICGIGGIGGCCATCCCCGCAGGCGCCTCAAGCATCGACATCCGCCAGCGCGGT7ACAAA 2151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTGACCGTGGAGGTCCTCTCCGTG----GGGAAGATGACACCGCCCCGGGTCCGCTAC 2388
689 IGGICAAGIICCACGGCGCGGACCIGGAACAITAICIGCIGACGCIGCIGGAAACAACAGGAAACA
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                                                                                                                 831 AAAGGCACTGCCTGTAGGAAGGTCTCAGGTTCTTTCACCCCCTTCAGTTATGGCTACAAT
                                                                    629 CCAAGCGTTTCGTGTCTATCCCGCGGTACGTGGAGACGCTGGTGGTCGCGGGACGAGTCAA
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Pred. No. 1e-47;
D; Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hirohata, Satoshi,
TILE OF INVENTION: Nucleic Acids Encoding Zilr
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT APPLICATION NUMBER: US/09/369,364A
NUMBER OF SEQ. ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
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 TGATCGTAGAAGATGAAAAATGGGGCCCAGAGGTGTCCGACAATGGGGGGCTTACACTGC 294
                                                                                                                                                                              GGGACACTGCCATCTTCACCAGGCAGGACCTGTGTGG----AGCCACCACTGTGACA
                          GCAACTICIGIGCCIGGCAGAAGAAGCIGAACAAAGIGAGIGACAAGCACCCCGAGIACI
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NAME/KEY: misc_feature

LOCATION: (1)...(5357)

OTHER INFORMATION: reprolysin (ADAM family of in the companies of incompanies)

LOCATION: (1)...(5357)

OTHER INFORMATION: n = A,T,C or G
US-09-392-184-5
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APPLICANT: RObison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEASE HOMOLOGS
FILE REFERENCE: 5800-55
CURRENT APPLICATION NUMBER: US/09/392,184
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 5357
                                                                                                                                                                                                                                                                                                            CCATCATCACCGACTTCCTGGACAGCGGG 1254
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                                                                                    3344 AGCCAGCCGGGACCTCTGCATCAACGCCATCTGTAAGAACGTGGGCTGTGACTTCGAGAT
                                                                                                                                                                                                        CCCAGCCGGCGCA------CGCGAGATCCGCATCCAAGAGGTTGCCGAGGTGC
                                                                                                                                                                                                                                                GAAGGIGACTGGACTCTTCACCAAGCCCATGCATGGCTACAATTTCGTGGTGGCCATCCC
                                                                                                                                                                                   CGCAGGCGCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGGCTGATCGGGGATGA
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APPLICANT: Hurskainen, Tiina L.
TIILE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases:
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 6
LENGTH: 3218
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Pred. No. 2.2e-43;
0; Mismatches 798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
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Best Local Similarity 51.4%;
Matches 933; Conservative C
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US-09-369-364A-6
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US-09-369-364A-6
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766 GCCAAAATGGTGGAGTACCACGGACAGCCGCAGGTTGAGAGCTATGTGCTGACCATCATG 825
                                                                                                                    885
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                                                          GCAACGGCGCGCGACTCTACCGCCATCCCAGCATCCTCAACCCCATCAACATGTTGTG
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Search completed: May 1, 2003, 22:52:44
Job time : 162 secs
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               TGGGTGCCCAAGTACTCCGGCGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGCCGAGCC 1866
                                                                      1867 AATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGACGGCACGCTGTGCTCT 1926
                                                                                                 GCGAATGAGTACTTTGCCAAGAAGCTGCGGACGCCTGTGTCGATGGCACCCCTGCTAC 1977
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                                                                                                                                                                                                                                                                                                                                    GGGCTGATCCCAGCGGCGCA------CGCGAGATCCGCATCCAAGAGGTTGCC 2205
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APPLICANT: Hurskalnen, Tilna L.
APPLICANT: Hurskalnen, Tilna L.
APPLICANT: Hurshata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SSEQ ID NO 3
LENGTH: 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09369364A Patent No. 6391610
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NAME/KEY: misc_feature
LOCATION: (296)
OTHER INFORMATION: n=T
NAME/KEY: misc_feature
LOCATION: (1443)
OTHER INFORMATION: n=A
NAME/KEY: misc_feature
LOCATION: (1457)
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US-09-369-364A-3
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                                                                          1603 GCCGTGCAGCTGGCCAGGAGGCAGTGCACCAACCCCACCCTGCCAACGGGGCAAGTAC 1662
                                                                                                                                                                                                                       1723 TCCGGAAAGACTTCCGGGAGGAGCAGTGTGAGGCTTTCAACGGCTACAACCACACACCAC 1782
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 Length 1520;
Score 215.8; DB 4; Length
Pred. No. 3.7e-38;
0; Mismatches 347; Indels
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 7.6%;
   Query Match 7.69
Best Local Similarity 56.09
Matches 456; Conservative
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1, 2003, 19:41:41 ; Search time 339 Seconds (without alignments) 9944.440 Million cell updates/sec
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2853
1 atgcttttgctgggcatcct......gcgtcctgaggccgtgctga 2853
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Published\_Applications\_NA:\*

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Database

## SUMMARIES

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	Description	Sequence 3.	Sequence 7	Sequence: 3	Sequence 1.	Seguence 5	Sequence 1	Sequence 13	Sequence 13	Sequence	Sequence 2, App]	Sequence 2, App]	Segmence	Sequence	Sequence	Sequence 35	Segmence	Segnence	Sequence	Sequence
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		US-09-965-631-3	US-09-965-631-7	18-10-163-316-3	53-316-1	965-631-5	US-09-965-631-1	17-597-13	US-10-097-580-13	145-023A-1	17-597-2	US-10-097-580-2	US-09-445-023A-2	US-10-105-929-1	US-09-918-171A-8	IS-10-174-590-351	6-758-351	5-737-351	JS-10-173-706-351	18-10-175-738-351
	Ð	5-60-SD	-60-SD	US-10-16	US-10-163-316-	60-Sn	5-60-SN	us-10-09	US-10-09	US-09-4	US-10-05	us-10-09	US-09-4	US-10-1	0S-09-6	US-10-17	US-10-17	US-10-17	US-10-17	US-10-17
	DB	10	10	6	σ	10	10	6	σ	10	6	σ	10	12	10	σ	σ	თ	6	6
	Query Match Length DB	2853	3446	2469	2940	1104	996	2184	2184	2184	2184	2184	2184	4676	3638	4407	4407	4407	4407	4407
ф	Query Match	99.8	8.66	80.5	80.5	38.1	33.5	22.3	22.3	22.3	22.0	22.0	22.0	22.0	20.8	20.4	20.4	20.4	20.4	20.4
	Score	2846.6	2846.6	2296.4	2296.4	1088	955.8	636	636	636	628.8	628.8	628.8	628.2	592	583.2	583.2	583.2	583.2	583.2
	Result No.		7	e	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19

Sequence 351, App Sequence 351	Human Proteases and Polynucleotides E	DB 10; Length 2853; 4; Indels 0; Gaps 0;
US-10-175-752-351 US-10-176-752-351 US-10-176-753-351 US-10-176-913-351 US-10-180-552-351 US-10-174-572-351 US-10-174-572-351 US-10-174-572-351 US-10-174-572-351 US-10-174-572-351 US-10-174-573-351 US-10-175-740-351 US-10-175-740-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-948-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351 US-10-176-993-351	NMENT Alel 89 4.0	Score 2846.6; Pred. No. 0; 0; Mismatches
2000 2000	Lion [158428]; Carl [158428]; Carl [158428]; Fritt [1684]; Carl [1684]	99.8%; milarity 99.9%; Conservative
0.000000000000000000000000000000000000	RESULT 1 US-09-965-631-3 Sequence 3, Applicati Sequence 3, Applicati BENERAL NO. US20020115 APPLICANT: FIDADIA TITLE OF INVENTION: FILE REFERENCE: LEX- CURRENT APPLICATION CURRENT APPLICATION PRIOR FILLING DATE: PRIOR PILLING DATE: PRIOR FILLING DATE: NUMBER OF SEQ ID NOS SOFTWARE: FASLESQ fo SEQ ID NO 3 LENGTH: 2853 LENGTH: 2853 TYPE: DNA US-09-965-631-3	Query Match Best Local Similarity Matches 2849; Conser

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TACTGGCGGGGTCCCGAGGACTCCGGGGGATCAGGGGACTCATTTTCAGATCACAGCATTT 180 CAGGAGGACTTTTACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCTTCTCC 240 

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ilarity 96.9%; Pred. No. 0;
Conservative 0; Mismatches
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Publication No. US20020197703A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 65552, A Human Matrix Met
TITLE OF INVENTION: Therefor
FILE REFERENCE: MPI001-025PIRNM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Matches 2379; Conserv
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LENGTH: 2469
TYPE: DNA
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US-10-163-316-3
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                                         Sequence 1, Application US/10163316

Sequence 1, Application US/10163316

Publication No. US2002019770341

GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: 65522, A Human Matrix Metalloproteinase and Uses:

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

CURRENT APPLICATION NUMBER: US/10/163,316

CURRENT FILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: 60/297,863

PRIOR PLILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2940
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2401 CCGCTGACCGTGGAGGTCCTCTCCGTGGGGAAGATGACACCGCCCCGGACCTGC
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                                                                                                                                                                                                                                                                                              Score 2296.4;
Pred. No. 0;
0; Mismatches
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LCCATION: (1)...(2940)

CTHER INFORMATION: n = A,T,C or G

US-10-163-316-1
                                                                                                                                                                                                                                                                                                80.5%;
96.9%;
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Matches 2379; Conservative
                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (472)...(2941)
FEATURE:
                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                             CCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCAGCCTTCACCACTGCC
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                                                                                          GAGACGCTGGTGGTCGCGGACGACTCAATGGTCAAGTTCCACGGCGCGGACCTGGAACAT
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38.1%; Score 1088; DB 10; Length 1104; 99.5%; Pred. No. 4e-281; ative 0; Mismatches 5; Indels 0; Garcine Construction of the control of the c	121 121 181 241 241 241 301 1301 1301 16	Db   16   16   16   16   16   16   16   1	7 7 7 8 8 8 9 9 9 11 11
CTGGCCAGGAGGCAGTGCACCAACCCTGCCAACGGGGGCAAGTACTGCGAGGA 16	2332 2392 1912 2452 1972 2512 2032 2572	TACAAA 21	2872 CCGCTGACCGTGGGGGAAGATGACACCGCCCGGACCTGC SULF 5 -09-965-631-5 Sequence 5, Application US/09965631 Patent No. US20020115842A1 APPLICANT: Friddle, Carl Johan FILE REFERENCE: Lax-021-09-27 CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US 60/236,689 NUMBER OF SEQ ID NOS: 7 SEQ ID NO 5 LENGTH: 1104 TYPE: DNA ORGANISM: homo sapiens

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APPLICANT: HINCOSE, KUNITAKA
APPLICANT: HAGOZAKI, MICHINOTI
APPLICANT: HAGOZAKI, MICHINOTI
APPLICANT: HAGOZAKI, MICHINOTI
APPLICANT: HASUSAHIMA
APPLICANT: HASUSAHIMA
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APPLICANT: MASUSAHIMA
APPLICANT: MUNDANTION: HUMBA ADANTS-1 protein, gene encoding the same,
TITLE OF INVENTION: Pharmaceutical
APPLICANT: CANOY
TITLE OF INVENTION: Composition and method of immunologically analyzin
TITLE OF INVENTION: COMPOSITION and method of immunologically analyzin
FILER REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/10/097,597
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 2184
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TATCTGCTGACGCTGCTGGCAACGGCGGCGCGACTCTACCGCCATCCCAGCATCCTCAAC
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Publication No. US20030022352Al
GENERAL INFORMATION:
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Best Local Similarity 60.7
Matches 1098; Conservative
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; LOCATION: (1)..(2184)
US-10-097-597-13
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                                                                                                                                                                       Sequence 1. Application US/09965631
Patent No. US20020115842A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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Pred. No. 8.4e-246;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 966
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y 99.8%;
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US-09-965-631-1
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Matches 957; Conserv
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APPLICANT: Inoquchi, E1j1
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Keiko
APPLICANT: Shioka, Keiko
APPLICANT: Kuno, Kouji
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TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: composition and method of
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT APPLICATION NUMBER: 09/445,023
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-10-03
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 14
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   Length 2184;
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Score 636; DB 9; 1
Pred. No. 2.8e-160;
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 Query Match 22.3%;
Best Local Similarity 60.7%;
Matches 1098; Conservative
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Sequence 13, Application US/09445023A
Patent No. US20020119167A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishida, Kukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzing human ADA
FILE REFERENCE: Q57092
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Pred. No. 2.8e-160;
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CURRENT APPLICATION NUMBER: US/09/445,023A CURRENT FILING DATE: 1999-12-03 PRIOR APPLICATION NUMBER: 1999-160422 PRIOR FILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin version 3.0 SEQ ID NO 13 LENGTH: 2184
                                                                                                                                  Query Match 22.3%;
Best Local Similarity 60.7%;
Matches 1098; Conservative 0
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Best Local Similarity 60.9%; Pred. No. 2.4e-158;
Matches 1080; Conservative 0; Mismatches 682;
  us/10097597
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(2184)
US-10-097-597-2
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OY 2302 AGCCTGCAGGCCCATCCTGGAGCCGTGACGTGGAGGTCCTCCGTGGGG 2361  11   1   1   1   1   1   1   1   1	7726	APPLICANT: Hacozaki, Eiji APPLICANT: Hakozaki, Michinori APPLICANT: Ishioka, Yukako APPLICANT: Matsushima, Kouji APPLICANT: Matsushima, Kouji APPLICANT: Kuno, Kouji TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMT FIRE REFERENCE: ASTAO2	PPLICATION NUMBER: LICHNG DATE: 2002-0 LICATION NUMBER: 09 ING DATE: 1999-12-0 LICATION NUMBER: JP LICATION NUMBER: JP ING DATE: 1997-06-0 SEQ ID NOS: 14	SEQ ID NO 2 SEQ ID NO 2 LENGTH: 2184 TYPE: DNA GRGANISM: Homo sapiens	; NAME/KEY: exon ; LOCATION: (1)(2184) US-10-097-580-2 Query Match Query Match 22.0%; Score 628.8; DB 9; Length 2184; Best Local Similarity 60.9%; Pred. No. 2.4e-158; Matches 1080; Conservative 0; Mismatches 682; Indels 12; Gaps 3;	QY         631 AAGCGTTTCGTGTCTATCCCGGGTACGTGGAGACGTGGTGGTCGCGGACGAGTCAATG 690           Db         31 AAGCGTTTGTGTCCAGCCCCGTTATGTGGAAACCATGCTTGTGGCAGACCAGTCGATG 90           QY         691 GTCAAGTTCCACGGCGGACCTGGAACATTATCTGCTGAGCGCGCTGCTGCAACGGCGGCG 750           Db         91 GTCAAGTTCCACGGCACTGGAACATTATCTGCTGCTGAACGCTGCTCGCAACGGCGGCG 750           Db         91 GCAAATTCCACGGCACTGCATTATCTGCTGCTTCATCGCTGCTCAACACGCTGCTCAATAACCAATTATCAACGTAACAATAACAATTATCAACGCTAACAATAACAATTATCAACGCTAACAATAACAATTATCAACGCTAACAATAACAATTATCAACGCTAACAATAACAATTATCAACGCTAACAATAACAATTATCAACGCTAACAATAAACAATTATCAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAACAATTAAAACAATTAAAAAA	751 CGACTCTACCGCCATCCCACCCATCAACATCGTTGTTGTCGAGCCCCCCACCACCACCCATCAACATCGTTGTGGCCAAGGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	271 271 931 331 991	Db 391 GGGATGGCTGATGTTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGAT 450

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                                                                                                        GCCATGGCTGATGTGGGTACCATGTGTGACCCCAAGAAGCTGCTCTGTCATTGAGGAC 1050
                                                    GACACAGCAATTCTTTTCACCAGACAGGACTTGTGTGGGGTCCCAGACATGTGATACTCTT 390
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   AGCATCGACATCCGCCAGCGCGGTTACAAAGGGCTGATCGGGGATGACAACTACCTGGCT 2181
                                         1528 AACATCGAAGTGAAACAGCGGAACCAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCC 1587
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Pred. No. 2.4e-158;
0; Mismatches 682;
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APPLICANT: HIROSE, KUNITAKA
APPLICANT: HAROSZAKI, MICHINOTI
APPLICANT: HAROZZAKI, MICHINOTI
APPLICANT: HAROZZAKI, MICHINOTI
APPLICANT: ISAIGA, YAKAKO
APPLICANT: MISHISHIMA, KOUJI
APPLICANT: MUNO, KOUJI
TITLE OF INVENTION: HUMAN ADAMTS-1 protein, gen
TITLE OF INVENTION: COMPOSITION and method of
FILE REFERENCE: 057092
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: UP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFUTHORS: PATENTIN VERSION 3.0
SEQ ID NOS: 14
SOFUTHORS: ALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                           AAGATGACACCCCCCGGGTCCGCTACTCCTTCT 2395
                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09445023A Patent No. US20020119167A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(2184)
US-09-445-023A-2
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
ITILE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83;
FILE REFERENCE: 09404/041001
CURRENT ELID OF THE 2002-03-25
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/059,108
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
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                      CGGGACCTGGTGTGAAGGGCAGTCTGCTGCGGTACAGCGGCACGGGCACAGCGGTGGAG 2301
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22.0%; Score 628.2; DB 12;
Best Local Similarity 57.1%; Pred. No. 3.9e-158;
Matches 1305; Conservative 0; Mismatches 913;
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; LOCATION: (460)...(3360)
US-10-105-929-1
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           CCGCTGCCCAATGCTAGCGCG-CGGCGCGCACACGCCAAGCCAGGCGCGCACACTTCT
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Patent No. US20020110894A1
GENERAL INFORMATION:
APPLICANT: Apressionen, Tiina L.
APPLICANT: Hirohata, Saroshi
TITLE OR INVENTION: Nucleic Acids Encoding Zinc Met
FILE REFERENCE: 26473/04193
CURRENT APPLICATION NUMBER: US/09/918,171A
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-08-06
PRIOR FILING DATE: 1999-08-06 Query Match 20.8%; Score 592; DB 10; Best Local Similarity 57.3%; Pred. No. 1.8e-148; Matches 1335; Conservative 0; Mismatches 905; ORGANISM: Mus musculus ADAMTS-8 NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 3638 NAME/KEY: CDS LOCATION: (278)..(2992) NAME/KEY: misc\_feature LOCATION: (3636) OTHER INFORMATION: n = T US-09-918-171A-8 US-09-918-171A-8 TYPE: DNA ö

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AATGCCTACAACCA---CACTGACCTGGATGGGAATTTCCTGCAGTGGGGTCCCCAAGTAT 2167
                               TCCGGCGTGTCTCCCCGGGACAAGTGCAAGCTCATCTGCCGAGCCAATGGCACTGGCTAC
                                                 2168 TCAGGAGTGTCCCCCCGAGACCGATGCAAGCTGTTTTGCAGAGCCCGTGGGAGGAGTGAG
                                                                                        2302 AGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTGACCGTGGAGGTCCTCTCCGTG---
                                                                            TTCTATGTGCTGGCACCCAAGGTGGTGGACGGCACGCTGTGCTCTCCTGACTCCACCTCC
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NUMBER OF SEQ ID NOS: 612
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LENGTH: 4407
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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## ALIGNMENTS

	BC003269 2931 bp mRNA linear HTC 07-AUG-2002	Mus musculus, Similar to a disintegrin-like and metalloprotease	(reprolysin type) with thrombospondin type 1 motif, 1, clone IMAGE:3499206, mRNA.	BC003269	BC003269.1 GI:14707747	HTC.	house mouse.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus	1 (bases 1 to 2931)	Strausberg, R.	Direct Submission	Submitted (20-FEB-2001) National Institutes of Health, Mammalian	Gene Collection (MGC), Cancer Genomics Office, National Cancer	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	USA	NIH-MGC Project URL: http://mgc.nci.nih.gov	Contact: MGC help desk	Email: cgapbs-r@mail.nih.gov	Tissue Procurement: Jeffrey Green M.D.	cDNA Library Preparation: Life Technologies, Inc.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Baylor College of Medicine Human Genome	Sequencing center Center code: BCM-HGSC	
BC003269	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL				~	COMMENT			•	•			

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

<sup>16154066</sup> seqs, 8097743376 residues Searched:

<sup>32308132</sup> Total number of hits satisfying chosen parameters:

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                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 9 Row: b Column: 7 This clone has the following problem: frame shifted.

Location/Qualifiers
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                    Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                             DB 11; Length 2931;
                                                                                                                                                                                                                                                                                            Score 634; DB 11; Length 29
Pred. No. 1e-125;
0; Mismatches 680; Indels
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                             : pCMV-SPORT6"
811 g .600 t
                                                                                                                                    1. .2931
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Best Local Similarity 61.0%;
Matches 1084; Conservative
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2241 2043 2001 2121 2301 1467 2821 AGAATCCGCAGCTTTAGTCCACTCAAAGAACCCTTAACCATCCAGGTTCTTATGGTAGGC 2521 AAGITIGATAAGIGIGGCGTITGTGGGAACGGTTCCACATGCAAGAAGGTGTCAGGA 2062 CICITCACCAAGCCCAIGCAIGCIACAATTICGIGGIGGCCAICCCCGCAGGGGCCICA 2242 CGGGACCTGGTGGTGAAGGGCAGTCTGCTGCGGTACAGCGGCACGGGCACAGCGGTGGAG AGCCTGCAGGCTTCCCGGCCCATCCTGAACCGCTGACGGTGGAGGTCCTCTCCGTGGGG CCAAAGAACGGAGGGAAGTACTGTGAAGGCAAACGAGTCCGCTACAGGTCCTGTAACATC 2224 GAGGACTGTCCAGACATAA---CGGAAAAACGTTCAGAGAGGAGCAGTGCGAGGCGCAC AATGAGTTTTCCAAAGCTTCCTTTGGGAATGAGCCCACTGTAGAGTGGACACCCAAGTAC TCCGGCGTGTCTCCCCCGGGACAAGTGCAAGCTCATCTGCCGAGCCAATGGCACTGGCTAC TICIATGIGCIGGCACCCAAGGIGGIGGACGCACGCIGIGCICTCCTGACICCACCICC AGCATCGACATCCGCCAGCGCGCTTACAAAGGGCTGATCGGGGATGACAACTACCTGGCT 2182 CTGAAGAACAGCCAAGGCAAGTACCTGCTCAACGGGCATTTCGTGGTGTCGGCGGTGGAG TGCTCGCGCACATGTGGTGGGGGGGGTGCAGCTGGCAGGAGGCAGTGCACCAAACCCCACC AACGGCTACAACCACAACCAACCAACCGGCTCACTCGCCGTGGCATGGGTGCCCAAGTAC GTCTGTGTCCAAGGCAAGTGCATCAAGGCTGGCTGTGATGGGAACCTGGGCTCCAAGAAG TGCACCGGGAAGGCCAAGGGACAGATGGTGCCAGACCCGCCACTTCCC~TGGGCCGGAT CTCAACAAGCACAG-----GGTGGATGGTTCCTGGGCCAAATGGGATCCCTATGGCCCC 2104 TGCTCAAGAACCTGTGGTGGTGGTGGTTCAATACACAATGAGAATGTGACAATGTGCTCAGTC CCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAGGGTGAAATACCGATCCTGCAACCTG GAGCCTGCCCCAGCTCAGCCTCCGGAAAGACTTCCGGGAGGAGCAGTGTGAGGCTTTC GCTTTTGGCGTGGGCTCCAAGCCCTGTCCTTACATGCAGTAC---TGCACCAAGCTGTGG GGCACCAGCTGTGGCGAGGGCAAGCTCTGCATCAAAGGGGCCCTGCGTGGAGAGACACAAA 2362 AAGATGACGCCCCGGGTCCGCTACTCTAT 2397 2302 2122 1822 1942 1408 1468 1582 1642 2164 1702 1762 2281 2341 1882 2461 1528 1804 1924 1351

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p mRNA linear EST 26-JUN-2001
musculus cDNA clone IMAGE:5044493
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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S NIH-MGC http://mqc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remil.nih.gov
Tissue Procurement Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)

Clone distribution: MGC clone distribution information can be http://image.llni.gov
Plate: LiAM1122 row: a column: 06
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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Pred. No. 6.6e-104;
0; Mismatches 112;
2881 CATGCTCCGACCCAAAATTAAATTCACCTACTTT 2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 743.
Location/Qualifiers
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                                                                                       BIIU3177
602889417F1 NCI_CGAP_Kid14 Mus
                                                                                                                                                         BI103177.1 GI:14554070
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Best Local Similarity 85.1%;
Matches 699; Conservative (
                                                                                                             5', mRNA sequence.
BI103177
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BG921734 681 bp mRNA linear EST 05-JUN-2001 602825569F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954456 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murićae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         And Albases 1 to 681)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs-"demail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLAM10915 row: i column: 17
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                                                                        1665
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                                                                                                                                      1666 GAGGGAGTGAGGGTGAAATACCGATCCTGCAACCTGGAGCCCTGCCCAGCTCAGCCTCC 1725
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                1607 TGCAGCTGGCCAGGAGGCAGTGCACCAACCCCACCCC-TGCCAACGGGGGGCLAAGTACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4954456"
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/organism="Mus musculus"
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Location/Qualifiers
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BG921734
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house mouse.
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KEYWORDS
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Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" 181\ c 206 g 141\ t
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                                                                                                                                                                                   1967 AGCTGCCTGTGATGGGAACCTGGGCTCCAAGAAGAGATCGACAAGTGTGGGGTGTGTG 2026
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                                                                                                     Score 512.6; DB 13; Length
Pred. No. 8.3e-100;
0; Mismatches 104; Indels
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Best Local Similarity 84.7%;
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URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa Hayashizaki,Y.
                                                                Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
ETEN Mouse ESTS Arakawa,T., et.al. 2001)
Unpublished (2001)
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="4631401M01"
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1056147
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                      2;
Length 961;
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Score 406; DB 10;
Pred. No. 7.3e-77;
0; Mismatches 100;
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14.28;
82.78;
                     Conservative
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          Similarity
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Matches 488;
 Query Match
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/db_xref="taxon:10090"
/clone="IMAGE:3153391"
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.E., Laegreid, W.W. and Reele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATCCGCCAGCGCGTTACAAAGGGCTGATCGGGGATGACAACTACCTGGCTCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 391.4; DB 10; Length 522;
Pred. No. 8.4e-74;
0; Mismatches 66; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF078689 544 bp mRNA linear
22090 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF078689.1 GI:10872519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%;
86.7%;
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Best Local Similarity 86.7
Matches 431; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 627)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oilgo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

159 c 177 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary
/tissue_torigin."
/tab_host="BH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1850 AGCTCATCTGCCGAGCCAATGGCACTGGCTACTTCTATGTG-CTGGCACCCAAGGTGGTG 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCTAATCTGCCGAGCCAATGGGACTGGCTACTTCTATGTAACTAGCACCTAAGSTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GCTACAATTITGIAGGCGCCACCCTGCTGGCGCCTCCAGCATGATATCCGTCAGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGCTGCTGCGACGGGAATCTGGTGCTCCAAGAAGAAATTTGACAACATGTGGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2262 CAGICIGCIGCGGTACAGCGGCACGGGCACAGCGGTGGAGAGCCTGCAGGCTTCCCGGCC
                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tyssue Procourement: Gilbert Emith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 627;
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llarity 83.6%; Pred. No. 1.3e-62;
Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM8537 row: a column: 16 High quality sequence stop: 530. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    1. 627
/organism="Mus musculus"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:3491991"
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504; Conserv
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                                                      REFERENCE
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                                                                                    Fax: 40. /oz 4. sus.

Fax: 40. /oz 4. sus.

Email: smith@email.marc.usda.gov
Single.pass sequencing. Bases called and alt_trimmed with phred
v0.980904 e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR PRIMETS
PCRARACGTAGACGATA
FORMARD: GGTATACGAGACACATA
BACKWARD: GTTTTCCCAGTCACACAGG
Plate: 43 row: P column: 17
Seq primer: ATTTAGGTGACACATAGG

Location/Qualifiers

1. 544
/organism="sus scrofe"
/organism="sus scrofe"
/db.xref="taxon:9823"
/clone_lib="Marc 2pig"
/lishubct="pooled"
/lab.host="booled"
/lab.host="Doublob"
/note="Voortor: DCMV SPORT6; Site_1: NotI; Site_2: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE281680 627 bp mRNA linear EST 26-OCT-2000 601099657F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491991 5',
                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Vector: pGMV SPORT6; Site_1: NotI; Site_2: Sal; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 349.6; DB 12; Length 544; Pred. No. 8.1e-65; 0; Mismatches 49; Indels 0;
                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:9156727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.3%;
Best Local Similarity 88.6%;
Matches 379; Conservative
Contact: Smith TPL
                                 PO Box 166, Clay C
Tel: 402 762 4366
Fax: 402 762 4390
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., While, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                        30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 11 2brafishWatson.wustl.edu
CDNA Library Preparation: Ning Wu. CDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Research Genetics web
                                                                                                                                                                                                                                              BE016461
fk73d10.x1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 3' similar to TR:054768 O54768 A DISINTEGRIN AND METALLOPROTEASE WITH THROWBOSPONDIN MOTIFS ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Site_1: ECORI; Site_2: Noti; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - Oligo(GT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified prima vector. Library is non-normalized. Library was constructed by Ming Wu. NOTE: Clones from this library are only available thru Research Genetics (www.resgen.com)."
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/db_xref="taxon:7955"
/dbone_lib="zebrafish Research Genetics C32 fin"
/tisone_lib="reperior"
/tisone_rype="fin"
/lab_host="GeneHogs (HS996, a phage-resistant isolate of
                                       2382 CCGCTACTCCTTCTATCTGCCCAAAGAGCCTCGGGAGGACAAGTCCTCTCATCCCAAGGA 2441
480 CATCCTGGAGCCACTCACCGTGGAGGTCCTGACGGTGGGGAAGATGACACCGACC---GT 536
                                                           note="Vector: pT7T3D-Pac with a modified polylinker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 8e-48;
0; Mismatches 239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      address: http://www.researchgenetics.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU Zebrafish EST Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7 ET from Amersham
High quality sequence stop: 489.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                       BE016461
BE016461.1 GI:8280907
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BI819909 738 bp mRNA linear EST 04-OCT-2001
603035454F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5176476 5',
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1439 row: 1 column: 13
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                             301 GAGGACAAGCGGCTGATGTCCTCCATCCTGACCTCCATCGACGCCTCCAACCCTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .213 GCCTGCAGTGCTGCCATCATCACGACTTCCTGGACAGCGGGCACGGTGACTGCCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/db_xref="taxon:9606"
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Location/Qualifiers
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BI819909
BI819909.1 GI:15931459
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                              GIGGGGIGIGIGGGGGAGACAAIAAGAGCIGCAAGAAGGIGACIGGACICIICACCAAĠC 2074
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9
                                                                                                                                                                             9.2%; Score 263.4; DB 13; Length 738; illarity 63.1%; Pred. No. 2.9e-46; Conservative 0; Mismatches 251; Indels 6;
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/clone="IMAGE:5176476"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                              Similarity
                                                                                                                                                 169
                                                                                                                                                                                                        Matches 440;
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BI733795
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library. 1 others
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                                                                                                                                                                    1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1914 row. column: 09
High quality sequence stop: 746.
Location/Qualifiers
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                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5359712"
/clone_lib="NIH_MGC_94"
BI733795.1 GI:15710808
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                                                       house mouse.
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Rakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyas, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koyas, S., Matsuyama, T., Myazaki, A., Nomura, K., Ohno, M., Royas, S., Matsuyama, T., Matsuyama, T., Salto, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Sano, H., Sasaki, M., Ragami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y., Takehashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

On Jun 30, 2000 this sequence version replaced gi:8885326.
Contact: Yoshihide Hayashizaki M. Sasarch Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-2021
Tel: 81-45-503-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB220373 RIKEN full-length enriched, adult male acrta and vein Mus musculus cDNa clone A530059019 3' similar to AF140673 Mus musculus putative secreted metalloprotease ADAWTS5 (Adamts5) mRNA, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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                                                                                                                                                 AGAAGAGATTCGACAAGTGTGGGGTGTGTGGGGGGAGACAATAAGAGCTGCAAGAAGGTGA 2056
                                                                                                                                                                                                                                                                                                                                           CCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGGCTGATCGGGGATGACAACTACC 2176
                                                  ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
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418 GCTACTTTTTGGTCTTACAGCCCCAAGGTTGTAGATGGCACTCCCTGTAGTCCAGACTCTA
                                                                         CTGGACTCTTCACCAAGCCCATGCATGGCTACAATTTCGTGGTGGCCATCCCCGCAGGCG
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken Contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lone_lib="RIKEN full-length enriched, adult male aorta
                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .041 CATTGAGGACGATGGGCTTCCATCAGCCTTCACCACTGCCCACGAGCTGGGCCACGTGTT 1100
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llarity 60.9%; Pred. No. 1.7e-42;
Conservative 0; Mismatches 257; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="aorta and vein"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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                                                                                                                                                                                                          further details.
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RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                         /tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="lal108"
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
/note="Site_1: Sal1; lim Mouse Genome Encyclopedia
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1018 GACCCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCAGCCTTCACCACT
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                                                                                                                   1. .660
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C230053J22"
                                                               e mouse tissues.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Upublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN.Genomic.
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

M. S. Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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URL:http://genome.gsc.riken.go.jp/,
URL:http://genome.gsc.riken.go.jp/,
Carninci,P., Shibata,Y., Hayacsu,M., Suqahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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BB651049 GI:16485303
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Fax: 81-45-503-9216
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TITLE JOURNAL COMMENT

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Arakawa,T., Carnini,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hlamoto,K., Hoti,F., Ishli,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyan,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,P., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                         BB642806 BIKEN full-length enriched, adult retina Mus musculus cDNA clone A930039D02 5', mRNA sequence.
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URL:http://genome-resegsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare [Iull-length cDNa libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1318 GCCAGCTACACCCTGAGCCAGCAGTGCGAGCTGGCTTTTGGCGTGGGGCTCCAAGCCCTGT 1377
                                  /clone_lib="RIKEN full-length enriched, adult_retina"
/tissue_type="retina"
/dev_stage="adult"
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        prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], CDNA was
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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/lab_host="DH10B (T1 phage-resistant)"
/hotb="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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143 c 180 g 135 t 304 others
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                                                                                                                                                                                                                                                       Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 8.5%; Score 241.8; DB 14; Length 951; Similarity 62.2%; Pred. No. 1.4e-41; 97; Conservative 0; Mismatches 238; Indels 3;
                   AGENCOURT_8920927 NCI_CGAP_Co24 Mus musculus cDNA clone. IMAGE:6395437 5', mRNA sequence.

    .951
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6395437"
                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 644.
Location/Qualiflers
                                                                         BQ930852
BQ930852.1 GI:22345883
                                                                                                                      house mouse.
Mus musculus
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TITLE
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BQ930852
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

En (1602)

En (1603)

In (1603)

In (1603)

In (1603)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.inh, gov

Tissue Procurement: DCTD/DPP

CDNA Library Preparation: Life Technologies, Inc.

CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:

http://mage.llnl.gov

Plate: LLAM9592 row: b column: 01

High quality sequence stop: 642.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             BF033017 945 bp mRNA linear EST 20-OCT-2000 601455701F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859104 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3859104"
/clone="lib="NIH_MGC_66"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
/note_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
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538 CATGACATTGTCACAATTCCTGCAGCCACCAACATTGAAGTGAAACATCGGAATCAA 597
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                                  2089 AATTICGIGGIGGCCAICCCCGCAGGCGCCTCAAGCAICGACAICCGCCAGGGGGGGTTAC
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Pred. No. 2.3e-39;
0; Mismatches 251;
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/db_xref="taxon:9606"
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BF033017.1 GI:10740729
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Best Local Similarity 61.8%;
Matches 422; Conservative
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1834 CCCCGGGACAAGTGCAAGCTCATCTGCCGAGCCAATGGCACTGGCTACTTCTATGTGCTG 1893
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                                         1714 AGCTCAGCCTCCGGAAAGAGCTTCCGGGAGGAGCAGTGTGAGGCTTTCAACGCTACAAC 1773
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                                                                                                                                                                               1774 CACAGCACCAACCGGCTCACTCTCGCCGTGGCTGGGTGCCCAAGTACTCCGGCGTGTCT
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GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

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Perfect score:
Sequence: Scoring table: Searched:

4109280 Total number of hits satisfying chosen parameters:

Word size :

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

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Pred. No. is the number of results predicted by chance to have a

em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	AJ315733	AX342635	AX31986U Sequen	AFUUZ988 HOMO	ACOSSTS HOMO	AP003459	AC025130 Homo	AC023429 Homo	AC101990 Mus m	AC126507 Rattus	AC125507 Ratt	8C10138	AC099229 Rattus no	AC022377 HOMO	AC018831	AC026218 HOMO	AC069271 Homo	AL139.159 Human	AC124	A:070	AF07258	X7487X	#C001	AB026	AE001:	273963 Hu	Continuation (	NL355321 Human	Nº004274 Oryza	ACU92553 Oryza ; C021/16 Homo 2	AL136092	AC120147 Oryza	ACU: 4890 Oryza	AC0231294 Human AC023025 Homo s	AC112482 HOMO S	AC117504 Homo sa		ALIGNMENTS		RNA linear PRI	isintegrin 15			metalloprotease; thrombospondin.		Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	
	a :	HSA315733	AX342635	AA319860	AC025130	AC023429	AP003459	AC025130	AC023429	AC101990	AC126507	AC126507	0 BC00966		AC022377	AC018831	AC026218	AC069271	AL139159	AC124158	AF070953	AF072582	HVACXPII		AB026907	AE001884	HSN62C4	AL583837	AL359821	AP004274	AC092553	AL136092	AC122147	AC078890	7	11248	AC11750	AL6714	ALIGN		2853			در	ıntegrin; m		Chordata; Primates;	
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a Query	Match	96.2	73.2	31.6	31.6	28.1	27.2	12.5	10.1	5.6	2.1	 	1.2	8.0	0.8	æ .	9 6	0.8	8.0	8.0	0.7	0.7	0	0.7	0.7	. 0 . 7	. 0		0.7	0.0		0.7	0.7			0.7	0.7	0.7			HSA315733	Homo sapien	gene). AJ315733	33.1	ס	Homo sapier	Eukaryota; Mammalia; E	
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/ LEADS 12 to 1- "MILLIAFAGRTAGGSEPEREVVVP IRLDPDINGRRYWRG
PEDSGDOGLIRQTITALPDAGFLAPARSTBEHGYPLOGTIGGSSDLRRCF
YSGDVNAREPDSFAAVSLCGGLRGAGGYRGAEVYISPLPNASPPAAORNSGGAHLLQRR
GVPGGPSGDPTSRCGYARGARYAILGALDPYKRARGFGESRSRRRSGRARREVSIPR
GVPGGPSGDPTSRCGYARMPALLALDPYKRAGFGESRSRRRSGRARREVSIPR
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SGLOKRANDCKGSAGQRTYPKDDARHRVVETOACGEPCPTWELSAWSPCSKSCGRGFG
SGLOKRANDCKGSGAGGREVPROPELDFCVLRPC
                                                                                                                                     Direct Submission
Submitted (26-JUN-2001) Cal S., Biochemistry and Molecular Biology,
University of Oviedo, Campus del Cristo, Asturias. 33006, SPAIN
Location/Qualifiers
1. .2853
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with Gisintegrin and thrombospondin-1 domains Gene 283 (1-2), 49-62 (2002)
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7 CCTCAAAGGGGCCTGCGTGGAGAGACACAACCTCAACAAGCACAGGGTGGATGGTTCCTG	7 GECCAAAIGGGAICCCIAIGGCCCCIGCTCGCGCACAIGTGGTGGGGGGGGTGCAGCTGGC	7 CAGGAGGCAGTGCACCAACCCCCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAG 	7 GGTGAAATACCGATCCTGCAACCTGGAGCCCTGCCCAGCTCAGCCTCCGGAAAGAGCTT	CCGGGAGGAGCAGTGTGAGGCTTTCAACGGCTACAACCACAGCACCGACCG	CGCCGTGGCATGGGTGCCCAAGTACTCCGGGTGTCTCCCCGGGACAAGTGCAAGGTCAT 	157 CTGCCGAGCCAATGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGTGGAGCGCACCACCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	GCTGTGCTCTCCTGACTCCACCTCCGTCTGTGTCCAAGGCAAGTGCATCAAGGCTGGCT	TGATGGGAACCTGGGCTCCAAGAAGATTCGACAAGTGTGGGGTGTGTGGGGGAGACAA 	TAAGAGCTGCAAGAAGGTGACTGCACTCTTCACCAAGCCCATGCATG	GGTGGCCATCCCCGCAGGGCGCTCAAGCATCGACATCCGCCAGGGGGTTACAAAGGGGT	7 GAICGGGGAIGACAACTACCIGGCICTGAAGAACAGCCAAGGCAAGIACCIGCICAACGG	7 GCATTITCGTGGTGGTCGGCGGGGGGGGCGCGGGGGGGGGG	7 CAGCGGCACGGCACAGCGGTGGAGAGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCTT	37 GACCGTGGAGGTCCTCTCCGTGGGAAGATGACACGCCCCGGGTCCGCTACTCTA	97 TCTGCCCAAAGAGCCTCGGGAGACAAGTCCTCTCCATCCCAAGGACCCCCGGGGACCCTC	57 IGTCTIGCACAACAGCGTCCTCAACCAACCAGGGGGGGGGCGGACCGACGGCCGACCGA	7 CCTGCAGGCTGGGTGGCAGCTGGGGGCCGTGCTCCGCGAGCTGCGCAGTGGCCT	7 GCAGAAGGGGGGGGGGGGCTCCGGCGCCGGGCAGGGCCCTGCCTG
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Tubouley, C. M., Delegeane, A. M., Baughn, M. R., Nguyen, D. B., Lee, E. A., Tribouley, C. M., Delegeane, A. M., Baughn, M. R., Nguyen, D. B., Lee, E. A., Hafalia, A., Khan, F. A., Wallia, N. K., Yao, M. G., Lu, D. A., Patterson, C. Tang, Y. T., Malsh, R. T., Azimzal, Y., Ramkumar, J., Xu, Y. and Reddy, R. Patent: WO 0198468-A 32 27-DEC-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 2930
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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RP11-211H6 map 11,
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Chemistry: Dye-terminator Big Dye; 100% of reads
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/note="assembly_fragment"
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83803 98393; conti
98394 98493; gap of
98494 117356; conti
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83702: con+
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68888: cont
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23535: 73535: 735
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4052: con
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40941: con
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                                                                                                                                                                                                                                                                                            Litton, B., Litton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Burket, G., Canlay G., Castle, A., Choepel, Y., Colagelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galaqan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, M., Howland, J.C., Illew, T., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRcque, K., Lawazares, R., Landers, T., Leboczky, J., McChan, F., Lawazares, R., Macdoria, M., McEwan, P., McGurk, A., McKernan, K., McPhan, S., Mandou, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T., O'Connol, P., Palani, J., Pantos, L., Waymon, C.H., O'Connor, T., O'Connol, P., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vonnier, C., Wilson, B., Wu, X., Wyman, D., Yewi, S., Wilson, B., Wu, X., Wyman, D., Yewi, S., Woung, C., Rulmer, A. and Zody, M.
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Direct Submission

Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 17295)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
McGarthy, M., McEwan, P., McGurk, A., McKernan, K., Merton, E.,
McGarthy, M., McEwan, P., McGurk, A., McKernan, K., Merton, E.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Ollivar, T.M., Olliver, J., Peterson, R., Pisani, C., Pollara, Y., Raymon, C.H., O'Connor, T., O'Donnell, P.,
Stange-Thomann, N., Stoyanovic, N., Subrearson, K., Trigilio, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Young, G., Zalnoun, J., Zimmer, A. and Zody, M.,
Nivert sinhaisain.
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Sesarch, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 3, 2000 this sequence version replaced gi:7158941.
All repeats were identified using RepeatMasker:
Smit. A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                         Lander, E.
                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, Homo sapiens chromosome 11, clone RP11-211H6
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      HTGS_PHASE1; HTGS_DRAFT
                                                                                                                         Mammalia; Eutheria; Pr. 1 (bases 1 to 172905)
                                                                                                                                                                                                                                                                            (bases 1 to 172905)
                                                            ORGANISM
                                                                                                                                                                                                         TITLE
JOURNAL
REFERENCE
AUTHORS
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COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Assembly program: Phrap, version 0.960731
Consensus quality: 161899 bases at least Q40
Consensus quality: 167402 bases at least Q30
Consensus quality: 169801 bases at least Q30
Insert size: 177000; agarose-fp
Insert size: 17105; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 14591 bp in length p of 100 bp contig of 18863 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117357 117456: gap of 100 bp
117457 140589: contig of 23133 bp in length
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140690 172905; contig of 32216 bp in length.
Location/Qualifiers
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contig of 10580 bp in length
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contig of 14714 bp in length
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f 1316 bp in length
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of 3892 bp in length
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of 1222 bp in length
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f 1193 bp in length
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14949: contig of 6805 bp in length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
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/note="assembly_fragment"
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?737. .4052
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122 1343: contig of
1344 1443: gap of
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122. .1343
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78867 ACATTATCTGCTGACGCTGCTGGCAACGGCGGCGCGACTCTACCGCCATCCCAGCATCCT 78808
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AC023429.19 GI:13569974
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                     CTACTACTACTGGCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTCAGATCACAGC 176
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                                             70362. .40941
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Matches 902; Conservative
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ACO23429 170682 bp DNA linear HTG 10-APR-2001
Homo sapiens chromosome 11 clone RP11-121M22, WOKKING DRAFT
SECUENCE, 7 unordered pieces
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HOMO sapiens.
HOMO sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I bases 1 to 170682)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Fauikner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M.,
Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D.,
Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onpublished

(bases I to 170682)

Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.

Direct Submission
Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                             ........ Genome Center
Center: Stanford DNA Sequencing and Technology Development
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Center clone name: RP11-121M22

Sequencing Vector: Minp18; X02513

Sequencing Vector: Minp18; X02513

Chemistry: Dye-primer; 12% of reads
Chemistry: Dye-primer; 12% of reads
Assembly program: Phrap; version 0.990319

Consensus quality: 167205 bases at least Q30

Consensus quality: 167255 bases at least Q30

Consensus quality: 167218 bases at least Q30

Consensus quality: 167255 bases at least Q30

Consensus quality: 167255 bases at least Q30

(unsert size: 170082; sum-of-contigs

(unsert size: 170082; sum-of-contigs

(unsert ycoverage: 9.0x in Q20 bases; sum-of-contigs

* NOTE: This is a "working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Apr 10, 2001 this sequence version replaced 91:13:62078.
GAACAAAGTGAGTGACAAGCACCCCGAGTACTGGGACACTGCCATCCTCTTCACCAGGCA
                                                                                                                                          CAAGGTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCT
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ARVUJ459
Homo sapiens genomic DNA, chromosome 11q, clone:RP11-211H5, complete sequence.
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Homo sapiens genomic DNA
Published only in Database (2001)
2 (bases 1 to 28000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hattori,M., Ishii,K., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (29-MAR-2001) Masshira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mal1:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Mar 7, 2002 this sequence version replaced gi:13488920.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         TTTCGTGTCTATCCCGCGGTACGTGGAGGCCTGGTGGTCGCGGACGAGTCAATGGTCAA
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    /organism="Homo sapiens"
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    /chromosome="11"

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Location/Qualifiers
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/note="assembly_name:Contig25"
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/note="assembly_name:Contig26"
/7166. .21089
/note="assembly_name:Contig27"
21190. .3414b
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48663. .109179
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ö 2079 GCATGGCTACAATTTCGTGGTGGCCATCCCCGCAGGCGCCTCAAGCATCGACATCCGCCA 2138 ; Length 28000; Indels δλ

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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 172965)

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Voung, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (J4-Nuc-Sonoz) Whitehead Institute/MIT Center for Genome Submission

Submitted (J4-Nuc-Sonoz) Whitehead Institute/MIT Center for Genome Coulmer, A.I. repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp:genome.washington.edu/FW/RepeatMasker:html

Http://ftp:genome.washington.edu/FW/RepeatMasker:html
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Bodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Galagam, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, P., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancageres, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, R., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miroda, C., Minenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roya, L., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainou, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Direct Submission, Marcher, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 211_H_6
Squencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161899 bases at least Q40
Consensus quality: 167402 bases at least Q30
Consensus quality: 167402 bases at least Q30
Insert size: 177000; agarose-fp
Insert size: 177000; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
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Web site: http://www.seq.wl.mit.edu
Wordtact: sequence.submissions@genome.wl.mit.edu
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WORKING DRAFT
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhqalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-211H6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGGTCCCTGCCTGTGATGCAGCCCATCGGCCCGTGGAGACACAAGCCTGCGGGGAGCC 2678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3833 GGACCCCCGGGGACCCTCTGTCTTGCACACGCGTCCTCAGCCTCTCCAACCAGGTGGA 3892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCTGCGGCAGTGGCCTGCAGAAGCGGGCGGTGGACTGCCGGGGCTCCGCCGGGCAGCG 2618
                    3533 GCGCGCTTACAAAGGGCTGATCGGGGATGACAACTACCTGGCTCTGAAGAACAGCCAAGG 3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCATCCTGGAGCCGCTGACCGTGGAGGTCCTCTCCGTGGGGAAGATGACACCGCCCCG 2378
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                                                                                                                                                                                                                                                                                                      CAAGTACCTGCTCAACGGGCATTTCGTGGTGTCGGCGGTGGAGCGGGACCTGGTGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCAGTCTGCTGCGGTACAGCGGCACGGGCACAGCGGTGGAGAGCCTGCAGGCTTCCCG
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Homo sapiens chromosome 11 clone RP11-211H6 map 11, 8
SEQUENCE, 16 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Research

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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL REFERENCE REFERENCE AUTHORS

AUTHORS

DEFINITION

RESULT 8 AC025130

ACCESSION

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Gaps

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ACO23429 170682 bp DNA linear HTG 10-APR-2001
Homo sapiens chromosome 11 clone RP11-121M22, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                              CAAGTACCTGCTCAACGGGCATTTCGTGGTGTCGGCGGTGGAGCGGGACCTGGTGGTAA 2258
                                                                                                                                                                                                                                                                                                                                    2139 GCGCGGTTACAAAGGGCTGATCGGGGATGACAACTACCTGGCTCTGAAGAACAJCCAAGG 2198
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                                                                                                                                                                                                                                                          2079 GCATGGCTACAATTTCGTGGTGGCCATCCCCGCAGGCGCCTCAAGCATCCACATCCGCCA 2138
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Bruno,D., Conn.L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J. Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
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Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Maco, J., Komp, C., Kortler, S., Lam, B., Marathe, R., Järrada, M., Morehouse, A.J., Nguyen, M., Oeffner, P., Pelm, C.J., Ram:rez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Apr 10, 2001 this sequence version replaced gi:13362078
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                                                                                                                                                                                  Score 358; DB 2; Length 172905; Pred. No. 2.1e-183;
                                                                                                                           1502 others
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens.
         98494. .117356
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117457. .140589
/note="assembly_fragment"
140690. .172905
/note="assembly_fragment"
a 41333 c 39516 g 46194 t
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                               100 bp
f 10580 bp in length
100 bp
f 13852 bp in length
                                                                                   2 121: gr of 100 bp
122 1343: contig of 1222 bp in length
344 1443: gap of 100 bp
444 2536: contig of 1193 bp in length
2637 2736: gap of 100 bp
4652 2736: contig of 1316 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83702: contig of 14714 bp in length
802: gap of 100 bp
98393: contig of 14591 bp in length
493: gap of 100 bp
117356: contig of 18863 bp in length
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13895 bp in length
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contig of 3892 bp in length
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14949: contig of 6805 bp in length
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54994 . 6888
/note="assembly_fragment"
68989 . 83702
/note="assembly_fragment"
83803 . 98393
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/note="assembly_fragment"
4153. 8044
/note="assembly_fragment"
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/note="assembly_fragment"
2737. 405?
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15050. .23535
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                                                                                                                                                                                                                                                                                                                                                           2 30361: gap of 100
2 40941: contig of 10
42 41041: gap of 100
42 54893: contig of 11
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
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122. .1343
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30362. .40941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="11"
/map="11"
                                                                                                                                                                                                                                                                                14950 15049: gap of
15050 23535: con
                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
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4153 8044: cor
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1378 CCTTACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTG 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                  DEFINITION
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JOURNAL
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AUTHORS
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REFERENCE
                                                                                                                                                                                                                                                           RESULT 10
AC101990
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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            Center clone name: 0.7

Center clone name: 0.7

Center clone name; 0.7

Center clone name; 0.7

Sequencing Vector: M13mp18; X02513

Chemistry: Dye-terminator Big Dye; 86% of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Assembly program: Phrap; version 0.990319

Consensus quality: 167216 bases at least 0.40

Consensus quality: 167218 bases at least 0.40

Consensus quality: 167218 bases at least 0.20

Insert size: 170423; agarose-fp
Insert size: 17082; sum-of-contigs
Ouality coverage: 9.0x in 020 bases; sum-of-contigs

* NOTE: This is a "working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbhirary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will.

* be preserved.
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gap of unknown length
contig of 14317 bp in length
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of 60517 bp in length
unknown length
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1956: gap of unknown length
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of 5109 bp in length
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1. .1856
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ilarity 100.0%; Pred. No. 3.4e-145;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
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/note="assembly_name:Contig26"
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109280, .170682
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/note="assembly_name:Contig27"
21190, .34145
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/note="assembly_name:Contig29
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/db_xref="taxon:9606"
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contig (
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gap of
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Direct Summission

Direct Summission

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Barren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barran, B., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Hunce, M., Illev, I., Johnson, R., Lindblad Toh, K., Liudblad, Toh, K., Liudblad, Toh, K., Liudblad, Toh, K., Liudblad, MacLean, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Moneus, L., Mihova, T., Nobu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Scaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
                                                                                                                                                                                                                                                                                                                                                                          AC101990 182656 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP24-371J2, WORKING DRAFT SEQUENCE, 16 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
TGCCAGACCCGCCACTTCCCCTGGGCCGATGGCACCAGCTGTGGCGAGGGCAAGCTCTGC
                                                                                                                                                                                                                      1498 CTCANAGGGGCCTGCGTGGAGACACAACCTCAACAAGCACAGGGTG 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC101990.2 GI:22381363
HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 182656)
Birren, B., Linton, L., Nusbaum, C., Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-371J2
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COMMENT

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Query Match
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ORIGIN
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AC126507/c
LOCUS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
OR Aug 21, 2002 This sequence version replaced gi:17060766.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fpgenome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flinished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 172000; agarose-fp
Insert size: 181156; sum-of-contigs
Quality coverage: 8.1 in Q20 bases; agarose-fp
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                   Center clone name: 371_J2

Center clone name: 371_J2

Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 178030 bases at least Q30

Consensus quality: 180647 bases at least Q20
                                                                                                                                                                                                                 77468 77567: gap of 100 bp
77568 108724: contig of 31157 bp in length
108725 108824: gap of 100 bp
108825 182656: contig of 73832 bp in length.
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contig of 12226 bp in length:
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57612: contig of 13925 bp in length
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of 1077 bp in length
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f 1759 bp in length
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f 1450 bp in length
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f 1846 bp in length
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contig of 3104 bp in length
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462 1538: contig of
1539 1638: gap of 10
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/clone="RP24-371J2"
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43587;
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6893: ~
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14977: con
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43688 576
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*** SEQUENCING IN PROGRESS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 16446 ACCATGTGACCCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCT**CCATCAGCC 16505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Loases 1 to 178764)
Muzny,D.M., Adams,C., Adio-Oduola,B., All-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burket,C., Burrell,K.L., Byrd,K.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chrvez,D.,
Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6%; Score 74; DB 2; L
100.0%; Pred. No. 2.4e-28;
iive 0; Mismatches 0;
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108825. .182656
/note="assembly_fragment"
a 41160 c 39770 g 48758 t
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12685. 14977
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15078. .18181
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43688. 57612
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/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
5048. .6893
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/note="assembly_fragment"
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1069 TTCACCACTGCCCA 1082
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
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Gabisi, A., Gao, J., Garcia, Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, M., Gunaratne, P., Hane, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Harlaws, A., Harnandez, J.,
Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Johnson, C., Hollins, E.,
Karlsson, E., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
I.J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, M., Martindale, A., Martinez, E.,
Maheshwari, M., Mapus, P., Martin, R., Martindale, A., Martinez, E.,
Mansenwari, M., Mapus, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., McLeed, M. P., Martin, R., Martinez, E.,
Massey, E., Mawhiney, E., McLeed, M. P., Meador, M., Nguyen, N.,
Oragung, N., Oveledo, R., Patens, P., Patton, S., Savery, G.,
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Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tamerisa, R., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, D.,
Williams, G., Williamson, A., Wilcey, R., Wooden, S., Worley, R.,
Williams, G., Williamson, A., Wilcey, R., Wooden, S., Worley, R.,
Prant, P., Rober, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wilcey, R., Wooden, S., Worley, R.,
Prant, H., Sham, S., Rober, R., Washington, C., Watlington, S.,
Weinston, R., Sham, R., Shon, J., Zorrilla, S., Nelson, D.,
Weinston, R., Sham, R., Shon, J., Zorrilla, S., Nelson, D.,
Weinston, R., Weinston, R., Watlington, S., Watling, S.,
Weinston, S., Watler, R., Watling, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 178764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a "working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124573 bases at least 040
Consensus quality: 131850 bases at least 020
Consensus quality: 137700 bases at least 020
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GZFU
Center clone name: CH230-254N12
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE AUTHORS TITLE

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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ONTE: This is a "working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178764)
Worley, K.C.
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Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
Submitted (24-JUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big bye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 124573 bases at least Q40 Consensus quality: 131850 bases at least Q20 Consensus quality: 137700 bases at least Q20
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1137: gap of unknown length
2256: contig of 1113 bp in length
2350: gap of unknown length
3579: contig of 1129 bp in length
4874: contig of 1195 bp in length
4974: gap of unknown length
674: contig of 1195 bp in length
6525: contig of 1551 bp in length
6525: qap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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Center clone name: CH230-254N12
------ Summary Statistics
Sequencing vector: Plasmid;
             Howard, S., Huber, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 178764)
Worley, K.C.
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AUTHORS
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alicoka, J.R., Ayele, M., Banks, T., Barbaria, J., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Bunde, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. D., Bunket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A., Doulawaite, K.J., Draper, H., Dugan-Rochas, S., Durbin, K.J., Earnbart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Garcia, A., Garner, T., Garza, N., Gill, R., Garnell, J.H., Guevara, W., Gunaratne, P., Hamilton, K., Harris, C., Harris, K., Harris, C., Harris, K., Hernandez, J., Holloway, C., Hollins, B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 150003 GTCTGTGTCCAAGGCAAGTCCAAGGCTGCTGTGATGGGAACCTGGGCTCCAAGAAG 149944
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Biren, Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., doubkgalter, B.,

Brown, A., Campoplano, A., Chang, J., Chazaro, B.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ferrelra, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

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Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D.,

Oliver, J., Peterson, R., Phunkhang, P., Plerre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,

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Zalinoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct, Submission

Nesearch, 320 Charles Street, Cambridge, MA 02141, JSA

Research, 320 Charles Street, Cambridge, MA 02141, JSA
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Mus musculus clone RP24-371J2, WORKING DRAFT SEQUENCE, 16 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1887 188926: gap of unknown length 927 188522: contig of 9596 bp in length 18523 188622: gap of unknown length 18623 178764: contig of 10142 bp in length. Location/Qualifiers 1.178764 (Adultises 1.178764) (Adultises 1.178764) (Adultises 1.278764) (Adultises 1.2787644) (Adultises 1.2787644) (Adultises 1
                                                                                                                                                           134187: gap of unknown length
143851: contig of 9664 bp in length
153951: gap of unknown length
151799: contig of 7748 bp in length
151799: qap of unknown length
158926: contig of 7027 bp in length
158926: gap of unknown length
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47487 a 39119 c 38897 g 45423 t 7838 others
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                                          contig of 6995 bp in length
gap of unknown length
contig of 8968 bp in length
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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unknown length
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100.0%; Pred. No. 5.7e-12;
Live 0; Mismatches 0;
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                                                                                                                              134087:
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Best Local Similarity 100.C
Matches 44; Conservative
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Mus musculus, Similar to a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1), clone IMAGE:3491991, mRNA,
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       22655 22754: gap of 100 bp 22755 31261: contig of 8507 bp in length 31262 31361: gap of 100 bp 31362 31361: gap of 100 bp 31362 43587: contig of 12226 bp in length 43588 43687: gap of 100 bp 4368 57612: contig of 13925 bp in length 57613 57712: gap of 100 bp 77467: contig of 13755 bp in length 77468 77557: gap of 100 bp 77568 108724: contig of 31157 bp in length 108725 10824: gap of 100 bp 100 bp 108725 10824: gap of 100 bp 100 bp 108725 10824: gap of 100 bp 100 bp 100 bp 1008725 10824: gap of 100 bp 100 bp 1008725 10824: gap of 100 bp 100 bp 1008725 100824: gap of 100 bp 100 bp 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 1008725 
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ture 108825, 18256
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/note="assembly_fragment"
22755. 31261
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/note="assembly_fragment"
57713. 77467
/note="assembly_fragment"
77568. 108724
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3498. .4947
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31362. 43587
/note="assembly_fragment"
43688. 57612
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/note="assembly_fragment"
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'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-371J2"
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., FitzGerald, M., Gage, D., Calgan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Macdonald, P., Major, J., Matthews, C., McChan, C., Macdonald, P., Major, J., Matthews, C., McChan, J., Maylor, J., Nguyen, C., Nicol, R., Mihova, T., Maran, C. H., O'Connor, T., O'Connell, P., O'Meil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wman, D., Young, G., Zainoun, J., Zembok, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17060766.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
Contact requence_tubmissions@genome.wi.mit.edu
Conter project Information
Center project name: 117833
Center clone name: 311_15.

Sequencing vector insandi, no% of reads
Sequencing vector: Plasmid; no% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 178030 bases at least Q30
Consensus quality: 179964 bases at least Q30
Consensus quality: 180647 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 181156; amn-of-contigs
Quality coverage: 8.1 in Q20 bases; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
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of 1759 bp in length
100 bp
of 1450 bp in length
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contig of 2293 bp in length
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10395: contig of 3402 bp in length
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18181: contig of 3104 bp in length
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6893: con
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ROD 07-AUG-2002

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Norway rat.
Rattus norvegicus
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                          ORGANISM
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     SOURCE
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QRGYKGLIGDDNYLALKNSQCKYLLNHFWYSAPREDLYNKGSVLRYSGTGANASSLO
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HTG: HTGS PHRES
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KRACGEPCPTWELGNWSPCSKSCGRGFKRRPLKCVGHGGRLLARDQCDLRRKPQELDF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3927)
Strausberg,R.
                                                                                                                                                                                                                     WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 9430
Web site:
Charact: (Dickson, Mark) mcd@epaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                     Submitted (29-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone="IMAGE:3491991"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clone) outgrowth infected with the virus MMTV."
/clone_lib="MOI_CGAP_Lu29"
/lab_host="DH108"
/note="MOI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Series: IRAK Plate: 8 Row: 1 Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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1. 3927
/organism="Mus musculus"
/db_xref="taxon:10090"
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## RESULT 1 AAH41003

ALIGNMENTS

Nove: human coding Type III adenylyl Human nervous syst Human nervous syst

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> Human metalloprotease MDTS6 cDNA. AAH41003 standard; cDNA; 2853 BP 23-AUG-2001 (first entry) AAH41003;

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/SIDS2/gcgdata/geneseg/geneseqn-embl/NA1982.bAr:\*/SIDS2/gcgdata/geneseg/geneseqn-embl/NA1983.bAr:\*/SIDS2/gcgdata/geneseg/geneseqn-embl/NA1984.bAr:\*

Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; ss. /product= "Metalloprotease" /note= "Aggrecanase activity" Location/Qualifiers 1..2853 /\*tag= a Homo sapiens 

11-NOV-1999; 99JP-0321740. 16-MAY-2000; 2000JP-0144020. 10-NOV-2000; 2000WO-JP07917 WO200134785-A1 17-MAY-2001.

(YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:

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Description	Human metallorote Human protease con	Human protease CDN Human protease PRT Human metalloprote	Human protease cDN Human metalloprote Rat metalloprotein
ID		ABK12894 AAS97182 AAD35570	AAD35568 AAA95831 AAA95827
DB	22	2 2 2 2	24 21 21
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Result No.	H 72 F	400	V 80 6

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This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents cDNA encoding the metalloprotease termed MDTS6.
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Indels T; 0 other; 22; ö DB BP; 522 A; 920 C; 903 G; 508 100.0%; Score 2853; 100.0%; Pred. No. 0; ive 0; Mismatches Conservative Best Local Similarity Matches 2853; Conserv Sequence 2853 Match Query

Gaps 0; Length 2853;

120 120 180 240 240 9. 9 CCAGAGCGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC CCAGAGCGGGAGGTAGTCGTTCCCCATCCGACTGGACCCGGACATTAACGGCCGCCGCTAC CAGGAGGACTITIACCIACACCIGACGCCGGAIGCICAGTICIIGGCICCCGCCIICICC ATGCTTTTGCTGGGCATCCTAACCCTGGCTTTCGCCGGGCGAACCGCTGGAGGCTTTGAG TACTGGCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTTCAGATCACAGCATTT 61 19 121 121 181 181 g ò qq g S S ð ò

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1200 1440 1080 1140 1260 1260 1440 1500 1560 1620 1020 1020 960 780 840 840 900 AAATACCGATCCTGCAACCTGGAGCCCTGCCCCAGCTCAGCCTCCGGAAAGAGCTTCCGG GAGGAGCAGTGTGAGGCTTTCAACGGCTACAACCACAGCACCAACCGGCTCACTCTCGCC 1381 TACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGGAGGTGTGC CAGACCCGCCACTTCCCCTGGGCCGATGGCACCAGCTGTGGCGAGGGCAAGCTCTGCCTC AAATGGGATCCCTATGGCCCCTGCTCGCGCACATGTGGTGGGGGGCGTGCAGCTCGCCAGG TATCTGCTGACGCTGCTGCCACCACCGCGCGCCACCTACCGCCATCCCCAGCATCCTCAAC TATCTGCTGACGCTGCTGCCAACGGCGGCGCGACTCTACCGCCATCCCAGCATCCTCAAC CCCATCAACATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCCCCAAG GTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCTGAAC CTGTGTGGAGCCACCTGTGACACCCTGGGCATGGCTGATGTGGGTACCATGTGTGAC TITGGGAAGCICCGAGCCAACCACAIGAIGICCCCGACCCICAICCAGAICGACCGIGCC AACCCCTGGTCAGCCTGCAGTGCTGCCATCACCGACTTCCTGGACAGCGGGCACGGT GACTGCCTCCTGGACCAACCCAGCAAGCCCATCTCCCTGCCCGAGGATCTGCCGGGCGCC TACATGCAGTACTGCACCAAGCTGTGGTGCACCGGGAAGGCCAAGGGACAGATGGTGTGC 1081 1141 1201 1321 1321 1381 1441 1441 1501 1501 1561 1561 1621 1621 1681 1681 1741 1741 1021 1081 1141 1201 1261 1261 1021 721 901 961 721 781 781 841 841 901 961 g do; g g QQ g g δ g δ Qγ δy qq ò g Ω g δ ŏ g QY δ οŽ ò δý 셤 δ g ò g ŏ g δý g

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	7 GTGCCAGACCCGCCACTTCCCCTGGGCCGATGGCACCAGCTGTGGCGAGGGCAAGCTCT	TGCCAGACCCGCCACTTCCCCTGGGCCGATGGCACCAGCTGTGGCGAGGGCAAGCTCT	97 CCTCAAAGGGGCCTGCGTGGAGACACACCTCAACAÀGCACAGGTGGATGGTTCCTG 	7 GGCCAAATGGGATCCCTATGGCCCCTGCTCGC	GCCAAATGGGATCCCTATGGCCCCTGCTCGCGCACATGTAGGGGGATGTGGGGGCCTGGCGGCGTGGAAAAAAAA	17 CAGGAGGCAGTGCACCAACCCCACCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAGT		GTGAAATACCGATCCTGCAATCTGGAGCCCTGCCCCAGCTCAGCCTCCGGAAAGA	37 CCGGGAGGAGCAGTGTGAGGCTTTCAACGCTACAACCACAGCACCAACCA	7 CGCGTGGGATGCCCAAGTACTCCGGCGTGTCTCCCCGGGACAAGTGCAAGC		57 CIGCCGAGCCAATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGACGGCAC	TGCCGAGCCAATGGCACTGGTTCTATGTGCTGGCACCCAAGGTGGTGGACGC	17 GCTGTGCTCTCCTGACTCCACCTCCGTCTGTGTCCAAGGGAAGTGCATCAAGGCTG	7 GCTGTGTCTCCTGACTCCACCTCCGTCTGTGTCCAAGGCAAGTGCATCAAGGCTGGC		77 TGATGGGAACCTGGGCTCCAAGAAGAGATTCGACAAGTGTGGGGGTGTGTGGGGGGAGAC	37 TAAGAGCTGCAAGAAGGTGACTGGACTCTTCACCAAGGCCATGCATG	97 GETGGCPATCCCGCAGGGGCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGGC		57 GATCGGGGATGACACTACCTGGCTCTGAAGAACAGCC	57 GATCGGGGATGACAACTACCTGGCTCTGAAGAACAGCCAAGGCAAGTACCTGCTCAACG	17 GCATTTCGTGGTGTCGGCGGTGGAGCGGGACCTGGTGGTGAAGGGCAGTCTGCTGCGGTA	17 GCATTICGTGGTGTCGGCGGTGGAGCGGGACCTGGTGGTGGTGAGGGCAGTCTGCTGGTGGT		77 CAGCGGCACGGCCACAGCGGTGGAGAGCCTGCAGGCTTCCCGGCCCATCCTGGAGCCG	3	37 GACCGTGGAGGTCCTCTCCGTGGGGAAGATGACACCGCCCGGGTCCGCTACTCCTTCT.	6	97 TCTGCCCAAAGAGCCTCGGGAGGACAAGTCCTCTCATCCCAAGGACCCCCGGGGACCCTT	57 TGTCTTGCACAACAGCGTCCTCAGCCTCTCCAACCAGGTGGAGCAGCCGGACGACGACGAGGCCGCAGGACGAGGCC
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                                                                                                                                                                               CCCTGCACGCTGGCTGGCAGCTGGGGGCCGTGCTCCGCGAGCTGCGGGAGTGGCCT
                                                                                                                                                     CAGCGCCTGGTCACCCTGCTCCAAGAGCTGCGGCCGGGGATTTCAGAGGCGCTCACTGAA
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probe for screening libraries
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strointestinal; Crohn's disease; cancer; erosis; autolumune disorder; dermatitis; quired immunodeficiency syndrome; AIDS; er; developmental disorder; epilepsy; by: epithelial disorder; neurological disorder; dometriosis; ss.
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his sequence lacks a stop codon"
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930 BP.
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The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and Immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g. cancer, developmental e.g. Duchenne and Becker proliferative e.g. cancer, developmental e.g. Duchenne and Becker muscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzaheimer's disease and reproductive e.g. infertility and endometriosis disorders. Numerous other examples of each disorder are given in the specification. The present nucleic acid sequence encodes the human protease PRTS-11 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         useful
                                                                                                                                                                                                                                                                      i AR, Lal P, Au-young J, Tribouley CM;
Nguyen DB, Lee EA, Hafalla A, Khan FA;
I, Patterson C, Tang YT, Walsh RT;
Ir J, Xu Y, Reddy R, Das D, Kearney L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g.
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Delegeane AM, Baughn MR, Nguye
Walia NK, Yao MG, Lu DAM, Pat
Azimzai Y, Lu Y, Ramkumar J,
                                                                                                                                          2000US-213955P.
2000US-215396P.
2000US-216821P.
                                                                                         2001WO-US19178
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                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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29-JUN-2000;
07-JUL-2000;
14-JUL-2000;
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176 TGAGCCAGAGCGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCG 116 250 236 310 296 370 356 416 3; Gaps ATTICAGGAGGACTITIACCTACACCTGACGCCGGATGCTCAGTTCTTGGCTCCCGCCTT CTCCACTGAGCATCTGGGCGTCCCCCTCCAGGGGCTCACCGGGGGCTCTTCAGACCTGCG ACGCTGCTTCTATTCTGGGGACGTGAACGCCGAGCCGGACTCGTTCGCTGCTGTGAGCCT GTGCGGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCCGAGTATGTCATTAGCCCGCT 73.2%; Score 2089; DB 24; Length 2930; llarity 99.8%; Pred. No. 0; Conservative 0; Mismatches 1; Indels 3; Best Local Similarity Matches 2379; Conserv Query Match 131 191 57 117 177 251 237 311 297 371 357 g ď ò g ò g δý 셤 qq ð δ

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         CAGGAGGCAGTGCACCAACCCCACCCCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAG
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The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissuss, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migrafine, pain, sexual dysfunction, mood disorders, attention disorders, organition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and inflammatory disorders (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human process and primmers of the invention.
                                                       tranquiliser;
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                                              cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 TGAGCCAGAGGGGGGGGGGGGGGTCCCATCCGACTGGACCCGGACATTAACGGCCGCCG
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                                                                                                                                     immune related disease; cardiovascular disease; neuronal disease;
migraine; sexual dysfunction; mood disorder; attention disorder;
cognition disorder; hypotension; hypertension; psychotic disorder;
dyskinesia; metabolic disorder; inflammatory disorder; ss.
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                                             cytostatic;
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AAS97182 standard; cDNA; 2937

RESULT 5 AAS97182

(first entry)

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GCATC	GCATC	CTATI	GCTCC	GCTCC	TAGCG	TAGCGC	TCCGG	11111	CGCCA	CGCCAT	TAGCCC	TAGCCG	SCTGGT	SCTGGI	SCTGAC	SCTGAC	CAACAT	CAACAT	CGCCAA	GGCAA	SAGTGA	SAGTGA	rggagc	GGAGC	SAGAAG	SAGAAG	SCTGGG	  cTGGG	SAAGCT	AAGCT	TGGTC	TGGTC	CTCCT	CICCI	ACCCT
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I I I I I I	GAAGGC         GAAGGC	CTGTGC         CTGTGC	GCACAC        GCACAC	regrec        regrec	CAAGTA         CAAGTA	CTCAGC        CTCAGO	CAGCAC           CAGCAC	CGGGA	CCCAA-	GGCAAC        GGCAAC	TGTGG         TGTGG	CCCAT	CGCCA       CGCCA	CAAGG        CAAGG	GTGAA        GTGAA	TCCCG	)        -	CCC 24
   GCTTTT	ACCGG(ACCGG)	ACCAGO               ACCAGO	AACAAC            AACAAC	ACATG1          ACATG1	366660 	CCCAGO	AACCAC	101000 1-1-1 101000	CTGGCA         CTGGCA	GTCCAAG         GTCCAAG	GACAAG        GACAAG	CCAAG	GACATC        GACATC	AACAGC         AACAGC	rggre       rggre	AGGCT        AGGCT	CACCG	CTCAT
   AGCTG	GGTGC        -	ATGGC 	CCTC	729292 	CCAACC	CCTGC	GCTACA	606161                   606161	ATGTGC           ATGTGC	TCTGTG	ATTC 	CTTCA	CATC	GAAG       GAAG	GGACC	CCTGC	GATGA	GTCCT
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LIIII	ACCAA 	CCCTG	GAGAG        GAGAG	66CCC	CCCA	CAACCT	GCTTT	CAAGTA         CAAGTA	GGCTAC	TCCAC	CCAA	GTGACT         GTGACT	300000  - - -	TACCTC	GCGGTC	606616        606616	CCGTG	CGGGAG
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CAGCTA	TTACAT        TTACAT	CCAGAC          CCAGAC	CAAAGG 	AAATG	AGGCA 	AAATA 	GAGGA	GTGGC               GTGGC	CGAGC        CGAGC	CTGTG        CTGTG	GATGG        GATGG	AAGAGO            AAGAGO	GTGGC       GTGGC	ATCGG        ATCGG	CATTT         CATTT	AGCGG(             AGCGG(	ACCGT(	CTGCC
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Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility; gene therapy; enzyme; gene; ss.
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ACATTATCTGCTGACGCTGCTGGCAACGGCGGCGCGACTCTACCGCCATCCCAGCATCCT
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                                         ACGC!!GCTTCTATTCTGGGGACGTGAACGCCGAGCCGGACTCGTTCGCTGCTGTGAGCCT
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                                                                                                                                                                                        Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility; gene therapy; enzyme; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding a human protease, useful as a hybridization probe for screening libraries and assessing gene expression patterns
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1104 BP; 189 A; 357 C; 345 G; 213 T; 0 other;
     2472 CTATCTGCCCAAAGAGCCTCGGGAGGACAAGTCCTCTCATCCC 2514
                                                                                                                                                                                                                                                                                                                    /product- "Human protease #3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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1..1104
/*tag= a
                                                                             AAD35570 standard; cDNA; 1104 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LEXI-) LEXICON GENETICS INC.
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P-PSDB; AAE22542.
                                                                                                                                                                Human protease cDNA
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                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                    26-JUL-2002
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776 836 836 968 896

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Human, ADAMTS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin Jomain; vaccine; nootropic; neuroprotective; antiparkinsonian; ecrebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury; ss.
                                                                                                           CAAGGTCACCGGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCCTGGCAGAAGAAGCT
                                                                                                                                                                                                                                                                                                                                CGTGGAGACGCTGGTGGTCGCGGACGAGTCAATGGTCAAGTTCCACGGCGCGGACCTGGA
                                                                                                                                                                                                                                                            CAACCCCATCAACATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCC
                                       CIGGAACCCCGCCAICCIACGGCCCTGGACCCITACAAGCCGCGGGGGGGGGTTCGG
                                                                                             GGAGAGTCGTAGCCGGCGCAGGTCTGGGCGCGCCAAGCGTTTCGTGTCTATCCCG;CGGTA
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/product= "ADAMTS-5"
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1..1143
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                                                                  /*tag= a
/product= "Human protease #1"
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                                         Location/Qualifiers
1..966
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                                                                                                                                                                27-SEP-2001; 2001WO-US30350
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                                                                                                           WO200226949-A2
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metalloproteinase ADAMTS-5 cDNA.
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   ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family of proteins bomain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                     Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTTCACCAGGCAGGACCTGTGTGGAGCCACCACCTGTGACACCCTGGGCATGGCTGAT 1002
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                                                                                                                                                                                                                                                                                          Length 1143;
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                                                                                                                                                                                                                                                                  Sequence 1143 BP; 240 A; 362 C; 326 G; 209 T; 6 other;
                                                                                                                                                                                                                                                                                         Score 481; DB 21;
Pred. No. 1.8e-211;
                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                      Claim 2; Fig 22; 129pp; English.
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99.8%;
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     WPI; 2000-594326/56
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                 P-PSDB; AAB21261
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The present sequence encodes rat metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disinterrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmung diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                vaccine; nootropic; neuroprotective; antiparkinsonlan; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease; human; aggrecanase; joint disease; osteoarthritis;
Rat; ADAWTS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adaptor primer SEQ ID 22 used in metalloprotease DNA isolation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1518 BP; 307 A; 470 C; 462 G; 279 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; L
8.6e-13;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "ADAMTS-5"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1.1515
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 13; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0264585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-594326/56.
P-PSDB; AAB21257.
                                                                                                                                                                                                                                                               Rattus norvegicus.
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This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents an adaptor primer used in the isolation and characterisation of the metalloprotease gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents
                                                                                 Metalloprotease with aggrecanase activity for treating joint diseases especially osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metalloprotease with aggrecanase activity for treating joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nomura N;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 30;
      Nagase T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer specific for human metalloprotease DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; L
. 0.0017;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 BP; 10 A; 6 C; 6 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preu. ...
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      Ohara O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 TTTTTCAGATCACAGCATTTCAGGAGGACT 190
                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 30;
                                                                                                                                            Example 13; Page 66; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 TITITICAGATCACAGCATTTCAGGAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 62; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishimura K, Abe K,
      Abe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH41017 standard; DNA; 41 BP
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16-MAY-2000; 2000JP-0144020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially osteoarthritis
      Yamaji N, Nishimura K,
                                           WPI; 2001-343602/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH41017;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
AAH41017/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
      δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host calls transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents an adaptor primer used in the isolation and characterisation of the metalloprotease gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease with aggrecanase activity for treating joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; primer; adaptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adaptor primer SEQ ID 23 used in metalloprotease DNA isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 30;
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                                                                                                                                                                                                                                                                                                                           Nagase
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0.0017;
thes 0;
osteopathic; antiarthritic; primer; adaptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 8 A; 6 C; 10 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB;
s; Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                       Ohara O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 66; 85pp; Japanese.
                                                                                                                                                                                                                                                             (YAMA ) YAMANOUCHI PHARM CO LTD (KAZU-) KAZUSA DNA RES INST.
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                                                                                                                                                                                                                                                                                                                         Abe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  llarity 100.0%; P. Conservative 0;
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                                                                                                                                                                                                    99JP-0321740.
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                                                                                                                                                          10-NOV-2000; 2000WO-JP07917.
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                                                                                                                                                                                                                                                                                                                                                                                                                       especially osteoarthritis
                                                                                                                                                                                                                                                                                                                     (amaji N, Nishimura K,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-343602/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 30; Conserv
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                                                                               WO200134785-A1.
                                                                                                                                                                                                  11-NOV-1999;
                                           Homo sapiens
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AAH41018 standard; DNA; 27 BP

a PCR primer used in the isolation and characterisation of the metalloprotease gene of the invention.

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Query Match

Matches

à 셤 AAH41016;

RESULT 13

AAH41016 ID AAH4

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This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents metalloprotease gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metalloprotease with aggrecanase activity for treating joint diseases especially osteoarthritis
                                                                                                                                            Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer specific for human metalloprotease DNA SEQ ID 10.
                                                                                                         PCR primer specific for human metalloprotease DNA SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 5 A; 6 C; 11 G; 5 T; 0 other;
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Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1534 AAGCACAGGGTGGATGGTTCCTGGGCC 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 63; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                            (YAMA ) YAMANOUCHI PHARM CO LTD: (KAZU-) KAZUSA DNA RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaji N, Nishimura K, Abe K,
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16-MAY-2000; 2000JP-0144020.
                                                                                                                                                                                                                                                                                                                  10-NOV-2000; 2000WO-JP07917
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-343602/36.
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                                                                                                                                                                                                         Homo saplens.
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                                   AAH41018;
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δλ
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                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metalloprotease with aggrecanase activity for treating joint diseases especially osteoarthritis
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                                                                      DB 22; Leny.
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                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer specific for human metalloprotease DNA.
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                                                  Sequence 41 BP; 5 A; 16 C; 13 G; 7 T; 0 other;
                                                                                       ch 1.1%; Score 30; DB 1 Similarity 100.0%; Pred. No. 0.0 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohara O,
                                                                                                                                                              1 ATGCTTTTGCTGGCCATCCTAACCCTGGCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 13 ATGCTTTTGCTGGGCATCCTAACCCTGGCT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 62; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishimura K, Abe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1999; 99JP-0321740
16-MAY-2000; 2000JP-0144020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0-NOV-2000; 2000WO-JP07917
                                                                                                                                                                                                                                                                                               AAH41016 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001 (first entry)
                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-343602/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200134785-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2001.
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Nagase T,

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Gaps

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17-MAY-2001

Query Match

Best Loca Matches

RESULT 14 AAH41018

g

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Length 27;

(YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST. 10-NOV-2000; 2000WO-JP07917. 11-NOV-1999; 99JP-0321740. 16-MAY-2000; 2000JP-0144020. 

Nagase T, Ohara O, Yamaji N, Nishimura K, Abe K, WPI; 2001-343602/36.

Nomura N;

Metalloprotease with aggrecanase activity for treating joint diseases especially osteoarthritis

Example 5; Page 63; 85pp; Japanese.

This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents metalloprotease gene of the invention.

Sequence 37 BP; 7 A; 14 C; 14 G; 2 T; 0 other;

0; Gaps Length 37; 0.9%; Score 27; DB 22; Length 37 100.0%; Pred. No. 0.042; arive 0; Mismatches 0; Indels Query Match 0.9% Best Local Similarity 100.( Matches 27; Conservative

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37 CTGGACTTCTGCGTCCTGAGGCCGTGC 11

ò g

us-10-009-332-2.oli.rng

2824 CTGGACTTCTGCGTCCTGAGGCCGTGC 2850

Search completed: May 2, 2003, 01:10:45 Job time : 622 secs

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May 1, 2003, 22:52:52; Search time 103 Seconds (Without alignments) 8494.649 Million cell updates/sec
                                                                                                                                                                             US-10-009-332-2
2853
1 atgettttgetgggeatcet......gegteetgaggeegtgetga 2853
                                                                                                                                                                                                                                                                                                                                                                                           882724
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                       OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                Word size :
                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                         Run on:
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Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/1/ina/packfiles1.seq:\* Database :

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

		Description	Segmence 7 Appli	·	31/		ì ,-	-	ï	11,	11,	3, 4	7	2	'n		1	55,	5,	2	7,	7,	9	7	9	1,	7	٦,	1,
SUMMARIES		ID	US-09-130-491-7	US-08-726-214-5	US-09-643-597-314	۱,	US-08-377-292-1	US-09-010-928B-1	US-07-862-021B-11	US-08-313-288B-11	PCT-US93-03164-11	US-08-872-757-3	US-08-737-715-1	US-09-103-840A-2	US-09-103-840A-2	US-09-103-840A-1	US-09-103-840A-1	US-08-914-375C-55	US-08-540-242A-5	PCT-US96-01471-5	US-08-688-609-7	US-09-002-832-7	US-08-688-908-6	US-08-540-242A-1	US-08-692-922-6	PCT-US96-01471-1	US-08-292-345B-1	-09-003-0	US-08-648-262-1
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		Length	2114	4533	311	2457	2487	2830	3226	3226	3226	3546	4149	4403765	4403765	4411529	4411529	426	438	438	444	444	445	504	504	504	701	702	702
ď	Query	Match	0.8	•	9.0		9.0	•	9.0	9.0	9.0	9.0	9	ò	v	9	9	9.0	9.0	9.0	9.0	9.0	9.0		٠		0.6.	9.0	9.0
		Score	23	19	18	18	18	18	18	18	18	18	18	18	18	18	18	17	17	17	17	17	17	17	17	17	17	17	17
	Result	NO.	7	7	ပ	4	S	9	7	Φ.	o,	10	c 11	12	c 13	14	c 15	16	17	81	19	07	77	22	23	24	25	26	7.7

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Sequence 1, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli	TANGO-76, AND TANGO-83	Length 2214; ; Indels 0; Gaps 0;	YCLASE
US-08-648-263-1 US-08-518-862C-5 US-09-120-772-1 US-08-137-785-2 US-08-142-569-1 US-08-63-694-7 US-08-694-501-7 US-08-694-501-7 US-08-694-501-7 US-08-488-218-1 US-08-488-214A-1 US-08-488-214A-1 US-08-488-211A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1 US-08-488-21A-1	ALIGNMENTS 91 NGO-73, TANGO-74, 9/130,491 0/058,108 0/054,961 rsion 3.0	Score 23; DB 4; Pred. No. 0.39; 0; Mismatches 0 2030 829	S6214 S. MAMMALIAN ADENYLYL CYCLASF SS THEREFOR & DUTKEE
702 12005 12005 14505 1480 1659 1659 1659 1659 1659 17093 27793 27	ation US/091304  N: tan, Douglas A. Tal, Andrew D.J. N: TANGO-71, TA 9404/041001  ON NUMBER: US/0 ON NUMBER: US 6 TE: 1997-09-05 ON NUMBER: US 6 TE: 1997-09-05 TE: 1997-09-06 TE: 1997-09-09-09-09-09-09-09-09-09-09-09-09-09-	0.8%; -y 100.0%; rrvative GTGTGGGGG	ion US/08726  !:     Wei-Jen     Na Infred G. NN: SOLUBLE EN: 31 DRESS: Old, White &
0.06 177 177 177 177 177 177 177 177 177 17	-7 Applica 6416074 6416074 Holtzma Goodear Goodear Goodear Goodear CENTING DAT LING	Match 0.8%; Local Similarity 100.0%; Local Sim	08-726-214-5 equence 5, Application US/0872 attent No. 6107076 GENERAL INFORMATION: APPLICANT: Tang, Wel-Jen APPLICANT: Gilman, Alfred G TITLE OF INVENTION: SOLUBLE TITLE OF INVENTION: AND USE. TITLE OF INVENTION: AND USE. ANDRESSED: ADDRESS: ADDRESSES: ARNOIG, White STREET: P.O. Box 4433 CITY: HOUSTON STATE: Texas
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-130-491- Sequence 7, Patent NO. 6 GENERAL INFO. 6 APPLICANT: BARLIER APPLICANT: BARLIER APPLICANT: CURRENT FILE BARLIER APPLICANT: ANDWERO FILE BARLIER FIL	Query Matc Best Local Matches Qy 2008 GA Db 807 GA	RESULT 2 US-08-726-214 ; Sequence 5, Patent No. GENERAL IN APPLICAN TITLE OF TITLE OF TITLE OF ONNERSPO CORRESPO SADDRES; STREET CITY: CIT

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; Sequence 1, Application US/08872757 ; Patent No. 6258584
86 TGGGCTCCAAGAAGAGAT 69
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Best Local Similarity
Matches 18; Conserve
                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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US-08-872-757-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCNGILL, PATTICIA D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 4533;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 18; DB 4; Length 311;
100.0%; Pred. No. 80;
                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: CONCURTENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEG ID NOS: 369
SOFTWARE: FASTED OF Windows Version 3.0
                                                                                                                                                                                                                                                                                       NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPRENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPRIX: (512) 474-77
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 314, Application US/09643597 Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0°;
100.0%; Pre-
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bangur, Chaitanya S
Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson, Robert A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                       LEGENT 4533 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Fan, Ligun
                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-726-214-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 19;
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1988 TGGCCTCCAAGAAGAGAT 2005

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Sequence, A. Application Us/00012/1/1
Sequence, A. Application Us/00012/1/1
Sequence, A. Application Us/00012/1/1
Sequence, A. Application Us/00012/1/1
Sequence, Application Us/00012/1/1
Septiment Second Sequence Sequen
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us-10-009-332-2.oli.rni

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The putative start codon is at
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                                                                                                                                                                                                                                                                                                                                                                                      Length 2830;
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Patent No. 5279966
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M
APPLICANT: Jessell, Thomas M
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREE: 30 Rockefeller Plaza
CITY: New York
STAME: New York
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                      /note= "Flagelliform DNA sequence
taken from the 5' region. The put
position 219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/07/862,021B
FILING DATE: 19920405
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Score 18; DB 2; Best Local Similarity 100.0%; Pred. No. 75; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 400:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: 42253 COP UI
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28,678
                                                                                           not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2234 CGGTGGAGCGGGACCTGG 2251
                                               LENGTH: 2830 base pairs
TYPE: nucleic acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3226 base pairs
            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         CDS
219..2830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 136..2543
US-07-862-021B-11
                                                                                                                                                                                    NAME/KEY: 1.2830
LOCATION: 1.2830
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                              linear
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                                                                                                          TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: N
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; LOCATION:
US-09-010-928B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-862-021B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                    FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION:
CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEBOUSE RD. SUITE 500E
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 2487; 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,292
FILING DATE: 23-JAN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B FILIG DATE: 22-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 18;
11810 East Miami River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MUTDHY Jr., Gerald M
REGISTRATION NUMBER: 29977
REFERENCE/DOCKET NUMBER: 1447-109P
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/243,435
                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US/08/117,367
ETLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-010-928B-1
; Sequence 1, Application US/09010928B
; Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.0.
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Corstanje, Brahm J.
REGISTRATION NUMBER: 34,804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-245-2858
TELEFAX: 513-741-3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 513-741-3012
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080 CCACGAGCTGGGCCACGT 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 CCACGAGCTGGGCCACGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2487 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: 11near
; MOLECULE TYPE: CDNA
US-08-377-292-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserva
                    Cincinnati
                                                            COUNTRY: U.S.A. ZIP: 45239-8707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22042
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Gaps

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3: Cooper & Dunham
30 Rockefeller Plaza
                  Dunham
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CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie &
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ), NAME/KEY: CDS
; LOCATION: 136..2543
PCT-US93-03164-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                       CITY: New York
STATE: New York
                                                                                              USA
                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-872-757-3
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                                                           Gaps
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                  Length 3226;
                                                           0; Indels
                                                                                                                                                                                                                                                                     GENERAL INCOMMATION:
GENERAL INCOMMATION:
GENERAL INCOMMATION:
GENERAL INCOMMATION:
CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE TO DUNAM LLP
STREET: 1185 Avenue of the Americas
CITTY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONING, EXPRESSION AND USES OF A NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                  core 18; DB 1;
Pred. No. 75;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; Pred. No.
                    0.6%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/313,288B FILING DATE: January 5, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-03164-11; Sequence 11, Application PC/TUS9303164; GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 11, Application US/08313288B Patent No. 5750502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Wilte, John P. 6.78
REGISTRATION NUMBER: 4002
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.6%; Soc
Best Local Similarity 100.0%; Pa
Matches 18; Conservative 0;
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APPLICANT: Klar, Avihu
TITLE OF INVENTION: CLONING,
TITLE OF INVENTION: NOVEL SEC
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1467 CCCCTGGTCAGCCTGCAG 1484
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                                                                                                  1203 CCCTGGTCAGCCTGCAG 1220
                                                                                                                      Db 1467 CCCTGGTCAGCCTGCAG 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3226 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                  Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 136..2543
US-08-313-288B-11
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US-08-313-288B-11
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03164
FILING DATE: 19930402
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08872757

Patent No. 6258584

GENERAL INVENARION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Aleksander
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES; METHODS AND USES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
75;
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 4002
TELECOMUNICATION INFORMATION:
TELEPAX: (212) 664-0525
TELERX: (212) 664-0525
TELEX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1203 CCCCTGGTCAGCCTGCAG 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1467 CCCCTGGTCAGCCTGCAG 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3226 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%
Best Local Similarity 100.0
Matches 18; Conservative
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OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Observed M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERBUES: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOGACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 18; DB 4; Length 4403765; 100.0%; Pred. No. 40; tive 0; Mismatches 0; Indel  0;
                                                                                                                                                                                                                                               Length 4149;
                                                                                                                                                                                                                                               0.6%; Score 18; DB 2;
00.0%; Pred. No. 74;
                                                                                                                                                                                                                                      Query Match U.00; CLAST TAGE NO. 74; Best Local Similarity 100.08; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application \text{US/O9103840A} Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 77,489 CCGGCGCCACCAAC 77506
                                                                                                                                                                                                                                                                                                                                 1701 GGAGCCCTGCCCCAGCTC 1718
                                                                                                                                                                                                                                                                                                                                                             3099 GGAGCCCTGCCCCAGCTC 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 CCGCCGCGCAGCGCAAC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                             MOLECULE TYPE: CDNA FEATURE:
                                                                                                             1..4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-103-840A-2/C
                                                                                      NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                               LOCATION:
                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-103-840A-2
                                                                                                                                                                                                    US-08-737-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ebina, Yousuke
TITLE OF INVENTION: MUTANT HUMAN INSULIN RECEPTOR DNA
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SUGHRUE, MION, ZINN, MACPEZ
2100 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 134827/1995
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/737,715
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
                                                                                    APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEFAX: 66141 FENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3546 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08737715
Patent No. 5958685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-4
TELECOMMUNICATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1080 CCACGAGCTGGGCCACGT 1097
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..2958
                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-872-757-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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OTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, CLAIR M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRASER, Claire M. APPLICANT: VENTER, OOD C. TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 18; DB 4; Length 4411529; ... 100.0%; Pred. No. 40; ... Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                  DB 4; Length 4403765; 40;
                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                               Query Match 0.6%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 40; Matches 18; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
TYPE: DNA CORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA

: ORGANISM: Mycobacterium tuberculosis

: OTHER INFORMATION: H37Rv

US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                       Db 3375303 TGGTGTCGGCGGTGGAGC 3375286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy 2225 TGGTGTCGCCGCTGGAGC 2242
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SOFTWARE: PatentIn Ver. 2.1
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Matches 18; Conservative
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LENGTH: 4411529
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LENGTH: 4411529
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US-09-103-840A-1/c
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US-09-103-840A-1
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0.6%; Score 18; DB 4; Length 4411529;

Query Match

Search completed: May 2, 2003, 05:13:52 Job time: 14589 secs

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2, 2003, 00:35:12 ; Search time 339 Seconds (without alignments) 9944.440 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Post-processing: Listing first 45 summaries

Published Applications_NA:* 1: /cqn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*	2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*	3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*	4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*	5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*	<pre>6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*</pre>	7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*	8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*	9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*	<pre>10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*</pre>	<pre>11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*</pre>	<pre>12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*</pre>	<pre>13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*</pre>	14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Query Match 94.5%; Score 2695; D Best Local Similarity 99.9%; Pred. No. 0; Matches 2795; Conservative 0; Mismatches

TYPE: DNA CORGANISM: homo sapiens US-09-965-631-3

DB 10; Lengrh 2853; Indels 116

57 TGAGCCAGAGGGAGGTAGTCGTTCCCATCCGACTGGACCCGGACATTAACGGCCGCCG 116

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117 CTACTACTGGCGGGGTCCCGAGGACTCCGGGGATCAGGGACTCATTTTTCAGATCACAGC 176 

117

•	Description	Sequence 3, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 7, Appli	٠,	Sequence 22019, A	Sequence 180, App	Sequence 60, Appl	Sequence 1835, Ap	Sequence: 15962, A	Sequence 85, Appl	Sequence 32286, A	Sequence 34926, A	Sequence 11410, A	Sequence 19861, A	Sequence 29711, A
	DI	US-09-965-631-3	US-09-965-631-7	US-10-163-316-3	US-10-163-316-1	US-09-965-631-5	US-09-965-631-1	US-10-105-929-7	US-09-931-457A-10	US-09-918-995-22019	US-09-925-297-180	US-09-938-842A-60	US-09-535-459-1835	US-09-918-995-15962	US-09-925-297-85	US-09-918-995-32286	US-09-918-995-34926	US-09-518-995-11410	US-09-864-761-19861	US-09-864-761-29711
	DB	101	10	σ	σ	10	10	12	6	6	10	6	6	6	10	6	6	6	10	10
	Match Length DB	2853	3446	2469	2940	1104	996	2114	1813	206	1827	1017	256	408	431	452	466	469	157	258
*	Match	94.5	94.5	50.3	50.3	36.3	31.7	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	9.0	9.0
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	υ	32		9.0	597		US-09-864-761-13150	Sequence 13150, A
		33		9.0	682		US-09-833-381-836	Sequence 836, App
		34		9.0	954		US-09-815-242-9757	Sequence 9757, Ap
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	3.	Segmence 3 Application [15/0996563]	a anni	icatto	0/511	9900	5631	
	, iš	Patent No. US20020115842A1	. uszoo	201158	42A1	,	1	
	<u>.</u>	GENERAL INFORMATION:	NFORMAT	ION:				
		APPLICANT: Friddle,	r: Frid		Carl Johan	han		
		APPLICANT:	T: H11		Erin			
	•	TITLE OF INVENTION:	INVENT	ION: N	lo. US2	0020	No. US20020115842Alel Human Proteases	ses and Polynucleotides Enco
		FILE REFERENCE: LEX-0241-USA	ERENCE:	LEX-0	241-US	K		
		CURRENT 2	APPLICA	TION N	UMBER:	'Sn	CURRENT APPLICATION NUMBER: US/09/965,631	
		CURRENT FILING DATE: 2001-09-27	FILING	DATE:	2001-	5-60	27	
	•	PRIOR APPLICATION NUMBER: US 60/236,68	PLICATI	ON NUM	BER: U	.s 60	0/236,689	
		PRIOR FILING DATE: 2000-09-29	LING DA	TE: 20	-60-00	29		
		NUMBER OF SEQ ID NOS:	F SEQ I	D NOS:	7			
		SOFTWARE	: FastS	EQ for	Windo	WS \	SOFTWARE: FastSEQ for Windows Version 4.0	
	S.	SEQ ID NO	3					
	••	LENGTH:	2853					
		TYPE: DNA	ΑA					

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IIII TGCT	CATT	ACCTT 	6676      	)   	TATC      TATC	9000 1111	8=8	TGAC      TGAC	GCAG	E E E	GGGT 	CAGCC	515	CCAGA	GGACA(        GGACA(	GGATO       GGATO	CTCC	55 =
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TCGT	GAGT       GAGT	0000 0000	CGCT	)  :  :	TCGT	11CC/	CTACC         CTACC	GAGA:	316	GCCATO          GCCATO	5=5	원그일	AATGT	ACCCT	GACTT        GACTT	CTGCC        CTGCC	GCGT 	GAAGGCCAAGG
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	GGCT	CAGO	SGAGAG               GAGAG	CTGGAC	)   	GAGT(        GAGT(	99	CAAGGT	KGGCTI           CGCTI	SAGT!       SAGT!	GACAC	CATTG2	CAACATO	CACATO 	- 10 - 10 - 10 - 10 - 10 - 10	CCAGCAAGC	용도용	CTGTG
IIII CGTG	CTIT	929 - 929	100g	22 <u>- 23</u>	걸=털	GAC	GCAAC	5 – 5	CTGAC		CTGTC	5 – 5		A = A	CAGTG 	CCCA	CAGT(	AAGC 
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δy	m	TGCCAGACCGCCACTTCCCCTGGGCCGATGGCACCAGCTGTGGCGAGGGCAAGC
qq	1437	   TG 149
Oy	1497	CAAAGGGGCCTGCGTGGAGACACAACTCAACAAGGAGGGTGGATGGTTCCTG 155
Ob	1497	CTCAAAGGGGCCTGCGTGGAGAGACACAACCTCAACAAGCACAGGGTGGATGGTTCCTG 15
Qy	20	GGCCAAATGGGGATCCCTATGGCCCCTGCTCGCCACATGTGGTGGGGGGCGTGCAGTTGC
QO	1557	GCCAAATGGGATCCCTATGGCCCCTGCTCGCGCACATGTGGTGGGGGCGTGCAGCTGGC 161
Oy G	1617	CAGGAGCCAGTGCAACCCCCACCCCTGCCAACGGGGGCAAGTACTGCGAGGGAGTGAG 1676
<u>a</u> :	- i	HOUNDER HOTGE CALCEACCECTACCECTGE CACGGGGGGAGTACTGE GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
δο d	<b>~</b> r	GSTGAAATACCGATCCTGCAACTGGAGCCCTGCCCCACCTCCGGAAAGAGCTT 1736
<u>a</u> :	1737	GIGAAAIACCGGGAAAGCIGGGGCCCIGCCCCGGCTCCGGGAAGGGCTT 1/3
5 A	n 'n	CCGGGAGGAGCAGTGTCAGCGCTATCAACGGCTACACACAC
, Qy	1797	GCCGTGGCATGGGTGCCCAAGTACTCCGGCGTGTCTCCCCGGGACAAGTGCAAGGTCAT 18
Db	1797	85
ΟY	1857	GCCGAGCCAATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGAGGGCGC
qa	1857	CCGAGCCAATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGGGGCGCAC 191
Oy	1917	IGEGCTCTCCTGACTCCACCTCCGTCTGTGTCCAAGGCAAGTGCATGAAGCTGGCTG
QQ	1917	GIGCTCTCTCTGACTCCACCTCCGTCTGTGTGTCCAAGGCAAGTGCATCAAGGCTGGCT
Qy	1977	GCTCCAAGAAGAGATTCGACAAGTGTGGGGGTGTGTGGGGGAGACAA 203
QQ	1977	GATGGGAACCTGGGGTCCCAAGAAGAGATTTCGACAAGTGTGGGGGTGTGTGT
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Qy	2217	CATTTCGTGTCGTCGCGGTGGAGCGGGACCTGGTGGTGAAGGGCAGTCTGCTGCGGTA 227
qa	2217	
Qy	2277	AGGGGCACGGGCACAGGGGGGGGGGGCCTGCAGGCTTCCCGGGCCCATCCTGGAGCCGCT 233
qq	2277	33
Qy	2337	CGTGGGGAAGATGACACCGCCCCGGGTCCGCTACTCCTTCTA 239
QQ	2337	ACCGIGGAGGICCICTCCGIGGGGAAGAIGACACCGCCCCGGGICCGCIACICCTICIA 239
Οy	2397	GAGGACAAGTCCTCTCATCCCAAGGACCCCCGGGGACCCTC 24
Db	2397	CTGCCCAAAGAGCCTCGGGAGGACAAGTCCTCATCCCAAGGACCCCCGGGGACCTC 24
ΟŸ	2457	ACCAGGTGGAGCAGCGGACGACAGGCC 2
qq	2457	GTCTTGCACAACAGGGTCCTCAGCCTCTCCAACCAGGTGGAGCAGCCGGACGACAGGCC 2

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GTGCGGGGGGCTCCGCGGAGCCTTTGGCTACCGAGGCGCCGAGTATGTCATTAGCCCGCT
                            ACATTATCTGCTGACGCTGGCAACGGCGCGCGACTCTACCGCCATCCCAGCATCCT
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APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: Brin
TITLE OF INVENTION: NO. US20020115842A1el Hum
FILE REFERENCE: LEX-0241-USA
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                        Sequence 7, Application US/09965631
Patent No. US20020115842A1
GENERAL INFORMATION:
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ilarity 99.9%;
Conservative
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Best Local Simil
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	1497 CCTCAAAGGGGCCTGCGTGGAGACACAACCTCAACAAGGACAGGGTGGATGGTTCCTG 1556	1893 CCTCAAAGGGCCTGCGTGGAAGACACAACCTCAACAAGCACAGGGTGGATGGTTCCTG 195	1557   GGCCAAATGGGATCCCTATGGCCCCTGCTGGCACATGTGGTGGGGGGGG	1617 CAGGAGGCAGTGCACCCCACCCCTGCCAACGGGGGCAAGTACTGCGAGGGGTGAG 1676 1111111111111111111111111111111111	1677 GGTGAAATACCGATCCTGCAACCTGGAGCCCTGCCCAGCTCAGCCTCCGGAAAGAGCTT 1736	CCGGGAGGAGCAGTGTGAGGCTTTCAACGGCTACAACCACAGCACCGACCG	CGCCGIGGCAIGGGIGCCCAAGIACTCCGGGGGIGTCICCCCGGGACAAGIGCAAGGTCAT 1856	CTGCCGAGCCAATGGCACTGGCTACTTCTATGTGCTGGCACCCAAGGTGGTGGACGCAC 1916.	GCTGTGCTCTCCTGACTCCACCTCGGTCTGTGTCCAAGGCAAGTGCATCAAGGCTGGCT	TGATGGGAACCTGGGCTCCAAGAAGATTCGACAAGTGTGGGGGTGTGTGGGGGGAGAA 2035. 	TAAGAGCTGCAAGAAGTGACTGGACTCTTCACCAAGCCCATGCATG	GGTGGCCATCCCCGCAGGCGCCTCAAGCATCGACATCCGCCAGCGCGGTTACAAAGGCT 2156,	57 GATCGGGGATGACAACTACCTGGCTCTGAAGAACAGCCAAGGCAAGTACCTGCTCAACGG 2216 	GCATTICGIGGIGGCGGGGGGGGGGGCCTGGTGGTGGAAGGGCAGTCTGCTGCGGTA 227	7 CAGCGGCACGGCACAGCGGTGGAGACCTGCAGGCTTCCCGGCCCATCCTGGAGCCGCT 23	GACCGTGGAGGTCCTCTCCGTGGGAAGATGACACGCCCCGGGTCCGCTACTCTTTA 23	TCTGCCCAAAGAGCCTCGGGAGGACAAGTCCTCTCATCCCAAGGACCCCGGGGACCCTC 245	TGTCTTGCACAACAGCGTCCTCAGCCTCTCCAACCAGGGGGGGG	CCCTGCACGCTGGGTGGCTGGCAGCTGGGGGCCCTGCTCCGCGAGCTGCGGCAGTGGCCT 257

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VERYION: 65552, A Human Matrix Metalloproteinase and Uses
VERYION: Therefor
NCE: MPIO1-025PIRNM
LICATION NUMBER: US/10/163,316
LICATION NUMBER: 60/297,863
CATION NUMBER: 60/297,863
S DATE: 2001-06-13
ED ID NOS: 10
astSEQ for Windows Version 4.0
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larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 0
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to. US20020197703A1
MATION:
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                                                     Sequence 1, Application US/10163316
Publication No. US20020197703A1
Publication No. US20020197703A1
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: ABLECT
FILE REFERENCE: MP101-025PIRNM
CURRENT APPLICATION NOWBER: US/10/163,316
CURRENT APPLICATION NUMBER: 60/297,863
PRIOR APPLICATION NUMBER: 60/297,863
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                              Length 1104;
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100.0%; Pred. No. v.
... 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/236,689
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
S SQ ID NO 5
LENGTH: 1104
                                                                                                                                    Conservative
                                                                             TYPE: DNA
CORGANISM: homo sapiens
US-09-965-631-5
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Best Local Similarity
Matches 1035; Conserv
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                                 CGTGGAGACGCTGGTCGCGGACGAGTCAATGGTCAAGTTCCACGGCGCGGACCTGGA
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Sequence 5, Application US/09965631

Patent No. US20020115842A1

GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. US20020115842A1e1 Human Proteases
FILE REFERENCE: LEX-0241-USA
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GENERAL INVOCATALION:

GENERAL INVOCATALION:

APPLICANT: Holtcman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

TUTLE OF INVORVINO: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83;

FILE REFERENCE: 09404/041001

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/130,491

PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-07

PRIOR PLILNG DATE: EARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: BARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: BARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: BARLIER FILING DATE: 1997-08-05

PRIOR FILING DATE: BARLIER FILING DATE: 1997-08-05

SOFTWARE: FASTERO FOR WINDOWS VERSION 3.0

SOFTWARE: FASTERO FOR WINDOWS VERSION 3.0
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Pred. No. 0.078;
0; Mismatches 0;
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; LOCATION: (3)...(1445)
US-10-105-929-7
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GGA 959
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US-09-931-457A-10
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US-10-105-929-7
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                                           1017 TGACCCCAAGAGAAGCTGCTCTGTCATTGAGGACGATGGGCTTCCATCAGCCTTCACCAC 1076
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Patent No. US20020115842A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
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Best Local Similarity
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LENGTH: 966
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US-09-965-631-1
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APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
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. 0.91;
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3.3;
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                            PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 180
LENGTH: 1827
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illarity 100.0%; Pred. No.
Conservative 0; Mismatc
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; LOCATION: (1524)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-180
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
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Best Local Similarity 100.C
Matches 21; Conservative
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Matches 20; Conserv
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US-09-535-459-1835
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LENGTH: 1017
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                                      APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes;
FILE REFERENCE: BB116 US CIP
CURRENT APPLICATION NUMBER: US/09/931,457A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/424,976
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR PILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-16-12
NUMBER OF SEQ ID NOS: 72
SEQ ID NOS: 72
SEQ ID NOS: 72
SEQ ID NO 10
SEQ ID NO 10
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100.0%; Pred. No. 0.27;
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Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
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100.0%; Pred. No. 1;
iive 0; Mismatches
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Publication No. US20030073623A1
GENERAL INFORMATION:
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| LCCATION: (1)...(506)
| OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22019
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Matches 21; Conservative
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Patent No. US20020157132A1
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ORGANISM: Homo sapiens
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; ORGANISM: Zea mays
US-09-931-457A-10
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US-09-925-297-180/c
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT PILL SPLING DATE: 20410-70-30
PRIOR APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILLING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (381)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-85
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100.0%; Pred. No.
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LOCATION: (325)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (334),
OTHER INFORMATION: n equals a,t,g, or
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; UCCATION: (1)...(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32286
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ORGANISM: Homo sapiens
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Matches 19; Conserv
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Matches 19; Conserv
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LENGTH: 452
                                                                                                                      NUMBER OF SEQ
                                                                                                                                       SOFTWARE: Par
SEQ ID NO 85
LENGTH: 431
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...erliCant: Naughton, Rebecca E.; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE; FILE REFERENCE: PD-1014 CIP.; CURRENT APPLICATION NUMBER: US/09/535,459; CURRENT FILING DATE: 2000-03-24; Prior application data removed - consult PALM or file wrapper. SOFTWARE: PERL Program

SOFTWARE: PERL Program

LENGTH: 256

TYPE: NN.
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) OTHER INFORMATION: Incyte ID No. US20030040615A1 rat00012080

) NAME/KEY: unsure

) CACATION: 205-206, 221

OTHER INFORMATION: a, t, c, g, or other

US-09-535-459-1835
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1090-01-00
PRIOR PHOR APPLICATION NUMBER: 105/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTERQ FOR WINDOWS VEISION 3.0
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12;
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: PCT/USO0/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rattus norvegicus
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US-09-918-995-15962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-918-995-15962/c
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LENGTH: 408
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CF320986 uz57h10.y AQ470250 Hz, 5071\_B AQ470250 Hz, 5071\_B AW465848 68315 MAR B01986 cSRL-145A3-EE281680 601099657 BB604671 BB604671 B103177 602899417 B1656088 149119 MA B1652086 603844521 BG921734 TETRAGOON PR195208 BB154064 A177414 TETRAGOON PR195208 BB154064 A177556 606054006 BB154064 BB154060 A110350 ESA MASS A1273690 tf85f08.x A1423690 tf85f08.x A1423690 tf85f08.x A1423690 tf85f08.x A1436963 ag09b04.s A1436963 ag09b04.s A1436963 mr53310.x ANO46359 UI-M-BHI-A1434663 mr52360.x ANO46359 UI-M-BHI-A143663 mr52360.x ANO46359 UI-M-BHI-A143663 mr52360.x

Scoring table:

Word size :

Searched:

Database :

score:

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Run on:

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AW130644
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2853
1 atgcttttgctgggcatcct.....gcgtcctgaggccgtgctga 2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32308132
                        GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      16154066 segs, 8097743376 residues
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                                                                                                                      using sw model
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Gapop 60.0 , Gapext 60.0
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A1698994 wc95f04.x AM430043 68812 MAR AA906648 UI-R-C0-h PF511038 UI-H-BI4-AA478616 zv19c12.s A1493824 tm92h0.x A1580450 tc34a06.x

AW430043 BF511038 AA996648

BE645522 7e71g08.x

ALIGNMENTS

L1202856 q154h11.x BF283275 EST447866 BI534593 397660 MA

BF078689 229090 MA AW935807 QV3-DT001 AQ806642 HS\_4758\_A BB612189 BB612189 AZ842795 ZW0141119 BE553572 Ur47b04.y

BF078689 AW935807 AQ809642 BB612189 AZ842795 BE553572

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Query Match Length

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Best Local Similarity
Matches 38; Conserv
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AQ809642
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KEYWORDS
SOURCE
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer.Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-0V3-DT0019-081
599-039-0086t3-1999-12-088t4-1)
Seq primer: puc 18 forward
High quality sequence start: 58
High quality sequence start: 58
High quality sequence stop: 109.
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//dev_stage="Addult"
//note="Organ: denis_drash; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
           Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;.
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., de Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Ragal,M.A., de Silva,W.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW935807 190019-081299-039-008 DT0019 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                             1.9%; Score 53; DB 12; Length 544;
100.0%; Pred. No. 5.1e-14;
tive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DT0019"
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW935807.1 GI:8111213
                                                                                                                                                                                                                                                                                                                   Similarity 100.
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BB612189 SIKEN full-length enriched, 0 day neonate skin Mus musculus cDNA clone 4631401M01 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                 HS.4758_A1_D11_T7A CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4758 Col=21 Row=G, DNA sequence. A0809642. GI:5728884 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metzzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequenching Center
University of Washington
University of Washington
High Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Fax: (206) 616-3887
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
tissue mRNA and cDNA amplification were performed under low stringency conditions.  
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                   Length 195;
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                                                                                                                                                             Indels
                                                                                                                                                                                                       ch 1.3%; Score 38; DB 17; I
I Similarity 100.0%; Pred. No. 7.9e-07;
38; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="Plate=4758 Col=21 Row=G"
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                                                                                                                   Score 39; DB 10;
Pred. No. 2.1e-07;
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                                                                                                               1.4%; Score 1.00.0%; Pred. No. 2.1.
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Location/Qualifiers
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                                                                                                                                             1 Similarity 100.
39; Conservative
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Class: BAC ends
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http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared fr.m a derivative
Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 469)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ842795
ZMO141I19F Mouse 10kb plasmid UUGCIM library Mus.musculus genomic clone UUGCZMO141I19 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                        Length 961;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                        Score 36; DB 10; I
Pred, No. 8.3e-06;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 5td Error: 0.00
Plate: 0141 row: I column: 19
Seq primer: CGTFGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                  449 ACAGCCAGGGCGCACACCTTCTCCAGCGCCGGGGTG 484
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
/clone="UUGC2M0141119"
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                              36; Conservative
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84112, USA
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                                                                                                      Fixed integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) nonredundant cDNA, Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, H., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primed with a primer [5' GAGAGAGCACTTTTTTTTTTTTTTTVN 3'], CDNA was GAGAGAGAGGAGAGGACCATTTTTTTTTTTTTTTTTTT 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.X., Shibata.X., Itoh
.M., Konno.H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa.Y., Izawa.M., Ohara.E.,
Watahiki,M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsuura
.S., Kawah.J., Okazaki,Y., Muramatsu.M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japan
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-922
Fax: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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/strain=FPRDN-3 misconing
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/clone='InbaCB:3153391"
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/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/note='Organ: manmary; Vector: pCMV-SPORT6; Site_1: SalI;
/note='Organ: Site_1: SalI;
/note='Organ: SalI; SalI;
/note='Organ: SalI; SalI;
/note='Organ: SalI; SalI;
/note='Organ: SalI; Sa
of pWD42 (gil4732114|gb|AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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IMAGE:3153391 5
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NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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Contact: Robert Strausberg, Ph.C.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0;
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11arity 100.0%; Pred. No. 2.1e-05;
Conservative 0; Mismatches 0;
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EST 29-DEC-2000

linear

mRNA

305 bp

BF320986

RESULT 7 BF320986 LOCUS

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400 bp DNA linear GSS 31-MAR-1999 HS_5071_B2_D07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=647 Col=14 Row=H, DNA sequence.
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao.S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: GapDS-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.llnl.gov/image/html/iresources.shtml
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 400)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzeli, S., Holzman, T.,
                                                                                                                                                                  Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 305)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
Thational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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uz57h10.yl NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3673219 similar to TR:09UP80 Q9UP80 METH1 PROTEIN. ;, mRNA sequence.
BF320986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB\N"
/db_xref="taxon:10090"
/clone="Inbance:367319"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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0.0048;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1765 GGCTACAACCACAGCACCAACCGGCTCACT 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 192.
Location/Qualifiers
1. .305
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                                                                                             BF320986.1 GI:11270026
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1433987
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Gaps

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GSS 13-JUL-1996

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Gaps

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Indels

; 0

10 others

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/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/cell_type="chimeric hamster somatic cell hybrid"
/note="Vector: SCos-1; Human Chromosome: 11 specific cosmid
library prepared from flow sorted human chromosome 11
derived from Chimese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, 11"
somatic cell hybrid, 31"
36 c 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 169)
Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M.,
Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S.,, Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer,K. and Garner,H.R.
                                                                       /organism="sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_nost="DHIOB"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B01986 13-JUL-16 CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145A3, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cSRL-145A3"
/clone_lib="cSRL flow sorted Chromosome 11 specific cosmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 28; DB 10; Length 415; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 27; DB 17; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
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Conservative 0; Mismatches
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Location/Qualifiers
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                т. .169
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Best Local Similarity
Matches 27; Conserv
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KEYWORDS
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                      FEATURES
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                             High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 7e1: (206) 616-3618
Fax: (206) 616-3818
Fax: 206) 616-3818
Fax: (206) 616-3818
Fax: 206) 616-3818
Fax: (206) 616-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 Vector at EcoRI sites" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the *minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 415)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
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EST discovery in swine
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Plate=647 Col=14 Row=H"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 400;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 29; DB
100.0%; Pred. No. 0.0
:ive 0; Mismatches
Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2164 GATGACAACTACCTGGCTCTGAAGAACAG 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 400.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 28 row: D column: 18
Seq primer: ATTTAGGTGACACTATAG.
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Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends
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Sus scrofa
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AW485848
LOCUS
DEFINITION
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VERSION
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SOURCE
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AUTHORS
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs
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BI103177
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JOURNAL
COMMENT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 247)
Alzawa, K., Arahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraka, T., Hirozane, T., Hodoyama, Y.,
Imotani, K., Ishli, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K.,
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                                                                                                             BE281680 627 bp mRNA linear EST 26-OCT-2000 601099657F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491991 5',
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Stem cell origin."
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
/library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

a 159 c 177 g 138 t
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL,)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMBSIT row: a column: 16
High quality sequence stop: 530.
Location/Qualifiers
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NIH-WGC http://mgc.nc1.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
(Uppublished (1999)

Contact: Robert Strausberg, Ph.D.
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100.0%; Pred. No. 0.47;
Lve 0; Mismatches 0; Indels
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/strain="C2ECH II"
/db_xref="taxon:10090"
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BE281680.1 GI:9156727
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BE281680
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KEYWORDS
SOURCE
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Email: genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp/
Carninci,P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayshizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayshizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTS (Alzawa,K. et al. 2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sclences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.rtc.riken.jo.jp) for
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0.9%; Score 25; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 0; Indels
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1. .247
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us-10-009-332-2.oli.rst

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORMARD: AGGAACAGCTATGACGAT
BACKWARD: GTTTTCCCAGTAGAGGAG
Plate: 62 row: B column: 2
Seq primer: ATTTAGGTGACATATAG.
Location/oulifiers

1. 464
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603344521F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5372261 5',
BI692986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Context: Robert Strausberg, Ph.D.

Email: Cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov
Plate: LLAM11947 row: j column: 06

High quality sequence stop: 664.
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 664)
Muth-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/note="Vector: pCMV SPORT6; Site_1: Not!; Site_2: Sall;
Library made from pooled tissue from day 20 and day 40 embryos."
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Pred. No.
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/clone="IMAGE:5372261"
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/strain="FVB_N"
/db_Aref="Laxon:10090"
/clone="InAction=11b="NOI_CGAP_Kid14"
/clone=Inb="NOI_CGAP_Kid14"
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/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI:
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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Smith, T. P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Techhologies, Inc.
CDNA Library Prayaration: Life Techhologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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0.9%; Score 25; DB 13; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels
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149119 MARC 4BOV Bos taurus CDNA 5', mRNA sequence.
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
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BE666088.1 GI:10026679
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                                                                                                  Mus musculus
                                                                           house mouse.
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0.8%; Score 24; DB 13; Length 664;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 24; Conservative 0; Mismatches 0; Indels

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Search completed: May 2, 2003, 04:28:09 Job time : 3943 secs

Appl Appli A

Sequence 17, Sequence 3, Pequence 2, Pequence 2, Pequence 2, Pequence 4, Pequence 4, Pequence 4, Pequence 13, Pequence 3, Pequence 3, Pequence 3, Pequence 3, Pequence 13, Sequence 14, Sequence 14, Pequence 14, Pequence 14, Pequence 14, Pequence 14, Pequence 14, Pequence 14, Sequence 16, Pequence 17, Sequence 17, Seq

US-09-411-329C-17 US-08-836-442-3 US-09-8018-601A-6 US-09-920-048-2 US-09-920-048-4 US-09-920-048-4 US-09-920-048-4 US-09-920-048-4 US-08-477-407-4 US-08-444-355-4 US-08-886-443-3 US-08-886-443-3 US-08-886-443-3 US-08-886-443-3 US-08-886-443-3 US-08-886-43-542-3 US-08-886-43-542-3 US-08-886-43-3 US-08-886-33-3

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Gencore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 17:10:24; Search time 15.41 Seconds

(without alignments)
1813.869 Million cell updates/sec

(without alignments)
1813.869 Million cell updates/sec

Sequence: 5164
Sequence: 1 MLLGILTLAFAGRTAGGFE......DQCNLHRKPQELDFCVLRPC 950

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*

Issued\_Patents\_AA:\*

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## Result Ouery Duery Duery

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SCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN 623
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                                      HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTYON: Nucleic Acids Encoding Zinc Metalloproteases
TITLE OF INVENTYON: Nucleic Acids Encoding Zinc Metalloproteases
TITLE OF INVENTYON: NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENTH: 905
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                                                                                                                                                                                                                                                                                                                                                                                 VGHGGRLLARDQCNLHRKPQE-LDFCVLRPC 950
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                                                                                                LAAMSCVAGWSGSFLLAGEEFTIQP------QGAGDSLDQPHRLQRWG-PGQR 160
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                                                                  FAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGA-----HLLQRRGVPGGP
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Patent No. 6451575

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFREENCE: DM6909

CURRENT APPLICATION NUMBER: US/09/122,126B

CURRENT FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 21
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                                                                   Length 837;
                                                                                     267; Indels
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                                                                37.1%; Score 1917; DB 4; 46.3%; Pred. No. 2.6e-151;
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HGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRDD
                                                                                 Matches 381; Conservative 123; Mismatches
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Sequence 13, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
 version 3.0
                                     sapiens
                                                                          Similarity
SOFTWARE: Patentin
SEQ ID NO 2
                          TYPE: PRT
ORGANISM: Homo
                                            US-09-122-126B-2
                                                                Query Match
                                                                          Best Local
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER PELICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-06
SALLIER FILING DATE: 1997-09-06
SOFTWARE: FALLING DATE: 1997-09-06
SOFTWARE: FALLING DATE: 1997-09-05
SOFTWARE: FALLING DATE: 1997-09-0
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Matches 339; Conservative 114; Mismatches 146; Indels
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RESULT 5 US-09-369-364A-2

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                                  APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hirohata, Satoshi,
TITLE OF INVENTION: Nucleic Acids Encoding Zin
FILE REPERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2.
Sequence 2, Application US/09369364A Patent No. 6391610
                                                                                                                                                                                        TYPE: PRT
ORGANISM: mus musculus ADAMTS-5
                           GENERAL INFORMATION:
APPLICANT: Apte, St
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PRGFSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRT 874
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding 21r
FILE REFERENCE: 264734007/10-30-00
CURRENT PAPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 1882
                                                                                                                                                                                         RESULT 6
US-09-369-364A-13
'Sequence 13, Application US/09369364A
'Patent No. 6391610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens ADAMTS-9
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NAME/KEY: MOD_RES
LOCATION: (521)
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                                                                                                                        CGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYN 591
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472 GKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRT
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TITLE OF INVENTION: AGERECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
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US-09-122-126B-15
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US-09-122-126B-15
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-AGGSGPQTWWRRRRRS-----ISRARQVELLLVADASMARLYGRGLQHYLLTLASIAN 299
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                                                                                                                                                         RLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYW
                                                                      HDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP
                                                                                                                                                                                                                                                                                                              431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                832 VQILATDPTKPLDVRYSFFVPKK-----STPK-----VNSVTSHGSNKVGSHTSQP
                                                                                                                                 DTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP
                                                                                                                                                                                                                                                                                                                                                                                                     TSCGEGKLCLKGACVER----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTN
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Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 264374007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369, 364A
NUMBER OF SOD DATE: 1999-08-06
NUMBER OF SOD DOS: 31
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Mus musculus ADAMTS-9
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Patent No. 6416974
GENERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
PILLE REFERENCE: 09404/041001
CURRENT APPLICATION: TANGO-73, TANGO-74, TANGO-83
FILE REFERENCE: 1998-08-07
CURRENT FILING DATE: 1998-08-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
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                                                                 325 -TICDILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK 383
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                                          ATSELKNSHSKDKRKIRMRKRRKRNSLADDVALLKSGLATKVLSGYSNQT...NNTRDRW 119
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3 AVISLCSGMMGTFRSHDGDYFIEPLQSVDEQEDEEEQNKPHIIYRHSTPQREPSTGKHAC
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APPLICANT: HOLEEMAN, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PASLES FILING DATE: 1997-08-06
LEARLIER FILING DATE: 1997-08-06
SEQ ID NO 8
LENGTH: 481
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                                                                                                                                                                                       40;
                                                                                                                                                   31.1%; score 1607; DB 4; Length 5
.larity 48.5%; Pred. No. 1e-125;
Conservative 108; Mismatches 152; Indels
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EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
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Patent No. 6416974
GENERAL INFORMATION:
                                                                                                          ORGANISM: Rattus rattus
                                                                                                                                                                       Local Similarity
es 282; Conserv
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US-09-130-491-8
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                                                                                          TYPE: PRT
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APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. 64449388el Human Proteases and Polynucleotides Encoding
FILE REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR PAPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                LDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 EI---LIVQILAIDPIKPLDVRXSFEVPKK-----STPK------VNSVISHGSNKV 458
                                 104 SGDVNAEPDSFAAVSLCGGLRCAFGYRGAEYVISPLPNASAPAAQRNSOG---AHLLQRR 160 | | : : : | | : | | | | | | | | | |
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                                                                                                                                                                                                                        ARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLT
              GHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCL
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Patent No. 6448388
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332; Conserv
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LENGTH: 1224
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                                                                                                                                         PWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCP- 460
                                                                                                                                                                                                           461 --YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLCLKGACVERHNLN--KHR 514
                                                                                                                                                                                                                                 | :||| : ::||:: ||||| : TSVEDICVQLWCRHRDSDEPICHTRNASLLWADGTPCGPGHLCLDGSCVLREEVENPKAV 116
                                                                                                                                                                                                                                                                                 VDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSA 574
                                                                                                                                                                                                                                                                                                                                                                           755 SLLRYSGTGTAVESLQASRPILEPLTVEVLSV-GKMTPPRVRYSFYLPKEPREDKSSHPK 813
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                     695 GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 814 DPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQR
                                                                                                                                                                                                                                                                                                                                                     SGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPK
                                                                                                                                                                                                                                                                                                                                                                                                                         VVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMH
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Batent No. 6391610

GENERAL INFORMATION:
APPLICANT: HOREMATION:
APPLICANT: HICHAEL
APPLICANT: HICHAEL
APPLICANT: HICHAEL
APPLICANT: HICHAEL
APPLICANT: HICHAEL
APPLICANT: Notleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                           Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 518;
                                                                   Query Match 24.7%; Score 1273; DB 4; Length 48
Best Local Similarity 47.0%; Pred. No. 6.3e-98;
Matches 236; Conservative 87; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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45.4%; Pred. No. 3.9e-97;
tive 73; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874 TVPACDAAHRPVETQACG-EPC 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa = M
US-09-369-364A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.5
Best Local Similarity 45.4
Matches 244; Conservative
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-130-491-8
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SEQ ID NO 22
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                                                                                                                                              GHNFGMIHDGEGNWCKKSEG----NIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAIC 490
                                                                                                                                                                                        475 KGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGG 534
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246
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                                                                                                                                                                                                                                         590 YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------VLHNSVLSLSNQVE----QPDDRP------PARWVAGSWGPC
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                                                                                                                                                                           LLDQPSKPI---SLPEDLPGASYTLSQQCELAFGVGSKPCPY---MQYCTKLWC--TGKA
            ATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-NKVSDK
                                                       LDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHG-ADLEHYLLTLL
                                                                                       HPEYWDTAILFTRODLCG - - ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL
                                                                                                                                 GHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC
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Sequence 5, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                              SEE: Pennie & Edmonds, LLP: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                        STREET:
CITY: Ne
                 US-09-491-522-5
RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 QIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAF 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGYMMCTAFRTFDPCKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHCFKGHCIWLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 GPKY-TGNAALTLRNECAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 YSGDVN--AEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG-AHLLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 VE-TLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.6%; Score 1217; DB 4; Length 1211; Best Local Similarity 33.1%; Pred. No. 1.1e-92; Matches 347; Conservative 133; Mismatches 405; Indels 162
                                                                                        for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LAFAGRTAG---GFEPEREVVVPIRLDPD------
                                                                                                                                                                                                                                               30,605
R: 8389-0060-999
                                                                                                                       US/09/491,522
                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ADTAGRAS Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-006
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
                                                                                                                                                                                                                                                                                                          TELERA: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
                                                            IBM Compatible
                                                          COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: Window SOFTWARE: FastSEQ for Window APPLICATION NUMBER: US/OFILING DATE:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       ropology: linear
XX: USA
10036-2811
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   COUNTRY:
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qq	556 DILKRDGSWGAMSPFGSCSRTCGTGVKFRTRQCDNPHPANGGRTCSGLAYDF 607	q	172 PARPGHAQ-PHVVYKRQAPERLAQRGDSS
Qy dq	563 RSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDK 615 :  :	Qy	200 ESRSRRRSGRAKRFVSIPRYVETLV
δλ	CKLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGV	δχ	255 HPSILNPINIVVVKVLLLRDRDSGPKVTG
අු		QQ	280 DPSIGNPIHITIVRLVLLEDEEEDLKITH
oy D	675 GGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ 732 	oy Dp	315 LFTRQDLCGATTCDTLGMADVGTMCDP
QY	733 -GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTP 791 	δ <sub>γ</sub>	373 -NVKVCEEVFGKLRANHMMSPTLIQIDRA :
QQ QD	792 PRVRYSFYLPKEPREDKSSHPKDPRG	δy d	431 ISLPEDLPGASYTLSQOCELAFGVGSKPC
QY		y d	
Qy Db		QY Db	
Qy Db	926 RLLARDQCNLHRKPQELDFCVLRPC 950 	Qy	610 VSPRDKCKLICRANGTGYFYVLAPKVVDG                     626 VNPCELHCRPANEYFAKKLRDACVDG
RE US	RESULT 14 US-09-369A-7 Sequence 7, Application US/09369364A : Partent No. 6391610	Qy	
	GENERIC NO. USITUDO: GENERAL INFORMATION: APPLICANT: Apte, Suneel APPLICANT: Hurskainen, Tiina L.	Oy Dp	727 ALKNSQ-GKYLLNGHFVVSAVERDLVVKG   ::       :   738 ALRSEDPEKYFLNGGWTIQ-WNGDYQVAG
	APPLICANT: Hirohata, Satoshi TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases FILE REFREENCE: 264734407/10-30-00	QY	785SVGKMTPPRVRYSFYLPKEPRE 
	CORRENT FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.1	Qy do	838 RPPARWVAGSWGPCSASCGSGL   :
s s s	SEQ 1D NO / LENGTH: 997 TYPE: PRT ORGANISM: Homo sapiens ADAMTS-7	Qy	885 VETQACCEPCPTWELSAWSPCSKS::    :    :   :  : :  902 IHREAGGHDEVPPPVESWHYGPWTKCTVT
	Query Match 23.3%; Score 1202.5; DB 4; Length 997; Best Local Similarity 34.9%; Pred. No. 1.4e-91; Matches 351; Conservative 116; Mismatches 379; Indels 159; Gaps 46;	RESULT US-09-3	RESULT 15 US-09-369-364A-17 ; Sequence 17, Application US/09369364A
VO QO	1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDP	GE S	Patent No. 6391610 GENERAL INFORMATION: APPLICANT: Apte, Suneel APPLICANT: HITCKAITON THING
Qy Db			; APPLICANT: Hirohata, Satoshi ; TITLE OF INVENTION: Nucleic Acids E ; FILE REFERENCE: 26473/4007/10-30-00 ; CURRENT APPLICATION NUMBER: US/09/36
Qy Db	92 TGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASA 144   :	ON SES	URRENT FILING DATE: 1999-08-06 UMBER OF SEQ ID NOS: 31 OFFWARE: PatentIn Ver. 2.1 Q ID NO 17
δλ	145 PAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG 199	** ** **	LENGTH: 1081 TYPE: PRT ORGANISM: Homo sapiens ADAMTS-10

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LVVADAKMVEYHGQPQVESYVLTIMNMVAGLFH 279
                                                                                  PCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWAD 489
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| |: | : | || || || || || || || || || GWSGWSAWSICSRSCGMGVQSAERQCTQPTPK 571
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SSAP-STCGV------QVYPELESRRERW 219
                                                                                                                                                                                                    RANPWSACSAAIITDFLDSGHGDCLLDQPSKP- 430
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                           LVVADESMVKFHG-ADLEHYLLTLLATAARLYR 254
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631 LAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFT 690
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                                                                                                                                                                                                                                                                                                                 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFREEQCEAFNG-----YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYV 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 DFREVOCAEFDSIPFRGKFYKWKTYR------GGGVK---ACSLTSLAEGFNFYTE 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLP----- 801
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                                                                                                        65 FLLNLTRSSRLLAGRVSVEYW--TREGLAWQRAARPHCLYAGHLQGQASSSHVAISTCGG 122
                                                                                                                                  LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGV--ASGW 180
                                                                                                                                                                                        --NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHG-AD 237
                                                                                                                                                                                                                                            LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQK 297
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                       Query Match 22.3%; Score 1152; DB 4; Length 1081; Best Local Similarity 31.5%; Pred, No. 2.5e-87; Matches 318; Conservative 120; Mismatches 400; Indels 172;
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Human protein sequ Human polypeptide Rat aggrecanase. Human aggrecan deg Human PRO1563 (UNQ

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Human Tango-71 pro Human secreted pro Protein; SEQ ID 12

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**AAB86950** AAB21264

Human metalloprote Human aggrecanase

Human aggrecanase

ABG30702 ABG30703

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Human ADAMTS-SI pr Human ADAMTS-9 ami Human protease #12 Human ADAMTS-9 alt Human metalloprote Human ADAMTS 1 Zn Human ADAMTS 9 Zn

Rat metalloprotein Rat Tango-76 prote Murine ADAMTS-8 am Human secreted pro

ALIGNMENTS

AAB90625

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Himan protess #2	Hilman protesse 72.	Human metalloprote	Himan protesses #3	Himan protesse #1	Himan metalloproto	Rat metalloprotein	HIMAD ADAMPS-1 DED	Mouse metalloprote
SUMMARIES	ΩI	AAG62299	AAE22541	AAU74751	AAU72899	AAE22542	AAE22540	AAB21261	AAB21257	AAW78435	AAB21265
	DB	22	23	23	23	23	23	21	21	20	21
	ouery Match Length DB	950	950	952	928	367	321	381	505	727	896
d	Query Match	100.0	98.0	70.8	8.99	36.3	31.6	18.6	16.2	1.8	1.8
	Score	950	931	673	635	345	300	177	154	17	17
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SULT 1	
AAG62299 ID AAG62299 standard: protein: 950 aa	
AC AAG62299;	
DI 23-AUG-2001 (first entry)	
XX DE Human metalloprotease MDTS6 protein. XX	
KW Metalloprotease: human: aggregaase: doint disease: osteoarthritis.	erthritio.
	, e : : : : : : : : : : : : : : : : : :
OS Homo sapiens.	
XX PN W0200134785-A1.	
17-MAY-2001.	
10-NOV-2000; 2000WO-JP07917.	
AX PR 11-NOV-1999; 99JP-0321740. PR 16-MAY-2000; 2000JP-0144020.	
AA (YAMA ) YAMANOUCHI PHARM CO LTD. PA (KAZU-) KAZUSA DNA RES INST.	
Yamaji N, Nishimura K, Abe K, Ohara O, Nagase T,	Nomura N;
AA WPI; 2001-343602/36. DR. N-PSDB; AAH41003.	
AA PT Metalloprotease with aggrecanase activity for treating joint diseases	int disease
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                                         This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritis cativity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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100.0%; Score 950; Dest Local Similarity 100.0%; Pred. No. 0; Matches 950; Conservative 0; Mismatches
                       Claim 1; Page 56-60; 85pp; Japanese.
osteoarthritis
                                                                                                                                                   950 AA;
 especially
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); novel human protein; NHP, protease; biological disorder; obesity; blood pressure; arthritis; connective tissue disorder; infertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHPS share structural similarity with animal processes particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG 199
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                                           ARWVAGSWGPCSASCGSGLQKRAVDCRGSAGORTVPACDAAHRPVETQACGEPCPTWELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is novel human protein (NHP), human protease
781 VEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPP
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                                                                                                                                                                                                                                                                                                                            AAE22541 standard; Protein;
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N-PSDB; AAD35569.
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Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM; Belegeane AM, Baughn MR, Nguyen DB, Lee-EA, Hafalia A, Khan FA; Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT; Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;

22-JUN-2000; 2000US-213955P. 29-JUN-2000; 2000US-21S96P. 07-JUL-2000; 2000US-218946P. 14-JUL-2000; 2000US-218946P.

13-JUN-2001; 16-JUN-2000;

27-DEC-2001

(INCY-) INCYTE GENOMICS INC

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Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer; cardiovascular; atherosclerosis; autoimmune disorder; dermatitis; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; cell prollferative disorder; developmental disorder; epilepsy; buchenne muscular dystrophy; epithelial disorder; neurological disorder; reproductive disorder; endometriosis.
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PNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG 199
                    NPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQ
                                                                             DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE
                                                                                                                                                       VFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG
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                                                                                                                                                                                                                                                                                                                                                                                        proliferative (e.g. cancer)disorders
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N-PSDB; ABK12894.
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Kallick DA;
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Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigrathe; analgasic; endocrine; notropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antinflammatory; aspartyl protease; cyteine protease; metalloprotease; serine protease; cancer; hematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; mandiather; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder.
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N-PSDB; AAS97182.
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Payne V;
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The invention relates to an isolated, enriched, or purified protease polypeptide (1) and polynucleotide (11) encoding (1). (1) may be used to screen for substances (5) that may modulate its activity. Administering S which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or hammarchopleitic origin, of the breast, colon, lung, prostrate, cervical, hearin, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, naurological disorders, hypotension, hypetrension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders uch as those above. Ad172876-AA0172910 represent human clissorders amino acid sequences of the invention.
           for substances that may
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           Novel protease polypeptide useful for screening for substances that be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
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Pred. No. 0;
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                                                                                    Figure 2G; 232pp; English.
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Best Local Similarity 99.9%;
Matches 755; Conservative (
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Human; novel human protein; NHP; protease; biological disorder; obesity;
high blood pressure; arthritis; connective tissue disorder; infertility;
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                                                                          Gaps
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                   200 ESRSRRRSGRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSIL
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    200 ESRSRRRSGRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSIL
                                                           260 NPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWOKKLNKVSDKHPEYWDTAILFTRO
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                                                                                                                  320 DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELG 364
                                                                                                                                320 DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELG 364
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                                                                                                                                                                                                                AAE22540 standard; Protein; 321
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                                                                                                                                                                                                                                                                                                                                                              gene therapy; enzyme.
                                                                                                                                                                                                                                                                          (first
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N-PSDB; AAD35568.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is novel human protein (NHP), human protease. NHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
STEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAETVISPL 139
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100.0%; Pred. No. 0;
1ve 0; Mismatches
                                                         GHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRP
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                                                                                                                                                        AAE22542 standard; Protein; 367 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001; 2001WO-US30350.
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Matches 345; Conservative
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                                                                                                                                                                                                                                            Human protease #3.
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                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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The present sequence is human metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell
                            199
                                                        259
                                                                                                           Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                        Human; ADAMTS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
               140 PNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG
                                                                     ESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Xaa= any amino acid"
Misc-difference 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "Xaa- any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                            AAB21261 standard; Protein; 381 AA
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                                                                                                                                                                                                                                                                                                Human metalloproteinase ADAMTS-5.
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Misc-difference 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Xaa≈ any
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N-PSDB; AAA95831.
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AAB21261
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migration, inflammation and/or angiogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
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                                                                                                                                                                                                                                                             255 HPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAI 314
                                                                                                                                        Gaps
                                                                                                                                                                                                                                       LFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV 374
                                                                                                                                                                                           16 HPSILNPINIVVVVVVVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; nootropic; neuroprotective; antiparkinsonian;
cerebroprotective; cytostatic; antiarthritic; immunosuppressive;
Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis;
                                                                                                                                                                                                                                                                                                         KVCEEVFGKLRANHMASPILIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disintegrin and metalloproteinase domain; thrombospondin domain;
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                                                                                                     Length 381;
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                                                                                                 18.6%; Score 177; DB
Llarity 100.0%; Pred. No. 3.1
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21257 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat metalloproteinase ADAMTS-5.
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N-PSDB; AAA95827.
                                                                                                                Best Local Similarity
Matches 177; Conserv
                                                                     AA;
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                                                                     Sequence
                                                                                                     Query Match
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The present sequence is mouse metalloproteinase ADAMTS-1. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
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                                                                                                                                                                                                                                                                                                                                                          Mouse; ADAMTS-1; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; erebroprotective; cytostatitic; antiparkinitic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autolimmune disease; brain tumour; brain injury.
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Mismatches 0;
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 17; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY49501 standard; Protein; 950 AA.
                                                                                                                                                                                            AAB21265 standard; Protein; 896 AA
                                                                                                                                                                                                                                                                                                                      Mouse metalloproteinase ADAMTS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5°,
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US06237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 AFTTAHELGHVENMPHD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 AFTTAHELGHVFNMPHD 372
                                                                 156 AFTTAHELGHVFNMPHD 172
                                                                                                                                                                                                                                                                             (first entry)
  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                           356 AFTTAHELGHVFNMPHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kelner GS, Clark M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594326/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             896 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200053774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38-MAR-1999;
                                                                                                                                                                                                                                                                             23-FEB-2001
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                                                                                                                                                                                                                                       AAB21265;
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AAY49501
ID AAY49
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a novel human metalloproteinase-disintegrin protein with a thrombospondin domain (ADAMTS-1). The protein may be used in drug compositions and foodstuffs, as an agent for decreasing the leukocyte and thrombocyte blood count and increasing the erythrocyte blood count, e.g. for treatment of inflammatory diseases such as rheumatoid arthritis, hepatitis, nephritis, Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metalloproteinase-disintegrin protein with a thrombospondin domain; ARDS; ADAMYS-1; drug composition; foodstuff; leukocyte; thrombocyte; hepatitis; blood; erythrocyte; inflammatory disease; rheumatoid arthritis; asthma; nephritis; crohn's disease; acute respiratory disease syndrome.
                                                                                                                                                                                                                                                                                                    262 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQ1 321
and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                             338 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQI 397
                                                                                                                                                                                         278 GPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 337
                                                                                                                                                   Gaps
                                                                                                                                                                                                                  Human metalloproteinase-disintegrin protein with thrombospondin domain - useful as leukocyte and thrombocyte decreasing and erythrocyte increasing agent
                                                                                                                                                   ;
0
                                                                                                        Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inoguchi E, Ishida Y, Ishioka K;
                                                                                                                                                 0; Indels
                                                                                                      16.2%; Score 154; DB 21; I
100.0%; Pred. No. 4.3e-145;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 20;
Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                   322 DRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI 355
                                                                                                                                                                                                                                                                                                                                                               398 DRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 51-52; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW78435 standard; Protein; 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KURE ) KUREHA CHEM IND CO LTD.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                 Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ADAMTS-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hakozaki M, Hirose K,
Kuno K, Matsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-070277/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                            Similarity
                                                               505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX17990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9855643-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1999
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Gaps

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AAY49501;

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The present sequence represents a murine ADAWTS-1 protein. ADAWTS-1 is a metalloproteinase. The specification describes another related metalloprotease, a C. elegans GON-1 protein, that lacks a transmembrane domain and possesses a predicted metalloprotease domain between residues 569-456. In C. elegans hermaphrodites, GON-1 is required for migration of two distal tip cells to produce elongated tubes, whereas in males, GON-1 is required the The protein is used in the method of the invention. The specification describes a metalloproteinse domain and a thrombospondin protein that contains a metalloproteinse domain and a thrombospondin
                                                                                                                                                           GON-1; metalloproteinase; cell migration; modulator; ADAMTS-1; metalloproteinase domain; thrombospondin domain; abnormal cell migration; organ shaping; sterility; cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain. The method comprises treating a target organism, having a developing gonadal cell that is responsive to the protein, with a test attributeable to the test compound. The compounds identified are potential therapeutic modulators of abnormal cell migration and organ shaping, e.g. for rendering animals (specifically nematodes) sterile and for inhibiting cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying modulators of proteins containing metalloprotease and thrombospondin domains, potentially useful for controlling cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ADAM-type metalloprotease MDTS4, SEQ ID NO:4.
                                                                                                                Amino acid sequence of a murine ADAMTS-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 17; DB 21; I
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB73549 standard; Protein; 950 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1C; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0087170.
99US-0129023.
                                                                                                                                                                                                                                                                                                                                                                                               99WO-US11918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         migration and organ shaping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 AFTTAHELGHVFNMPHD 372
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                                                              13-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                     W09961656-A2
                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                  12-DEC-1999.
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                      AAY53899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of
anglogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to anglogenesis including abnormal.
wound healing, inflammation, rheumatoid arthritis, psoriasis,
candometrial bleeding disorders, diabetic rethinopathy, some forms of
macula degeneration, haemangiomas, and arterial-venous malformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
complisation (chemotaxis) of immune cells. The etiology of these
immune deficiencies or disorders may be genetic, sometic, such as
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat inflammatory
conditions, both chronic and acute conditions. The products can also be
used for detection and diagnosis. AA323002 to AA323080, and AA449503 to
AA449511 represent sequences given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                      Human, METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; mecula degeneration; hæmangioma; detection; arterial-venous malformation; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 17; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Fig 1; 457pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0072298.
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                                                            10-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IRUE/) IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HAST/) HASTINGS G A. (RUBE/) RUBEN S M.
                                                                                                              Human METH1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-590684/50.
N-PSDB; AAZ32000.
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                                                                                                                                                                                                                                                                                                                                                                   WO9937660-A1.
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-1999;
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Gaps

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AAY53899 standard; Protein; 950 AA.

RESULT 12
AAY53899
ID AAY53

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invention.

Sequence Query Match

Length 950; 0; Indels 99US-0318208

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10-AUG-1999;
13-AUG-1999;
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                                                                                      (SMIK )
(BETH-)
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                                                                                                                                                                                                                                       The invention relates to the novel human ADAM (A Disintegrin And Metalloprocease)-type metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS6 or MDTS5 genes, the recombinant production of MDTS4 and MDTS5, and antibody specific for MDTS4 or MDTS5, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; METHI; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; sclerodermi, crebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; oblater Webber syndrome; plaque neovascularisation; telanglectasia; haemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                           A new metal protease and its preparation for use as an anti-cancer and
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 22; Length 950;
Pred. No. 1.3e-07;
0; Mismatches 0; Indels
Human; MDTS4; ADAM-type metalloprotease; drug screening; A Disintegrin And Metalloprotease; cancer; arthritis.
                                                                                                                                                                                                                        Claim 1; Page 12-14; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50002 standard; Protein; 950 AA.
                                                                                                                                                                                                                                                                                                                                                               1.8%; Scorv
v 100.0%; Pre
                                                                                                                                     (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                 sequence represents human MDTS4,
                                                                                              99JP-0196584.
                                                                                                                   99JP-0196584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000WO-US14462.
                                                                                                                                                                                                    anti-arthritic therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                             379 AFTTAHELGHVFNMPHD 395
                                                                                                                                                                                                                                                                                                                                                                                                                356 AFTTAHELGHVFNMPHD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8 Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                          WPI; 2001-275950/29.
N-PSDB; AAH20224.
                                                                                                                                                                                                                                                                                                                                                     950 AA;
                                                    JP2001017183-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200071577-A1.
                                 Homo sapiens.
                                                                                             09-JUL-1999;
                                                                                                                  09-JUL-1999;
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                                                                        23-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human METH1
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AAB50002
ID AAB50
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The present sequence is human METH1 (ME for metalloprotease and TH for thrombospondin). METH1 can be used for inhibiting angiogenesis in an individual, and for treating cancer, benjagn tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque necvascularisation, telangiectasis, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH1 can also be used in birth control. METH1 can also be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITGL-TSP; integrin ligand; angiogenic disease; cancer; atherosclerosis; chronic inflammatory disorder; rheumatoid arthritis; tissue remodeling; macular degeneration; diabetic retinopathy; Alzheimer's disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METH1 and METH2 polynuclectides and encoded polypeptides, used to inhibit anglogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iruela-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH; Fornwald JA, Terrett JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 17; DB 22; I
100.0%; Pred. No. 1.3e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                 SMITHKLINE BEECHAM CORP.
BETH ISRAEL DEACONESS MEDICAL CENT.
IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human integrin ligand polypeptide ITGL-TSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW80285 standard; Protein; 967 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Fig 1; 768pp; English.
99US-0144882.
99US-0147823.
99US-0373658.
                                                                                                                                                                                                 HUMAN GENOME SCI INC
                                                                                                                                2000US-0183792
                                                                                                    99US-0171503
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                                                                                                                                                                                                                                                                                                                                  HASTINGS G A.
                                                                                                                                                                                                                                                                                        (IRUE/) IRUELA ARIEPE
(HAST/) HASTINGS G A.
(RUBE/) TRUENS S M.
(JONA/) JONAK Z L.
(TRUL/) TRULLI S H.
(FORN/) FORMALID J A.
(TERR/) TERRETT J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-025136/03.
N-PSDB; AAC90057.
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                                                                                                                                                                                                                                                                                                                                                      This represents a human integrin ligand polypeptide ITGL-TSP. ITGL-TSP polypeptides can be used in the treatment of angiogenic diseases such as cancer, cancer metastasis, chronic inflammatory disorders, rheumatoid attrititis, atheroscierosis, macular degeneration or diabetic retinopathy, restenosis, Alzheimer's disease and tissue remodeling. They can be used to treat a subject in need of enhanced activity or expression of the ITGL-TSP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                        DNA encoding integrin ligand polypeptide ITGL-TSP - used to treat anglogenic diseases, restenosis, Alzheimer's disease and in tissue remodeling
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                                                                                                                                                             Fronwald JA, Hastings GA, Jonak ZL, Terrett JA;
Trulli SH;
                                                                                                                                                                                                                                                                                                                              Claim 11; Pages 6-9; 24pp; English.
                                                                                              (HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                              98EP-0300575.
                                                             97US-0845496.
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N-PSDB; AAV66508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 AA;
                              27-JAN-1998;
                                                             24-APR-1997;
28-0CT-1998.
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Search completed: April 29, 2003, 17:22:32 Job time : 52 secs

396 AFTTAHELGHVFNMPHD 412

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Sequence 13, Application US/09130491

Sequence 13, Application US/09130491

Patent No. 6416974

GENERAL INFORMATION:

APPLICANT: HOLICAMEN DOUGLAS A.

APPLICANT: GOOGMAIL, ANDREW D.J.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT APPLICATION NUMBER: US/09/130,491

CURRENT FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: US 60/058,108

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-09-06

NUMBER OF SEQ ID NOS: 16

NUMBER OF SEQ ID NOS: 16
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US-09-130-491-2
; Sequence 2, Application US/09130491
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: HOLTEMEN. DOUGLAS A.
; APPLICANT: GOOGBEAL1, ANGEW D.J.
; TILLE OF INVENTION: TANGO-71, TANGO-73, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 18, Appl
Sequence 29, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 29, Appl
Sequence 44, Appl
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Pred. No. 9.4e-08;
0; Mismatches 0;
US-08-487-568-18

US-08-817-561-29

US-09-311-9218-29

US-07-646-531D-7

US-08-187-7708-13

5426100-7

US-08-187-7708-13

US-08-57-3098-29

US-08-57-3098-44

US-08-557-3098-44

US-08-557-3098-44

US-08-557-3098-44

US-08-557-3098-44

US-08-256-44

US-08-834-306-44

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US-08-256-44
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100.0%; Pre
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Best Local Similarity 100.
Matches 17; Conservative
    TYPE: PRT
CORGANISM: Mus musculus
US-09-130-491-13
    -09-130-491-13
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LENGTH: 608
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                                                                                                                                             April 29, 2003, 17:20:53; Search time 24 Seconds (without alignments) 1164.657 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                      GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-130-491-2

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US-09-122-126B-2

US-09-36-364A-15

US-09-36-364A-15

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US-07-801-812A-18
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                                                                                                                                                                                                                                                                                                                                                                                         262574 seqs, 29422922 residues
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                                                                                                             protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length
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No.
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Gaps

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Sequence 15, Application US/09369364A
Patent No. 6391610
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; Sequence 8, Application US/09130491
; Patent No. 6416974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens ADAMTS-9
                                                                                                                                                                                                                                                                                                              ) ORGANISM: Mus musculus ADAMTS-9
US-09-369-364A-15
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US-09-364A-13
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Best Local Similarity 100.
Matches 13; Conservative
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272 AHELGHVFNMPHD 284
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LOCATION: (521)
                                                                         GENERAL INFORMATION:
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LOCATION: (468)
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US-09-369-364A-13
RESULT 5
US-09-369-364A-15
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APPLICANT: HOLIZMAN, Douglas A. '
APPLICANT: GOOGBAIL, Andrew D.J.
TITLE OF INVENTON: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
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                                                                                              Length 967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.5%; Score 14; DB 4; Length 551
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                    0; Indels
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APPLICANT: Bristol. Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REPERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
LENGTH: 837
                                                                                                Score 17; DB 4; L
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER APLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-06
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09122126B Patent No. 6451575
                                                                                  1.8%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                   RESULT 3
US-09-130-491-16
Sequence 16, Application US/09130491
Patent No. 6416974
                                                                                                                                                                         356 AFTTAHELGHVFNMPHD 372
                                                                                                                                                                                              Query Match 1.4
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                   Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 HFPWADGTSCGEGK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 HFPWADGTSCGEGK 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 DTAILFTRODLCG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Rattus rattus
US-09-130-491-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-122-126B-2
       ; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-491-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-122-126B-2
                                                                                                    Query Match
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APPLICANT: HOLIZEMEN, Douglas A.
APPLICANT: GOOGEAL1, ANGTEW D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09369364A

Sequence 13, Application US/09369364A

Sequence 13, Application US/09369364A

Sequence 13, Application Sequence 1

APPLICANT: Apre. Sunce 1

APPLICANT: Hirohata, Satoshi

TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

FILE REFERENCE: 26473/4007/10-30-00

CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.1
APPLICANT: Apte, Suneel APPLICANT: Apte, Suneel APPLICANT: Hurskainen, Tiina L. APPLICANT: Hurskainen, Tiina L. APPLICANT: Hirchata, Satoshi TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases CURRENT APPLICATION WUBBER: US/09/369,364A CURRENT FILING DATE: 1999-08-06 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 13; DB 4; Length 874; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 13; Conservative 0; Mismatches 0;
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Sequence 9, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:

APPLICAWT: Abte, Sunce!

APPLICAWT: Hurskainen, Tiina L.

APPLICAWT: Hurskainen, Tiina L.

APPLICAMT: Hurskainen, Tiina L.

TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases;

FILE REFERENCE: 26473/4007/10-30-00

CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06

SOUTHWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGHH: 905

HURSHOW PARENCE: PATENCE PATENC
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; Sequence 2, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Hurskalmen, Tilna L.
; APPLICANT: Historiata, Satcoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 2647340077.10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%; Score 12; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 12; Conservative 0; Mismatches 0;
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 8
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CORGANISM: mus musculus ADAMTS-5
US-09-369-364A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
watches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Rattus rattus US-09-130-491-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603 WVPKYSGVSPRD 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 WVPKYSGVSPRD 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 WVPKYSGVSPRD 213
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                                       Gaps
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SSETURARE: Patentin Ver. 2.1
SEG ID NO 22
LENGTH: 518
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                                                                                                                                                                             1.2%; Score 11; DB 4; Length 930;
100.0%; Pred. No. 0.075;
tive 0; Mismatches 0; Indels
1.2%; Score 11; DB 4; Length 930; 100.0%; Pred. No. 0.075; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 22, Application US/09369364A; Patent No. 6391610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/09491522
; Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens ADAMTS-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: MOD_RES
; LOCATION: (99)
; OTHER INFORMATION: Xaa = M
US-09-369-364A-22
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2
Best Local Similarity 100.
Matches 11; Conservative
   Ouery Match 1.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-126B-15
                                                                                             376 CDTLGMADVGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 CDTLGMADVGT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 CDTLGMADVGT 386
                                                                          327 CDTLGMADVGT 337
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US-09-491-522-11
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GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
FILE REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT PILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1224
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US-09-369-364A-5
Sequence 5, Application US/09369364A
Sequence 5, Application US/09369364A
Sequence 5, Application US/09369364A
GENERAL INFORMATION:
APPLICANT: Alte, Suneel
APPLICANT: HIrshara, Saroshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
            FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                                                                                                                                                      8389-0060-688
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Pred. No.
      SOFTWARE: FastSEQ for Windows Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                          FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-49-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/09930872
; Patent No. 6448388
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1%;
Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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; ORGANISM: homo sapiens
US-09-930-872-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-491-522-5
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597 PCSRTCGGGV 606
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US-09-930-872-4
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                             APPLICANT: Colige, Alain
APPLICANT: Laplafre, Charles M.
APPLICANT: Laplafre, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
NUMBER OF SEQUENES: 17
CORRESPONDENCE AND THE PRODUCTION, METHODS AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPOND
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Pred. No. 0.86;
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                                                                                                                                                                                                                                                                                                                                                                                    ZOUNTIL USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettee
COMPUTER: IBM COMPAITIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows.Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0.8
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ADTAMS, SAMUEL B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650-493-5556
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COMPUTER READABLE FORM:
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US-09-491-522-11
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704 DKCGVCGGDN 713
GENERAL INFORMATION:
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COUNTRY:
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US-09-491-522-5
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Search completed: April 29, 2003, 17:24:27 Job time : 26 secs

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April 29, 2003, 17:10:25; Search time 35.9135 Seconds (without alignments) 2738.218 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.
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/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                    US-10-009-332-1_COPY_213_950
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Human metalloprote	Human protease #2.	Human protease PRT	Human metalloprote	Human ADAMTS-1 pro	Human METH1 protei	Human ADAM-type me	Human METH1. Homo	Human integrin lig	Human Tango-71 pro
ΩΙ	AAG62299	AAE22541	AAU74751	AAU72899	AAW78435	AAY49501	AAB73549	AAB50002	AAW80285	AAY04142
DB	22	23	23	23	20	20	22	22	19	70
% Query Match Length DB	950	950	952	928	727	950	950	950	196	196
% Query Match	100.0	100.0	98.9	95.6	55.9	55.8	55.8	55.8	55.8	55.8
Score	4043	4043	3998	3743.5	2260	2254	2254	2254	2254	2254
Result No.	н	7	e	4	S	9	7	œ	Ġι	10

Metalloprotease with aggrecanase activity for treating joint diseases

## ALIGNMENTS

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Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                    Nomura N;
                                                                                                                                                                                                                                                    Nagase T,
                                                                                                                                                                                                                                                   Tamaji N, Nishimura K, Abe K, Ohara O,
                                                          Human metalloprotease MDTS6 protein.
AAG62299 standard; protein; 950 AA.
                                                                                                                                                                                                                     (YAMA ) YAMANOUCHI PHARM CO LTD.
(KAZU-) KAZUSA DNA RES INST.
                                                                                                                                                                                        11-NOV-1999; 99JP-0321740.
16-MAY-2000; 2000JP-0144020.
                                                                                                                                                                      10-NOV-2000; 2000WO-JP07917.
                                      23-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                      WPI; 2001-343602/36.
N-PSDB; AAH41003.
                                                                                                                               WO200134785-A1.
                                                                                                            Homo sapiens
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Protein;

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AAE22541 standard;
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                                     This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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                                                                                                                                                                                                                FVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                                                                                                                                                                                                                                                        ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP
                                                                                                                                                                                                                                                                                                                                  TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                           Length 950;
                                                                                                                                                                                 Indels
                                                                                                                                                           100.0%; Score 4043; DB 22;
100.0%; Pred. No. 4.2e-311;
ive 0; Mismatches 0;
                     Page 56-60; 85pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNLHRKPQELDFCVLRPC 738
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osteoarthritis
                                                                                                                                                                        Best Local Similarity 100. Matches 738; Conservative
                                                                                                                                                                       Similarity
                                                                                                                                         950 AA;
                                                                                                                                         Sequence
                                                                                                                                                              Query Match
Best Local
                     Claim 1;
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Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility; gene therapy; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid encoding a human protease, useful as a hybridization probe for screening libraries and assessing gene expression patterns -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is novel human protein (NHP), human protease. NHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 36-38; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                              (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                          29-SEP-2000; 2000US-236689P.
                                                                                                                                                                                                                                                                               27-SEP-2001; 2001WO-US30350
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hes 738; Conserv
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                                      Human protease
                                                                                                                                                                                                    WO200226949-N2.
                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                           04-APR-2002
26-JUL-2002
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                                                                                                                                                                                                                                                                                                                                     Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer; cardiovascular; atherosclerosis; autoimmune disorder; dermatitis; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; cell proliferative disorder; developmental disorder; epilepsy; buchenne muscular dystrophy; epithelial disorder; neurological disorder; reproductive disorder; endometriosis.
               812
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                                                                                         RTVPACDAAHRPVETQACGEPCPTWELSAWSPCSKSCGRGFQRRSLKCVGHGGRLLARDQ 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue H, Elliott VS, Gandhi AR, Lal P, Au-Young J, Tribouley CM; Delegeane AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA; Walla NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT; Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L; Kallick DA;
HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS
                                               PKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKP
                                                                               MHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVV
                                                                                                               KGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHP
                                                                                                                       KDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQ
                                                                                                                                                       Human protease PRTS-11 protein sequence
                                                                                                                                                                                                                                                                    AAU74751 standard; Protein; 952
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22-JUN-2000; 2000US-213955P.
29-JUN-2000; 2000US-21596F.
07-JUL-2000; 2000US-216621P.
14-JUL-2000; 2000US-218946P.
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                                                                                                                                                                                                                                                                                                      (first entry)
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N-PSDB; ABK12894.
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The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and myocardial infarction, autoimmune/inflammatory e.g. acquired immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g. cancer, developmental e.g. Duchenne and Becker muscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzheimer's disease and reproductive e.g. infertility and endometriosis disorders. Numerous other examples of each disorder are given in the specification. The present protein sequence represents the human protease PRTS-11 protein of the invention.
       useful
(e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLATAARLYRHPSILNPINIVVVKVLLL 272
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Twenty one human proteases (referred to as PRTS-1 to PRTS-21), in the diagnosis, treatment and prevention of gastrointestinal gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders
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                                                                                                                             177pp; English
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les 735; Conservative
                                                                                                                          Claim 1; Page 144-146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or heading to dispin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, exual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dystinesias), metabolic disorders and inflammatory disorders uch as those above. AA072876-AA072910 represent human cid sequences of the invention.
                                                                                                                                                                                                                                         Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; antimiflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoletic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; dyskinesia; metabolic disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substances that may
 873 GQRTVPACDAAHRPVETQACGEPCPTWELSAWSPCSKSCGRGFQRRSLKCVGHGGRLLAR 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protease polypeptide useful for screening for substances that be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenepeel S;
                                                                                                                                                                                                                 Human metalloprotease partial protein sequence #11
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                                                                                                                                 AAU72899 standard; Protein; 928 AA.
                              04-MAY-2001; 2001WO-US14431
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N-PSDB; AAS97182.
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                                                                                                                      AAU72899
ID AAU7
                                                                                                         RESULT
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Score 3743.5; DB 23; Length 928; Pred. No. 2.1e-287;

92.6%;

Query Match Best Local Similarity

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Metalloproteinase-disintegrin protein with a thrombospondin domain; ARDS; ADAWIS-1; drug composition; foodstuff; leukocyte; thrombocyte; hepatitis; blood; erythrocyte; inflammatory disease; rheumatoid arthritis; asthma; nephritis; Crohn's disease; acute respiratory disease syndrome.
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                                                            ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP
                                                                                                          HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS
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metalloprotease thrombospondin (METH) proteins METH1 and METH2
metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of
angiogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to angiogenesis including abnormal
wound healing, inflammation, rheumatoid arthritis, psoriasis,
endometrial bleeding disorders, diabetic retinopathy, some forms of
macula degeneration, haemangiomas, and arterial venous malformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
or mobilisation (chemotaxis) of immune cells. The etiology of these
immune deficiencies or disorders may be genetic, somatic, such as
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat inflammatory
conditions, both chronic and acute conditions. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                551 DIMYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKK----K 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency.
                                                            657 SAGQRIVPACDAAH--RPVETQACGE-PCPIWELSAWSPCSKSCGRGFQRRSLKCVGHGG
                                   SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRG
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                                                                      607 ES----FNAIPTFS---
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98US-0098539.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human METH1 protein.
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                                                                                                                                                                                                                                                                       Human metalloproteinase-disintegrin protein with thrombospondin domain - useful as leukocyte and thrombocyte decreasing and
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Best Local Similarity 54.3%; Pred. No. 4.2e-170;
Matches 405; Conservative 129; Mismatches 172;
                                                                                                                                                            Ishida Y,
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Kuno K, Matsushima K;
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                                                                                                                     KURE ) KUREHA CHEM IND CO LID
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                                              98WO-JP02449.
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and diagnosis. AA232002 to AA232080, and AAY49503 to sequences given in the exemplification of the present
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                                                                 40;
                                                  Length
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                                                Query Match 55.8%; Score 2254; DB 20; Best Local Similarity 54.0%; Pred. No. 1.8e-169; Matches 403; Conservative 131; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ADAM-type metalloprotease MDTS4, SEQ ID
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GVLSHESCDPLKKPKHFIDFCTMAEC
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detection a
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The invention relates to the novel human ADAM (A Disintegrin And Metalloprotease)-type metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and archritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 specific for MDTS4, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                             as an anti-cancer and
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nman; MDTS4; ADAM-type metalloprotease; drug screening;
Disintegrin And Metalloprotease; cancer; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             new metal protease and its preparation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 12-14; 22pp; Japanese.
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N-PSDB; AAH20224.
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                                                                                                                            JP2001017183-A.
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The present sequence is human METH1 (ME for metalloprotease and TH for thrombospondin). METH1 can be used for inhibiting anglogenesis in an individual, and for treating cancer, benjug tumours, an ocular anglogenic disease, rheumatodia arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial anglogenesis, coronary collaterals, cerebral collaterals arteriovenous malformations, ischaemic limb anglogenesis, Osler-Webber syndrome, plaque mevascularisation, telangiectasia, haemophiliac joints, anglofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH1 can also be used in birth control. METH1 can also be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                       RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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           of disorders such as cancer,
                                                                                                                                                                                                                                                                                 Length 950;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                              Query Match 55.8%; Score 2254; DB 22; Best Local Similarity 54.0%; Pred. No. 1.8e-169; Matches 403; Conservative 131; Mismatches 172;
           ne treatment
psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLLARDQCNLHRKPQE-LDFCVLRPC 738
                                               Claim 15; Fig 1; 768pp; English
           the
          inhibit angiogensis in th
rheumatoid arthritis and
                                                                                                                                                                                                                                                     950 AA;
                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                          Human; METH1; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; ocronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis, obster Webber syndrome; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
                                                          829
VISAKPGYHDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLSTLEQ
                                           SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRG
                                                                                                     ES------FNAIPTFS------AWVIEEWGECSKSCELGWQRRLVECKD
                                                                                                                                   SAGQRTVPACDAAH--RPVETQACGE-PCPTWELSAWSPCSKSCGRGFQRRSLKCVGHGG
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BETH ISRAEL DEACONESS MEDICAL CENT.
IRUELA-ARISPE L.
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924 GVLSHESCDPLKKPKHFIDFCTMAEC
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99US-0147823.
99US-0373658.
99US-0171503.
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Terrett JA;
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RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
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Fornwald JA,
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10-AUG-1999;
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(RUBE/)
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                            ES------FNAIPTES------AWVIEEWGECSKSCELGWORRLVECKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRG
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                                                                                        KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
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97US-0054966.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This represents a human integrin ligand polypeptide ITGL-TSP. ITGL-TSP polypeptides can be used in the treatment of anglogenic diseases such as cancer, cancer metastasis, chronic inflammatory disorders, rheumatoid arthritis, atherosclerosis, macular degeneration or diabetic retinopathy, restenosis, Alzheimer's disease and tissue remodeling. They can be used to treat a subject in need of enhanced activity or expression of the ITGL-TSP polypeptide.
                                                                                                                                                                                                       ITGL-TSP; integrin ligand; anglogenic disease; cancer; atherosclerosis; chronic inflammatory disorder; rheumatoid arthritis; tissue remodeling; macular degeneration; diabetic retinopathy; Alzheimer's disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDEQKGPEVISNAALILERNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGM 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding integrin ligand polypeptide ITGL-TSP - used to anglogenic diseases, restenosis, Alzheimer's disease and in remodeling
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Best Local Similarity 54.0%; Pred. No. 1.8e-169;
Matches 403; Conservative 131; Mismatches 172;
                                                                                                                                                                              Human integrin ligand polypeptide ITGL-TSP
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924 GVLSHESCDPLKKPKHFIDFCTMAEC 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Pages 6-9; 24pp; English.
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(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                       AAW80285 standard; Protein; 967
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                                                                                                                                                 (first entry)
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                                      The present sequence represents human Tango-71. Tango polypeptides are useful for identifying compounds which bind the polypeptide via direct binding, competition binding assays or Tango-71, -73, -74, 76 or -83-mediated signal transduction. Tango polypeptides are also useful for identifying modulating compounds by determining effect on Tango activity. Tango polypeptides and nucleic acids are useful for diagnosing diseases related to aberrant expression of Tango, and Tango polypeptides are useful for asising antibodies which can be used in diagnostic assays for detection of Tango, and also for generating anti-idiotype antibodies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                             55.8%; Score 2254; DB 20; Length 967; 54.0%; Pred. No. 1.8e-169;
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 54.0%; Pred. No. 1.8e-169;
Nes 403; Conservative 131; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 941 GVLSHESCDPLKKPKHFIDFCTMAEC 966
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Claim 8; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                      prevention and protection
                                                                                                                                                                                                                                                                                                 967 AA;
                                                                                                                                                                                                                                                                                                 Sequence
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QQ Op Oy Oy

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The present invention relates to human METH1 and METH2 (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatcoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in hirth control. METH can also be used in the present invention.
                                                                                                                            Human; METH1; metalloprotease; thrombospondin; angiogenesis inhibition;
                                                                                                                                        cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb angiogenesis; Osler Webber syndrome; plaque neovascularisation; telangiectasia; hemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
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BETH ISRAEL DEACONESS MEDICAL CENT.
IRUELA-ARISPE L.
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AAB50011 standard; Protein; 968
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99US-0147823.
99US-0373658.
99US-0171503.
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                                                              (first entry)
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Fornwald JA, Terrett JA;
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                                                                                              Protein; SEQ ID 125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RUBEN S M.
JONAK Z L.
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                              19-MAR-2001
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                               AAB50011;
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(RUBE)
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
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                                                                                RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                        ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                               241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                        PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416
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                                                                                                                        181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                        DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDK
                                                1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLLATAARLYRHPSILNPINIVVVKVLLL
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                                40;
                 968;
                 Length
                                Indels
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                DB 22;
.8e-169;
es 172;
                55.8%; Score 2254; D.larity 54.0%; Pred. No. 1.8e Conservative 131; Mismatches
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942 GVLSHESCDPLKKPKHFIDFCTMAEC
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                           Local Sim
nes 403;
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inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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to generate
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ben SM, Shi Y, Youn
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Rosen CA, Ruben SM,
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                                                                                                                        Location/Qualifiers
                                                                                                                                                          'label- unknown
                                                                                                                                                                                            label- unknown
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97US-0052989.
97US-0051919.
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Ni J, Olsen HS,
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N-PSDB; AAX04374.
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02-OCT-1997;
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Yu GL;
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fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in
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                                                                                                                                                                                                                                           Length 967;
                                                                                                                                                                                                                                    tch 55.4%; Score 2241; DB 20; al Similarity 53.8%; Pred. No. 2e-168; 401; Conservative 131; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLLARDQCNLHRKPQE-LDFCVLRPC 738
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GVLSHESCDPLKKPKHFIDFCTMAEC 966
                                                                                                                                                                             (see AAX04311 for described uses)
                                                                                                                                                                                                         967 AA;
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                                                                                                                                                                                                                                      Query Match
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Matches
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RESULT 13

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The present sequence represents a murine ADAWTS-1 protein. ADAWTS-1 is a metalloproteinase. The specification describes another related a metalloprotease, a C. elegans GON-1 protein, that lacks a transmembrane domain and possesses a predicted metalloprotease domain between residues CS 69-456. In C. elegans hermaphrodites, GON-1 is required for migration of a single linker cell to produce a single is required for migration of a single linker cell to produce a single clongated tube. The protein is used in the method of the invention. The specification describes a method for identifying a modulator of a protein that contains a method for identifying a modulator of a protein that contains a method for identifying a modulator of a protein that contains a methologonia compound, and determining a target organism, having a developing gonadal cell that is responsive to the protein, with a test compound, and determining any change in migration or shape of the cell attributable to the test compound. The compounds identified are attributed to the rest compound. The compounds identified are structubuted and later adulators of abnormal cell migration and organ shaping, e.g. for rendering animals (specifically nematodes) sterile and for inhibiting cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                  cell migration; modulator; ADAMTS-1;
thrombospondin domain; abnormal cell migration;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying modulators of proteins containing metalloprotease a thrombospondin domains, potentially useful for controlling cell
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                                                                                                                              Amino acid sequence of a murine ADAMTS-1 protein.
                                                                                                                                                                                                         cancer metastasis.
                 AAY53899 standard; Protein; 950 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WISC ) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1C; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                            98US-0087170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        migration and organ shaping
                                                                                           (first entry)
                                                                                                                                                                  GON-1; metalloproteinase;
                                                                                                                                                                                                         organ shaping; sterility;
                                                                                                                                                                                       metalloproteinase domain;
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13-APR-1999;
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                                                                                           13-MAR-2000
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                                                      AAY53899;
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FTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER
                                                                                                                                                                                           DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDK
                                                                                                                                                                                                                                 ------FNAIPTFS-----EWVIEEWGECSKTCGSGWQRRVVQCRD
                           241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN
                                     300 KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                                                                            357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF
                                                                                                                                            SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRG
                                                                                                                                                                                                                                                                                                                                      GRLLARDQCNLHRKPQE-LDFCVLRPC 738
                                                                                                                                                                                                                                                                                                                                                         GGVLSNESCDPLKKPKHYIDFCTLTQC 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse metalloproteinase ADAMTS-1.
                                                                                                                                                                                                                                                                                                                                                                                                         AAB21265 standard; Protein; 896
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The present sequence is mouse metalloproteinase ADAMTS-1. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell magration, inflammation and/or anglogenessis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
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Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                     DB 21; Length 896;
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                                                                                                                                                                                                                                                                                                                                                 Matches 375; Conservative 115; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                   51.9%; Score 2096.5; DB 2554.2%; Pred. No. 4.8e-157;
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                                                                Disclosure; Fig 17; 129pp; English
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Best Local Similarity
                                                                                                                                                                                                                                                                                          896 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                    Human; ADAMTS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropto; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; autoimmune disease; brain tumour; brain injury.
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Pred. No. 3.3e-147;
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308
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                              AAB21261 standard; Protein; 381 AA.
                                                                                                                          Human metalloproteinase ADAMTS-5.
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Best Local Similarity 94.0%;
Matches 358; Conservative
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                                                             AAB21261;
RESULT 15
              AAB2126
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Indels

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HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL 87

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                                                                                                         208 GDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMV
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Human ADAMTS-9 ami

AAU72897 AAB86950 AAB72280 AAB72286 AAB72286 AAW75426

Juman metalloprote Rat metalloprotein

AAB72287 AAB21255 AAB21252

ALIGNMENTS

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Human metalloprotease MDTS6 protein
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   April 29, 2003, 17:10:25; Search time 46.2301 Seconds (without alignments) 2738.218 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic. Nomura Nagase T, ò Ohara (YAMA ) YAMANOUCHI PHARM CO LID. (KAZU-) KAZUSA DNA RES INST. Yamaji N, Nishimura K, Abe K, 11-NOV-1999; 99JP-0321740. 16-MAY-2000; 2000JP-0144020. 10-NOV-2000; 2000WO-JP07917 WPI; 2001-343602/36. N-PSDB; AAH41003. WO200134785-A1. Homo sapiens 17-MAY-2001. Human protease PRT Human metalloprote Rat metalloprotein ADAM-type me METH1. Homo Human METH1. Homo Human integrin lig Protein; SEQ ID 12 Human metalloprote Human METH1 protei protease #2

Description

SUMMARIES

Human

AAG62299

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ВВ

Query Match Length

Score

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Result

Human

AAE22541 AAU74751 AAU72899 AAB21257 AAY49501 AAB73549 AAB7369002 AAB80285 AAB500011

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5164 5156 5111 4856.5 2497.5 2480.5 2480.5 2480.5 2480.5 2480.5

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Metalloprotease with aggrecanase activity for treating joint diseases

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                                                 The invention includes protein and bNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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                                        invention relates to a metalloprotease with aggrecanase activity
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                    Claim 1; Page 56-60; 85pp; Japanese.
osteoarthritis
                                                                                                                                                                              Matches 950; Conservative
                                                                                                                                                                    Similarity
                                                                                                                                    950 AA;
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Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility; gene therapy; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is novel human protein (NHP), human protease. NHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
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ARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPACDAAHRPVETQACGEPCPTWELS
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99.9%; Pred. No. 0;
Live 0; Mismatches
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            NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEH
                                       YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN
                                                                KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA
                                                                                          HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
                                                                                                  DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVC
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The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and polypeptides of the livrention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g. cancer, developmental e.g. Duchenne and Becker muscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzheimer's disease and reproductive e.g. infertility and endometriosis disorders. Numerous other examples of each disorder are given in the specification. The present protein sequence represents the human protease PRTS-11 protein of the invention.
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                                                                                                                                                                                                                                                                                                                           Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM; Delegeane AM, Baughn MR, Nguyen DB. Lee EA, Hafalia A, Khan FA; Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT; Azimzi Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Twenty one human proteases (referred to as PRTS-1 to PRTS-21), in the diagnosis, treatment and prevention of gastrointestinal gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders
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22-JUN-2000; 2000US-213955P.
29-JUN-2000; 2000US-215396P.
07-JUL-2000; 2000US-21682IP.
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The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering screen for substances activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migralne, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders also has also be useful as a diagnostic tool for a disease or disorder such as those above. AAD72876-AAD72910 represent human
                                                                                                                                                                     Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA
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                                        Manning
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94.7%; Pred. No. 0;
ive 0; Mismatches
                                        s,
                                                                                                                                                                                                                                                                                   Claim 28; Figure 2G; 232pp; English.
                                        Sudarsanam
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(SUGE-) SUGEN INC.
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                                           Plowman GD,
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                                                               Payne V;
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The present sequence is rat metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
DGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGL 719
                                                                                                                                                    IGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPL 779
                                                                                                                                                                                                      TVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRP 839
                                                                                                                                                                                                                     PARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPACDAAHRPVETQACGEPCPTWEL 899
                                                                                                                                                                                                                                                                                PARWVAGSWGPCSASCGSGLOKRAVDCRGSAGORTVPACDAAHRPVETQACGEPCPTWEL 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; nootropic; neuroprotective; antiparkinsonian;
cerebroprotective; cytostatic; antibarthritic; immunosuppressive;
Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis;
autoimmune disease; brain tumour; brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; ADAMTS-5; metalloproteinase; ADAM;
a disintegrin and metalloproteinase domain; thrombospondin domain;
                                                             VAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPK-VVDGTLCSPDSTSVCVQGKCIKAGC
                                                                                                                                                                                                                                                                                                          SAWSPCSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRPC 950
                                                                                                                                                                                                                                                                                                                       INC.
                                                                                                                                                                                                                                                                                                                                                                                                 AAB21257 standard; Protein; 505 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat metalloproteinase ADAMTS-5.
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contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 MASPILIQIDRANPWSACSAAIIIDFLDSGHGDCLLDQPSKPIILPEDLPGTSYSLSQQC 372
                                                                                                                                                                                                                                                                                                                                                   13 RHSQGAHLLQRRGAPVGPSGDPTSRCGVASGWNPAILRALDPYRPRRTGVGESHNRRRSG 132
                                                                                                                                                                                                                                                                                                                                                                                                                  MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERH 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARR--QCTNPTPANGGKYCEGVRVKYRSCN 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency.
                                                                                                                                                                                                                                                                89 QGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 VLLERDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 388
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                                                                                                                                                                                                                                                                                  13 QRLTGSSLDLRRCFYSGYVNAEPDSFAAVSLCGGLRGAFGYQGAEYVISPLPNTSAPEAQ
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RAKRRYSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK
                                                                                                                                                                                                                                                                                                                                   149 RNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSG
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                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                21; Indels
                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                               Score 2497.5; DB 2. Pred. No. 1.3e-185;
                                                                                                                                                                                                                                  8; Mismatches
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                                                                                                                                                                                                                                    Matches 462; Conservative
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                                                                                                                                                                                                                                                                                               metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of
anglogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to anglogenesis including abnormal
wound healing, inflammation, rheumatoid arthritis, psoriasis,
cancer and other disorders, related to anglogenesis including abnormal
wound healing, inflammation, rheumatoid arthritis, psoriasis,
cancer and other disorders, and arterial-venous maiformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
or mobilisation (chemotaxis) of immune cells. The etalogy of these
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat infiammatory
conditions, both chronic and acute conditions. The products can also
used for detection and disagnosis. AAZ32002 to AAZ32080, and AAY49503 to
AAY49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                          New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS------PQDPALQGVGQP-TGTGS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLLLGILTLAFAGGTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 48.0%; Score 2480.5; DB 20; Length 950; Best Local Similarity 48.9%; Pred. No. 6.8e-184; Matches 485; Conservative 154; Mismatches 251; Indels 101;
                                                                                                                                                               SM;
                                                                                                                                                                Ruben
                                                                                                                                                                                                                                                                              Claim 10; Fig 1; 457pp; English.
                                                                                                                                                                GA,
                                                99WO-US01313
                                                                       98US-0072298
98US-0098539
                                                                                                                                                                  Hastings
                                                                                                            (IRUE/) IRUELA-ARISPE L.
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                       WPI; 1999-590684/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    950 AA;
                                                                                                                                                                  Iruela-Arispe L,
                                                                                                                                                                                                     N-PSDB; AAZ32000
                                               22-JAN-1999;
                                                                        23-JAN-1998;
28-AUG-1998;
                        29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
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an anti-cancer and
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684 KVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 VDCRGSAGQRTVPACDAAH--RPVETQACGE-PCPTWELSAWSPCSKSCGRGFQRRSLKC
                                                                   SCNLEPCFSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN
                                                                                                                                                                                                                                                    GTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCK
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A Disintegrin And Metalloprotease; cancer; arthritls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ADAM-type metalloprotease MDTS4, SEQ ID NO:4.
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Human; METHI; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; lischaemic limb angiogenesis; Osler-Webber syndrome; plaque neovascularisation; telangiectasia; hemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control.
                                                                                                        VDCRGSAGQRTVPACDAAH--RPVETQACGE-PCPTWELSAWSPCSKSCGRGFQRRSLKC 920
    PREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRA
                                                                   ----KES------PNAIPTFS------AWVIEEWGECSKSCELGWQRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trulli SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Jonak ZL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETH ISRAEL DEACONESS MEDICAL CENT. IRUELA-ARISPE L.
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LSHDGGVLSHESCDPLKKPKHFIDFCTMAEC
                                                                                                                                                                 VGHGGRLLARDQCNLHRKPQE-LDFCVLRPC
                                                                                                                                                                                                                                                                     AAB50002 standard; Protein; 950
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Fornwald JA, Terrett JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN GENOME SCI INC
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99US-0147823
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99US-0171503
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N-PSDB; AAC90057.
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JONAK Z L.
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22-FEB-2000;
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10-AUG-1999;
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(HAST/)
(RUBE/)
(JONA/)
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FORN/)
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(BETH-)
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                                                  The invention relates to the novel human ADAM (A Disintegrin And Metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 specific for MDTS4, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present
                                                                                                                                                                                                                                                                                                                                                      61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
                                                                                                                                                                                                                                                                                                                                                                             DQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 119
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Pred. No. 6.8e-184;
4; Mismatches 251; Indels 101; Gaps
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                                                                                                                                                                                                                                                                                                             KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
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                          Claim 1; Page 12-14; 22pp; Japanese.
                                                                                                                                                                            sequence represents human MDTS4
                                                                                                                                                                                                                                                               485; Conservative 154;
                                                                                                                                                                                                                                    48.0%;
anti-arthritic therapeutic
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                                                                                                                                                                                                        950 AA;
                                                                                                                                                                                                        Sequence
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                           The present sequence is human METH1 (ME for metalloprotease and TH for thrombospondin). METH1 can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumnurs, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunlon fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, crebral collaterals, arteriovens malformations, ischaemic limb angiogenesis, osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH1 can also be used in birth control. METH1 can also be used in diagnostic methods for the prognosis of cancer.
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                                                                                                                                                                                                                                                                                Query Match 48.0%; Score 2480.5; DB 22; Length 950; Best Local Similarity 48.9%; Pred. No. 6.8e-184; Matches 485; Conservative 154; Mismatches 251; Indels 101;
Claim 15; Fig 1; 768pp; English.
                                                                                                                                                                                                                                                  950 AA;
                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                        ITGL-TSP; integrin ligand; anglogenic disease; cancer; atherosclerosis; chronic inflammatory disorder; rheumatoid arthritis; tissue remodeling; macular degeneration; diabetic retinopathy; Alzheimer's disease; human;
                                                                                                           920
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tissue
SAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKE | :|:|::|| | | :::|::|| | stleodimyrgvvlrysgssaalerirsfsplkepltiqvltvgnalrpkikytyfvkk
                                                                                                                         PREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRA
                                                                                ----FNAIPTFS------AWVIEEWGECSKSCELGWORRL
                                                                                                            VDCRGSAGQRTVPACDAAH - - RPVETQACGE - PCPTWELSAWSPCSKSCGRGFQRRSLKC
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48.9%; Pred. No. 7e-184;
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SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                             AAW80285 standard; Protein; 967
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Trulli SH;
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(first entry)

19-MAR-2001

Protein; SEQ ID 125

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61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
                                                                                                                                                                                   GRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV 267
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-----RAP---GHGTTRLRAF
                                                                                  115 AAVSLCGGLRGAFGYRGAEYVISPLPNAS:--APAAQRNSQGA----HLLQ--RRGVPGG
                                                                                                                                                         197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPOWS-----PODPALOGVGOP-TGTGS
                                                                                                                                   166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS
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The present invention relates to human METH1 and METH2 (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003.

METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonution fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, cleroderma, trachoma, vascular adhesions, myocardial angiogenesis, cononary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, osler webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or therosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer. The present sequence is a protein isolated in the present invention.
                                                                            Human; METH1; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischemnic limb angiogenesis; Osler Webber syndrome; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH;
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BETH ISRAEL DEACONESS MEDICAL CENT.
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99US-0144882.
99US-0147823.
99US-0373658.
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2000US-0183792
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Terrett JA;
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HASTINGS G A.
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JONAK 2 L.
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Fornwald JA,
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22-FEB-2000;
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24;

Gaps

Best Loca Matches

AAB50011 standard; Protein; 968

RESULT 10 AAB50011 AAB50011;

Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;

(first entry)

15-JUN-1999

AAY04142;

Human Tango-71 protein

Homo sapiens WO9907850-A1

detection.

us-10-009-332-1.rag

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                                                                                        115 AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG 165
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SCNLEDCPDN-NGKIFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSFKDRCKLICQAK
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                                                                                                                                                                                                                                          HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
             PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS
                                           61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
                                                                                                                                                                                GRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
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New TANGO polypeptides and nucleic acids encoding them - useful diagnostic agents and for treating disorders caused by aberrant expression of TANGO

Claim 8; Fig 1; 84pp; English.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC

Holtzman DA;

Goodearl ADJ,

WPI; 1999-167426/14.

N-PSDB; AAX19955.

98WO-US16502 97US-0058108. 97US-0054966.

06-AUG-1998;

18-FEB-1999

06-AUG-1997; 05-SEP-1997;

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The present sequence represents human Tango-71. Tango polypeptides are useful for identifying compounds which bind the polypeptide via direct binding, competition binding assays or Tango-71, -73, -74, 76 or -83-mediated signal transduction. Tango polypeptides are also useful for identifying modulating compounds by determining effect on Tango activity. Tango polypeptides and nucleic acids are useful for diagnosing diseases related to aberrant expression of Tango, and Tango polypeptides are useful for raising antibodies which can be used in diagnostic assays for detection of Tango, and also for generating antibodies so prevention and protection.
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AAY04142 standard; Protein; 967

RESULT 11 AAY04142 ID AAY04

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma: lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                               684 KVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVV 743
308 KILVIHDEQKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTC 367
                                                                                                                                                                              |: || || || || || 48 CQFTFGEDSKHCPDAASTCSTLMCTGTSGGGVLVCQTKHFPWADGTSCGEGKWCINGKCVN 547
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STLEQDIMYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKK 845
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                                                                                                                                                    HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
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AAW78189
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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 movel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX04311-X04410; amino acid sequences AAX04311-X04410; amino acid sequences AAX06155, which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Y, Young F
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Ruben SM, Shi
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Moore PA, Ni J, Olsen HS, Rosen CA, Rui
Yu GL;
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              'label- unknown
                                      /label= unknown
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N-PSDB; AAX04374.
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                                                                                  QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
                                                                                                                                               AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG
                                                                                                                                                                                                      197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS-----PODPALQGVGQP-TGTGS
                                                                                                                                                                                                                          208 GRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
                                                                                                                                                                                                                                                                KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
                                                                                                                                                                                                                                                                                                     DILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN
                                                                                                                                                                                                                                                                                                                                          HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
                               Length 967;
                                                 101;
                                                  255; Indels
                              47.6%; Score 2458.5; DB 20;
11arity 48.5%; Pred. No. 3.6e-182;
Conservative 154; Mismatches 255; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGHGGRLLARDQCNLHRKPQE-LDFCVLRPC 950
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              296
                                                    Matches 481;
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                                                                                                                                                                                                                                                             GON-1; metalloproteinase; cell migration; modulator; ADAMTS-1; metalloproteinase domain; thrombospondin domain; abnormal cell migration; organ shaping; sterility; cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain. The method comprises treating a target organism, having a developing gonadal cell that is responsive to the protein, with a test compound, and determining any change in migration or shape of the cell attributable to the test compound. The compounds identified are potential therapeutic modulators of abnormal cell migration and organ shaping, e.g. for rendering animals (specifically nematodes) sterile and for inhibiting cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TARQEDEYLHLIPDAQFLAPARSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APPAAQRNSQGA----HLLQRRG 161
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llarity 47.7%; Pred. No. 3.6e-181;
Conservative 158; Mismatches 250; Indels 113;
                                                                                                                                                                                                      Amino acid sequence of a murine ADAMTS-1 protein.
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AAY53899 standard; Protein; 950
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Matches 476; Conserva
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13-APR-1999;
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Clark M,
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453; Conserv
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                                                                               38-MAR-2000;
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                                                                                                                               Kelner GS,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; ADAMTS-1; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian;
                                                                                                                                                                                                                                                            619 ICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGD
                                                                                                                                                                                                                                                                                              NKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLN
                                                                                                                    443 TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
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                                                                                                                                                                                                                                                                                                                                                            162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRR-------
                                        ----RRGSGGAKCGVMD------DETLPTSDSRPESONTRNOWPVRDPTPQDAGKP
                                                      ----SGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI
                                                                                       NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC
                                                                                                                                                     383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
                                                                                                                                                                                                                    GACVERHNINKH - - - RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse metalloproteinase ADAMTS-1.
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The present sequence is mouse metalloproteinase ADAMTS-1. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
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cerebroprotective; cytostatic; antiarthritic; immunosuppressive;
Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis;
autoimmune disease; brain tumour; brain injury.
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1.3e-171;
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Conservative 143; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             Metalloproteinase-disintegrin protein with a thrombospondin domain; ARDS; ADAMTS: -1; drug composition; foodstuff, leukocyte; thrombocyte; hepatitis; blood; erythrocyte; inflammatory disease; rheumatoid arthritis; asthma; nephritis; Crohn's disease; acute respiratory disease syndrome.
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                                                                                                                                                            NKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLN 738
                                                                                                                                                                     GSTCKKMSGIVTSTRPGYHDIVTIPAGATNIEVKHRNQRGSRNNGSFLAIRAADGTYILN 764
                                                                                                                                                                                                          824
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                                                                       FMKKKTES -----FNAIPIFS -----EWVIEEWGECSKTCGSG
      VTGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLY
                                                                                                                            619 ICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGD
                                                                                                                                                                                                   TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGOMVCQTRHFPWADGTSCGEGKLCLK
                                        GACVERHNINKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                                                                                                                                                           GHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSF
                                                                                                                                                                                                                         YLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSG
KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human metalloproteinase-disintegrin protein with thrombospondin domain - useful as leukocyte and thrombocyte decreasing and erythrocyte increasing agent
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Kuno K, Matsushima
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N-PSDB; AAX17990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624
                                     This sequence represents a novel human metalloproteinase-disintegrin protein with a thrombospondin domain (ADAMTS-1). The protein may be in drug compositions and foodstuffs, as an agent for decreasing the leukocyte and thrombosyte blood count and increasing the erythrocyte blood count, e.g. for treatment of inflammatory diseases such as rheumatoid arthritis, hepatitis, nephritis, crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
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                                                                                                                                                                                                                                                                            Length 727;
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                                                                                                                                                                                                                                                                          44.0%; Score 2274; DB 20; ilarity 54.4%; Pred. No. 5.4e-168; Conservative 129; Mismatches 173;
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Claim 1; Page 51-52; 82pp; Japanese.
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Matches 408; Conserv
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April 29, 2003, 17:14:33 ; Search time 56 Seconds (without alignments) 3495.442 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

Database :

sp\_rvirus:\*
sp\_bacteriap:\*

sp\_archeap:\*

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Aggrecanase-1 (Fragment).
Aggrecanase-1 (Fragment).
Edgus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type I motif.
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SEQUENCE FROM N.A.
MEDLINE-21856482; Pubwed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Flannery C.R., Little C.B.; Flannery C.R., Little C.B.; Expression and activity of equine aggrecanases."; Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF368321; AAK53425.1; -.
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192 AA; 20670 MW; 9013B0E19FCE8C56 CRC64;
                                                                                                                                           06562C747634A8BD CRC64;
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Catarrhini; Hominidae;
                                                                                                                                                                                            Query Match 7.5%; Score 71; DB 11; Best Local Similarity 100.0%; Pred. No. 1.1e-67; Matches 71; Conservative 0; Mismatches 0;
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InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; an_MTpeptdse.
PROSTIE; PS50215; ADAM_MEPRO; I.
PROSTIE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                        340 AA; 37021 MW;
EMBL; BC009667; AAH09667.1;
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 2.
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NCBI_TaxID=9796;
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                                                                                                                                                                                                                               500 LKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVR 559
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                                                                                       ESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSIL 259
                                                                                                                                                                                                                                                                                                                                                                                                                           VFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLC 499
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
motifs 1 (ADAMTS-1) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butherla; Rodentia; Sciurognathi; Muridae; Mus.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 133.5 kDa protein.
Hypothetical lass kDa protein.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-FETAL LUNG;
MEDLINE-2118678212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
EMBL; AJ345098; CAC87943.1; -.
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Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
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SEQUENCE 1223 AA; 133871 MW; 36394AC4D92F170F CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                             InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR000809; TSP1.
IPR001421; Reprolysin; 1.
IPR001421; Reprolysin; 1.
IPR001TE; PS50191; TSP1, 4.
IPR0SITE; PS50192; TSP1, 1.
IPR0SITE; PS50015; TSP1; 1.
INTEGTIN; PROFERSE; Metalloprotease.
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100.0%; Pred. No. 0.48;
ive 0; Mismatches
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         InterPro; IPR002870; Pep_M12B_propep
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nes 10; Conservative
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SENBL; AF366351; AAL79814.1; SEQUENCE 1159 AA; 127336 MW; A5B130149BF7FF34 CRC64;
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Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
BEBL; ABJ35734; CAC86015.1; -.
Integrin; Protease.
SEQUENCE 1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MUN-2002 (TrEMBLrel. 21, Last annotation update)
A disintegrin-like and metalloprotease with thrombospondin type
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BECTION BLOOM SECUENCE A., VON Bredel11779638;
BOLZ H., RAMÍTEZ A., VON Brederlow B., Kubisch C.;
"Characterization of ADAWTS14, a novel member of the ADAWTS metalloproteinase family.";
Blochim. Blophys. Acta 1225(2001).
EMBL; ASS8666; ALAL02295.1; -.
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100.0%; Pred. No. 0.46;
tive 0; Mismatches 0; Indels
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Last annotation update)
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Matches 10; Conservative
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ADAMTS14.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemonchus contortus (Barber pole worm).
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
                          Madan A., Dickhoff R., Shaffer T., James R., Lasky S., Hood L.; "Complete sequence of the gene for presentlin 1."; Submitted (Nov-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AP109907; AR297963.1; --. HSSP; P12111; 2KNT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 10; DB 4; Length 1235; 100.0%; Pred. No. 0.49; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133477 MW; A0B44CCE4F38E350 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Thrombospondin.
                                                                                                                                                                       InterPro; 12111; 78001
InterPro; 1PR003598; 1g_c2.
InterPro; 1PR00306; 1g_MHC.
InterPro; 1PR000223; Kunitz_BPTI.
InterPro; 1PR00084; TSP1.
Pfam; PF00047; 1g; 3.
Pfam; PF00047; 1g; 3.
Pfam; PF000047; 1g; 3.
Pfam; PF000090; tsp_l; 5.
PROMOTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SWART; SW00131; KU; 1.
SWART; SW00209; TSP1; 5.
PROSITE; PS00280; PRTI_KUNITZ_1; 1.
PROSITE; PS00280; PRTI_KUNITZ_1; 1.
PROSITE; PS0029; TSP1; 4.
Hypothetical protein; Immunoglobulin domain; Serine protease inhibitor:
SEQUENCE 1235 AA; 133477 MW; A0B44CCE4F38E3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1572 AA.
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InterPro: IPR0002623; Kunitz_BPTI.
InterPro: IPR000884; TSP1.
InterPro: IPR000884; TSP1.
Pfam; PP00014; Kunitz_BPTI; 6.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 6.
SMART; SM00011; EGF_11ke; 1.
SMART; SM00131; KU; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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MISLOR R., Alnscough R., Anderson K., Baynes C., Berks M.,

Allscon R., Alnscough R., Anderson K., Baynes C., Berks M.,

RA Gratton M., Dear S., Durbhin R., Favello A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Ranaldon N., Smith A., Sonnhammer B., Staden R., Sulston J.,

Rhierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Ratson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

R. Clegans R.,

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                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Sukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
NcBL_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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InterPro; IPR00184; TSP1.
InterPro; IPR000184; TSP1.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF00090; tsp1; 14.
SMART; SM00209; TSP1; 18.
PROSITE; PS50215; ADAW_MEPRO; 1.
PROSITE; PS50042; TSP1, 6.
PROSITE; PS00042; TSP1, 6.
SPROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 2165 AA; Z44397 MW; FCC3DABAAA9C4888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gajadsty S.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F25H8.3.
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01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
     2165 AA.
PRT;
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EMBL, 269361; CA93288.1; -
EMBL, 269360; CAA93288.1; JOINED.
EMBL, 269360; CAA93287.1; -
EMBL, 269361; CAA93287.1; -
EMBL, 269361; CAA93287.1; -
EMBL, 269361; CAA93287.1; JOINED.
HSSP, P15167; IDTH.
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InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PP01421; Repro; 1.
Pfam; PR00030; tSp_1; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS500215; ADAM_NEPRO; 1.
PROSITE; PS500142; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
NON_TER 269 269
SEQUENCE 269 AA; 29193 MW; 97A1CA80B334528
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAMTS18 protein.
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Matches
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Q9EPX2
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDINE-99457716; PubMed=10528409;
MEDINE-99457716; PubMed=10528409;
NardiJ.S., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
NardiJ.S., all alraye multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca sexta.";
Insect Biochem. Mol. Biol. 29:883-897(1999).
EMBL; AF078161; AF074457.1; -.
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                                       Lacunin precursor.

Manduca saxta (Tobacco hawkmoth) (Tobacco hornworm).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Meoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Sphingiodea; Sphingidae; Sphinginae; Manduca.

NCBI_TaxID=7130;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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100.0%; Pred. No. 1.1;
ive 0; Mismatches 0; Indels
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                01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aggrecanase-2 (Fragment).
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InterPro: IPR004099; Ig_C2.
InterPro: IPR003509; Ig_C2.
InterPro: IPR003066; Ig_MRC.
InterPro: IPR00223; Kunitz_BPTI.
InterPro: IPR00223; Kunitz_BPTI.
InterPro: IPR00221; WAP.
Pfam; PF0047; Ig; 2.
Pfam; PF00047; Ig; 2.
Pfam; PF00047; Ig; 2.
Pfam; PF00048; Wap: 1.
PRINTS; PR00759; BASICPTASE.
PROPOM: PD000225; Kunitz_BPTI; 10.
SMART; SM00131; KU; 10.
SMART; SM00209; TSPI; 7.
PROSITE; PS00217; WAP: 1.
PROSITE; PS00217; WAP: 1.
PROSITE; PS00217; WAPI KUNITZ_1; 8.
PROSITE; PS00209; BPIL KUNITZ_2; 10.
PROSITE; PS50029; TSPI; 7.
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InterPro; IPR001590; Reprolysin.
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hes 10; Conservative
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71 PCSRTCGGGV 80
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MEDIANNS-21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization of
seven novel human ADAMTSs, a family of metalloproteinases with
disintegrin and thrombospondin-1 domains.";
Charley 49-62(2002).

EMBL; AJ311903; CAC83612.1;
SEQUENCE 1081 AA; 119655 MW; 0438BF645676461E CRC64;
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STRAIN-CD-1;
MEDLINE-20530499; PubMed=11076767;
Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,
Kramerova A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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269 AA; 29193 MW; 97A1CA80B33452FA CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 5.3;
0; Mismatches
                                                 0.9%; Score 9; DB 6;
100.0%; Pred. No. 1.5;
iive 0; Mismatches
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100.0%; Pred
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26 POTENTIAL.
231936 MW; 038F707952623120 CRC64;
                                                                     PRINTS; PRO0003; WAD! T. AUSULPHCORE.

PRINTS; PRO0003; WAD! T. AUSULPHCORE.

PRINTS; PRO00022; Kunitz_BPTI; 3.

PRON0409; IGC2; 2.

SMART; SM00409; IGC2; 2.

SMART; SM00130; Kul; 3.

SMART; SM00209; TSP1; 7.

SMART; SM00209; TSP1; 7.

SMART; SM00210; WAD! 7.

PROSITE; PSC00280; BPTI_KUNITZ_1; 3.

PROSITE; PSC00280; BPTI_KUNITZ_1; 3.

PROSITE; PSC0022; EGFI; UNKNOWN_1.

PROSITE; PSC0022; EGFI; 3.

MALTIX PICTEIN; Serine Protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 9; DB 5;
100.0%; Pred. No. 9.9;
iive 0; Mismatches
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           Pfam; PF00047; 19; 2.
Pfam; PF00041; Kunitz_BPT1; 3.
Pfam; PF00090; tsp_1; 5.
Pfam; PF00095; wap; 1.
 InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                            21.74 AA;
                                                                                                                                                                                                                                                                                                                                           528 CSRTCGGGV 536
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                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Sieron A.L., Prockop D.J., Fessler J.H.; "Papilin in development; a pericellular protein with a homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Extracellular matrix protein papilin precursor.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Eptrygota, Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SEQUENCE 1280 AA; 138824 MW; AE287705E561AF30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2174 AA.
                                                                                                                                                                                                                                                                          SMART; SMO0409; IG; 3.
SMART; SMO0408; IGC2; 3.
SMART; SMO010; IG_like; 2.
SMART; SMO0110; IG_like; 2.
SMART; SMO013; KU; 1.
SMART; SMO0209; TSP1; 5.
PROSITE; PSC01200; BPT_KUNITZ_1; 1.
PROSITE; PSC0129; BPT_KUNITZ_2; 1.
PROSITE; PSC0199; ODR_DC_2_2; UNRNOWN_1.
                                                                                      InterPro; IPR000183; Decarbxylse2.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig.11ke.
InterPro; IPR003060; Ig.MHC.
InterPro; IPR002223; Kulitz_BPTI.
InterPro; IPR000884; TSPI.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00223; Kunitz_BPTI.
InterPro; IPR00084; TSPI.
                            ADAMTS metalloprotéinases.";
Devolopment 127:5475-5485(2000).
EMBL; AF314171; AAG41980.1; -.
HSSP; P12111; ZKNT.
                                                                                                                                                                                        Intervior Acceptage 3. Pfam; PF00047; 1g; 3. Pfam; PF00014; Kunitz BPT; 1. Pfam; PF00090; tsp_1; 5. PRINTS; PR00759; BASICPTASE. ProDom; PD000222; Kunitz_BPTI; 1
                                                                                                                                                                                                                                                                Kunitz_BPTI; 1.
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InterPro; IPR000561; EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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38 PCSRTCGGG 46
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Length 2174;

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April 29, 2003, 17:22:09; search time 27 Seconds (without alignments) 3382.507 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                               283224 seqs, 96134422 residues
                                                                             protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote alpha-mannosidase ryanodine-binding hypothetical prote neurofibromin - mo hypothetical prote nitrogen regulator nitrogen regulator gene ADAMTS-1 prot hypothetical prote hypothetical prote procollagen N-endo hypothetical prote probable ABC trans coccidiosis-relate metalloproteinase PTS system, IIC co hypothetical prote NADHZ dehydrogenas probable flagellar immunodominant mic nitrogen regulator nitrogen regulator hypothetical prote conserved hypothet nitrogen regulator nitrogen regulator nitrogen regulator Description SUMMARIES 747158 T100355 T100355 T21871 T21871 721871 845510 86538 A41293 A81293 A81293 A81293 A81293 A81293 A81293 A81293 A81293 G81738 AH3226 T00017 % Query Match Length DB 951 11205 21165 21165 21165 21165 21065 440 607 607 712 712 712 718 718 7049 96 1277777788888888888888 Score 71114 1100 1100 88 88 88 88 77 77 No. Result

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Gaps

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Query Match 1.5%; Score 14; DB 2; Length 550; Best Local Similarity 100.0%; Pred. No. 1.5e-05; Matches 14; Conservative 0; Mismatches 0; Indels

hypothetical prote probable rhodamese virulence-associat hypothetical prote hypothetical prote ribosomal protein ribosomal protein ribosomal protein hypothetical prote nitrogen regularor hypothetical prote bnaJ protein homol hypothetical prote conserved hypothet rrypsin inhibitor trypsin inhibitor trypsin inhibitor trypsin inhibitor	ALIGNMENTS  ALIGNMENTS  sion 22-Jan-1999 #text_change 21-Jul-2000  Matsushima, K.  ion and chromosomal mapping of the mouse ADAMTS-1  8110583; PMID:9441751  from GB/EMBL/DDBJ  IND:92809056; PIDN:BAA24501.1; PID:92809057  ivj  4/1; 539/3; 602/1; 660/3; 719/2  i repeat homology  rype 1 repeat homology <thr3>  Score 17; DB 2; Length 951;  Pred. No. 1.9e-08;  Mismatches 0; Indels 0; Gaps 0;</thr3>	FZp762C1110.1 - human (fragment) (man) quence_revision 20-Apr-2000 #text_change 20-Apr-2000 S.; Mewes, H.W.; Weil, B.; Wiemann, S. n Sequence Database, March 2000 379 L:AL162080 adult melanoma (MeWo cell line); clone DKFZp762C1110
AB3048 D69827 AI0244 AI0244 B49205 C70059 C70059 C70059 C71122 T1182 T11	mouse) evision; ;; Matsus zation and D:981105; H444/1; Matsus 295VJ 444/1; Matsus 295VJ 605 Missus	0.1 - huma 1sion 20-A , H.W.; We Database, Database, noma (MeWo
пнинипипипипипипи	e mousse mousse e_revis ( , S.; M morib:98 morib:98 morib:98 morib:98 morib:98%; S 0.0%; e 0; 372 morib mori	C111 _rev ewes ence
125 131 132 132 133 143 143 143 160 161 167 172 172 172	ALIGNM  Trians and the state of	protein DKF2p762C1110.1 - mo sapiens (man) r-2000 #sequence_revision T47158 T47158 the Protein Sequence Datal muber: Z24379 T47158 liminary liminary ences: EMBL:AL162080 L source: adult melanoma
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	RESULT 1 T00017 gene ADAMTS-1 protein - mouse C; Date: 22-Jan-1999 #sequence_C; Accession: T00017 C; Accession: T00017 A; Title: The exon/intron organ A; Reference number: 214055; MU A; Accession: T00017 A; Status: prelininary; transla A; Residues: 1-951 - KUN> A; Consereferences: EMBL:AB001 A; Conserreferences: EMBL:AB001 A; Conserreferences: EMBL:AB001 A; Conserreferences: EMBL:AB001 A; Conserreferences: EMBL:AB001 C; Genetics: ADAMTS-1 A; Antrons: 228/1: 343/3; 388/1 C; Superfamily: thrombospondin F; 542-598/Domain: thrombospondin Best Local Similarity 100. Matches 17; Conservative Oy 356 AFTTAHELGHVFNMPHD 39	
WWWWWWWWWWW#44444 OHUW4WMVWWWWWWWAW	RESULT 1 T00017 Gene ADAMTS-1 Gene ADAMTS-1 G'Species: Mus G'Accession: G'Accession: G'Accession: A'Ritle: The A'Ritle: The A'Ritle: The A'Ritle: The A'Residues: 17 A'Resi	RESULT 2 T47158 T47158 C;Species: Ho C;Species: Ho C;Date: 20-Ap C;Date: 20-Ap C;Bum, H.; B Submitted to A;Reference nA;Aceference nA;Aceference nA;Aceference nA;Aceference nA;Aceference nA;Status: pre A;Ross-refer nA;Coss-refer nA;Coss-ref
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probable ABC transport ATP-binding chain STY1861 [imported] - Salmonella enterica sub C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
        Rigajasty, S.
submitted to the EMBL Data Library, February 1996
A; Reference number: 219413
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Cross-references: EMBL: Z69360; PIDN: CAA93287.1; GSPDB: GN00022;. CESP: F25H8.3
A; Experimental source: clone F25H8
R; Gajasty, S.
submitted to the EMBL Data Library, February 1996
A; Reference number: 219949
A; Reference number: 219949
A; Reference number: 219949
A; Restdues: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; Amble Cull Companiental Source: clone T13H10
C; Genetics: clone T13H10
C; Genetics: clone T13H10
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coccidiosis-related antigen - Eimeria tenella (fragment)
N;Alternate names: thrombospondin-related antigen, 100K
C;Species: Eimeria tenella
C;Species: Eimeria tenella
C;Species: D3-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 07-May-1999
C;Accession: A45517; 22781
R;Clarke, L.E.; Tomley, F.M.; Wisher, M.H.; Foulds, I.J.; Boursnell, M.E.G.
Mol. Biochem. Parasitol. 41, 269-280, 1990
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0.63;
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100.0%; Pred. No. 9.8;
ative 0; Mismatches
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C; Accession: T21371; T24896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         615 CSRTCGGGVQ 624
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                                                                                                                                                                                                                     hypothetical protein KIAA0688 - human
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: 10-reb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00355
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 16-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: 214142; MUID:98403880; PMID:9734811
A;Reference number: 214142; MUID:98403880; PMID:9734811
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AB014588; NID:93327189; PIDN:BAA31663.1; PID:93327190
A;Experimental source: brain
C;Genetics:
A;Gene: KIAA0688
C;Superfamily: thrombospondin type 1 repeat homology
C;Superfamily: thrombospondin type 1 repeat homology
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NiAlternate names: procollagen N-proteinase
C; Species: Bos primigenius taurus (cattle)
C; Accession: T18517
R; Colige, A.; Nusgens, B.V.; Lapiere, C.M.
submitted to the EMBL Data Library, February 1996
A; Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.
A; Reference number: 218941
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1205 <COL>
A; Residues: 1-1205 <COL>
A; Cross references: EMBL:X96389; NID:e990769; PID:e228215; PIDN:CAA655253.1
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
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100.0%; Pred. No. 0.00023;
tive 0; Mismatches 0; Indels
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0.39;
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Matches 10; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                 108 HFPWADGTSCGEGK 121
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                                          HFPWADGTSCGEGK
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C;Function:
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C;Genetics:
A;Gene: SP0250
C;Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-de
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C;Species: Agkistrodon contortix contortix (southern copperhead)
C;Decies: Agkistrodon contortix contortix (southern copperhead)
C;Date: 17-Dec-1906 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Accession: S66260; S74263
R;Selistre de Araujo, H.S.; Ownby, C.L.
Arch. Biochem. Biophys. 320, 14-148, 1995
A;Title: Molecular cloning and sequence analysis of cDNas for metalloproteinases from br
A;Accession: S66260
A;Molecule type: mRNA
A;Accession: S66269; MUID:95314311; PMID:7793974
A;Accession: S74263
A;Accession: S74263
A;Accession: S74263
A;Accession: S74264
A;Residues: 188-206 <SED-A
C;Superfamily: atrolysin C
C;Keywords: hydrolase; metalloproteinase; zinc
C;Keywords: hydrolase; metalloproteinase; zinc
F;118/Domain: signal sequence #status predicted <SIG>F;118/Domain: propeptide #status predicted <ARGO-F;118/Domain: propeptide #stat
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A;Molecule type: DNA
A;Residues: 1-440 <KUR>
A;Crosireferences: GB:AE005672; PIDN:AAK74429.1; PID:g14971719; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: D95029
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, science 293, 496-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: D95029
A;Accession: D95029
A;Title: Regions of an Eimeria tenella antigen contain sequences which are conserved in A;Reference number: A45517; MUID:90377296; PMID:2204833 A;Accession: A45517 A; Eatus: preliminary
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F;304.384,344-551,346-368/Disulfide bonds: #status predicted
F;329,333,339/Psinding site: zinc, catalytic (His) #status predicted
F;330/Active site: Glu #status predicted
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C; Superfamily: thrombospondin type 1 repeat homology
F;136-198/Domain: thrombospondin type 1 repeat homology <THR5>
                                                                                                                                                                                                                                                                                                                                                                                      Length 206;
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100.0%; Pred. No. 18;
tive 0; Mismatches
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100.0%; Pred. No. 10;
tive 0; Mismatches
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Best Local Similarity 100.0%
Matches 8; Conservative
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Best Local Similarity 100...
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-206 <CLA>
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C.Genetics:
A.Geneme: mitochondrion
A.Genetic code: SGC1
C.Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C.Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C.Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - redhead mitochondrion (Species: mitochondrion Aythya americana (redhead) (Date: 16-Uul-1999 #text_change 03-Jun-2002 (Jacession: T11032 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 (Jacession: T11032 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 (Jacession: T11032 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 (Jacession: T11032 #stelle: Multiple independent origins of mitochondrial gene order in birds. A;Reference number: 217242 #stelle: Multiple independent origins of mitochondrial gene order in birds. A;Recession: T11032 #stelle: Zi7242 #stelle: Zi72424 #stelle: Zi7242 #stelle: Zi7242 #stel
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                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PTS-EIIC [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: G97900
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    Length 440;
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100.0%; Pred. No. 19;
tive 0; Mismatches
Query Match 0.8%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 19; Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                            C; Accession: A81293
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf Reference number: A81250; MUID:20150912; PMID:10688204
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Eimeria tenella
C; Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: A45638
R; Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Blochem. Parasitol. 49, 277-288, 1991
MylItle: Sequence of the gene encoding an immunodominant microneme protein of Eimeria te
A; Reference number: A45638; MUID:92131064; PMID:1775171
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A;Cross-references: GB:AF012905; GB:M73495; NID:g2707732; PIDN:AAD03350.1; PID:g2707733
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
C;Superfamily: thrombospondin type 1 repeat homology; von Willebrand factor type A repeat homology cWMAl>
F;348-218/Domain: thrombospondin type 1 repeat homology cTHR2>
F;309-371/Domain: thrombospondin type 1 repeat homology cTHR2>
F;372-432/Domain: thrombospondin type 1 repeat homology cTHR3>
F;343-493/Domain: thrombospondin type 1 repeat homology cTHR5>
F;560-610/Domain: thrombospondin type 1 repeat homology cTHR5>
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-608 <PAR>
A; Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73889.1; PID:g696889
A; Expenimental source: serotype O2, strain NCTC 11168
C; Genetics:
A; Gene: flgK; Cj1466
probable flagellar hook-associated protein Cj1466 [imported] - Campylobacter jejuni (st4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T25061
R;Cofttage, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19975
                               C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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0; Mismatches
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tive 0; Mismatches
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A; Molecule type: DNA
A; Residues: 1-712 <TOM>
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alpha-mannosidase (EC 3.2.1.24) - Emericella nidulans
C; Species: Emericella nidulans, Aspergillus nidulans
C; Species: Emericella nidulans, Aspergillus nidulans
C; Species: 22-oct-1999 #sequence_revision 22-oct-1999 #text_change 11-May-2000
C; Accession: T30552
R; Eades, C.J.; Gilbert, A.; Goodman, C.D.; Hintz, W.E.
Glycobiology 8, 17-33, 1998
A; Title: Identification and analysis of a class 2 alpha-mannosidase in Aspergillus ni, Areference number: 220843; MUID:98119762; PMID:9451011
A; Accession: T30525
A; Accession: T30525
A; Accession: T30525
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:AF016850; NID:92407175; PID:92407176; PIDN:AAB70514.1
Gaps
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C;Superfamily: Saccharomyces alpha-mannosidase
C;Reywords: glycosidase; hydrolase
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GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

April 29, 2003, 17:18:08; search time 16 Seconds (without alignments) 2462.657 Million cell updates/sec

US-10-009-332-1 950 1 MILIGILTLAFAGRTAGGFE......DQCNLHRKPQELDFCVLRPC 950

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\*

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IDE3_ERYLA IDE3_ERYVA CFTR_MACNU SP25_DROME VG77_HSV11 FRDB_PROVU PK1_MPVOP CITG_KLEPN GGH_RAT	K6PF_AQUAE
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## ALIGNMENTS

OTHERNADA.	SUL S1_	OC EUKaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBL_TaxID=9606; RN [1] RN [1] RP SEQUENCE FROM N.A. RR Gasas C., Pritchard M.A., Estivill X., Arbones M.L.; RT "Cloning, characterization and mapping on human chromosome 21 of the RT orthologue of murine Adamts-1."; RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	RE SEQUENCE FROM N.A.  RC TISSUB-Endothelial cells;  RX MEDLINE-20247184; PubMed-10785405;  RA Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,  RA Rosenthal A., Thierauch K.H.;  RT "Differential gene expression by endothelial cells in distinct  RT anglogenic states.";  RL Eur. J. Blochem. 267:2820-2830(2000).	2012511410-	ONEETOEKK	

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                                                                                                                                                                                                                                                                                      Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordslek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.; "The DNA sequence of human chromosome 21.";
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DOMAIN: THE SPACER DOWAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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CYSTEINE SWITCH (POTENTIAL).
CYSTEINE SMITCH (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTĒNTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF170084; AAF15317.1; -.
EMBL; AF060152; AAD48080.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF207664; AAF23772.1;
EMBL; AB037767; BAA82584.1; AIT_INIT.
EMBL; AP001697; BAA95502.1; -.
EMBL; AL162080; CAB82413.1; -.
                                                                                                                                                                                                                                               SEQUENCE OF 418-967 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M12.222; -.
Genew; HGNC:217; ADAMTS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              967
198
401
402
411
559
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Blum H., Bauersa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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MIM; 605174;
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SIGNAL
PROPEP
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liver 20:165-173(2000).

Liver 20:165-173(2000).

-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE
INVOLVED IN ITS TORNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY
SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER
CACHEXTA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY
SIMILARITY).
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-I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WUQ1; Q9ER11;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-1 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1).
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adriana M. Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUB-Brain;
Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.
                                                                                                                    N-INKED (GLCNAC. .) (POTENTIAL).
N-INKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> A (IN REF. 4 AND 5).
Q -> H (IN REF. 1).
S -> N (IN REF. 1).
S -> N (IN REF. 1).
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STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-20304099; Pubmed-10847486;
Diamantis I., Luethi M., Hoesli M., Reichen J.;
Cloning of the rat ADAMTS-1 gene and its down regulation in endothelial cells in cirrhotic rats.";
                                                                                                                                                                                                                                                                                                                                 Score 17; DB 1; Length 967; Pred. No. 8.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Little S.P.; "Induction of a disintegrin and metalloprotease with the thrombospoint type I motif (ADAMTS)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMITARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                            1.8%; Score 100.0%; Pred. No. 8.2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          967 AA.
                                             TSP TYPE-1 2.
TSP TYPE-1 3.
                                                                                                    POLY-LYS.
CYS-RICH.
                                                                                                                                                                                                                                                                                      105383 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 AFTTAHELGHVFNMPHD 412
                                                                                                                                                                                                                                                                                                                                    Query Match 1.8
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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724
849
908
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967
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527
561
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                                                                                                                                                                                                                             468
561
967 AA;
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CONFLICT
SEQUENCE
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                                                                                                                               CARBOHYD
                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                           PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00042; TS91, 2.
PROSITE; PS00407; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                  ZINC (CATALTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALTIC) (BY SIMILARITY).
ZINC (CATALTIC) (BY SIMILARITY).
DISINTEGRIN LIKE.
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC. ..) (POTENTIAL). (GLCNAC. ..) (POTENTIAL). (GLCNAC. ..) (POTENTIAL). (GLCNAC. ..) (POTENTIAL).
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KFRSSQ -> RSRGSL (IN REF. 2).
V -> A (IN REF. 2).
R -> P (IN REF. 2).
L -> TR (IN REF. 2).
L -> TR (IN REF. 2).
R -> G (IN REF. 2).
TMLV -> WILK (IN REF. 2).
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CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105705 MW; F93C864F6DCDB4CF CRC64;
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8.2e-09;
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N-LINKED (GLCNAC:
N-LINKED (GLCNAC:
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L -> V (IN REF.
I -> T (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATS1_MOUSE STANDARD; PRT; 968 AA. P97857, 054768; A30-MAY-2000 (Rel. 39, Created) 16-0CT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          TSP TYPE-1 2.
TSP TYPE-1 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                             InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR0001590; Reprolysin.
InterPro; IPR000184; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 6.
Pfam; PF01421; Reprolysin; 2.
Pfam; PF01562; Pep_M12B_propep; 2.
SMART; SM00209; TSP1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
N-LINKED
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                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                 SPACER
                                                                    EMBL; AF149118; AAD34012.1; -. EMBL; AF304446; AAG29823.1; -. MEROPS; M12.222; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
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9957
11998
9967
7720
9452
721
722
723
724
9962
962
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607
936
962
967 AA;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                             ACT_SITE
METAL
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CARBOHYD
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METAL
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE.

SIMILARITY: BELONGS TO PERTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene.";
J. Biol. Chem. 272:556-562(1997).
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Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACITVITY (BY SIMILARITY). ACITUE METALLICAPROFASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-1-LEU-1692 STE, WITHIN THE CHONROITIN SULFARE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
                                       metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND INDUCTION.
MEDILINE-20243757; Pubmed=10781075;
ROBKER R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuno K., Lizasa H., Ohno S., Matsushima K.; "The exon/intron organization and chromosomal mapping of the mous ADAMTS-1 gene encoding an ADAM family protein with TSP motifs."; Genomics 46:466-471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuno K., Terashima Y., Matsushima K.;
"ADAMTS-1 is an active metalloproteinase associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97150761; PubMed-8995297;
Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20389568; PubMed=10930576;
Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka Mohno H., Matsushima K.;
"ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan.";
"FEBS Lett. 478:241-245(2000).
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.) (A disintegrin and m
with thrombospondin motifs 1) (ADAM-TS1).
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MEDLINE-99303657; PubMed-10373500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 274:18821-18826(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~98110583; PubMed~9441751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMESHIFT IN POSITION 7.
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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NCBI_TaxID=10116;
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METAL
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CARBOHYD
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     the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATS4_RAT
OPERSP7, OPERSP8, OPERSP6,
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amontation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                            MEROPS; M12.222;

MEROPS; M12.222;

MEDPOS; M12.222;

MEDPOS; M12.223;

MEDPOS; M12.23;

MEDPOS; M12.23;

MEDPOS; M12.23;

MEDPOS; M12.23;

MEDPOS; M12.23;

MEDPOS; M13.3;

MEDPOS; M12.33;

MEDPOS; M12.33;

MEDPOS; M12.34;

MEDPOS; M13.34;

MEDPOS;
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(POTENTIAL).
(POTENTIAL).
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ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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8.2e-09;
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E->0: LOSS OF ACTIVITY.
N -> S (IN REF. 2).
T -> S (IN REF. 2).
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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(CATALYTIC)
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TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 17; DB
ilarity 100.0%; Pred. No. 8.5
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP TYPE-1 2.
TSP TYPE-1 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ARG.
                                                                                                    EMBL; AB001735; BAA24501.1; ALT_INIT.
EMBL; D67076; BAA11088.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINCZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105841 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 AFTTAHELGHVFNMPHD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425
968 AA;
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nes 17; Conserv
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ADAMTS4.
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METAL
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CARBOHYD
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ATS4_RAT
ID ATS4
AC 09ES
AC 09ES
DT 15-J
DT 15-J
DD 15-J
DD ADAN
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CN ADAN
CO RALT
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                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-:- TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
-:- DOMAIN: THE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
-:- DOMAIN: THE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
-:- DOMAIN: THE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
-:- FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX.
-:- SIMILARITY: BELONGS TO PEPTIORS FAMILY MIZB.
-:- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                                                    STRAIN=Wistar; TISSUE=Brain;
MEDLINE=20415831; PubMed=10961658;
Satoh K., Suzuki N., Yokota H.;
"ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin motifs) is transcriptionally induced in beta-amyloid treated rat astrocytes.";
                                                                                                                                                                                                      Neurosci. Lett. 289:177-180(2000).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY INVOLYED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGRECAN IN ARTHRITIC DISEARES.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-1-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ALA.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
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63A428753167C7EF CRC64;
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100.0%; Pred. No. 7.6e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
ADAMTS-4.
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB042272; BAB16474.1; -...
EMBL; AB042271; BAB16473.1; -...
EMBL; AB042273; BAB16475.1; -...
InterPro; IPR00150; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Ffam; PF00090; tsp_1; Z...
Pfam; PF01421; Reprolysin; 1.
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00209; TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DTAILFTRQDLCG
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Best Local Similarity
Matches 13; Conser
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SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Scor.
100.0%; Pre
                                                                                                                                                                                     InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
                                                                                                    EMBL; AB014588; BAA31663.1; --
EMBL; AF148213; AAD41494.1; --
EMBL; AY044847; AAL02262.1; --
MEROPS; M12.221; --
Genew; HGNC:220; ADAMTS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90224 MW;
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 DTAILFTRODLCG 323
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77
626
682
837 AA;
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METAL
ACT_SITE
METAL
METAL
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DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CONFLICT
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CONFLICT
SEQUENCE
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CHAIN
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ATS9_HUMAN
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ò
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Burn T.C., Arner E.C.;
Burn T.C., Arner E.C.;
Burn T.C., Arner E.C.;

"The thrombospondin motif of aggrecanase-I (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";

J. Biol. Chem. 275:25791-25797(2000).

-I. FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. COULD ALSO BE A ONE CRITICAL FACTOR IN THE EXACERBATION OF NEURODEGENERATION IN ALZHEIMER'S DISEASE.

-I. CAMPALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-1-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATS4_HUMAN STANDARD; PRT; 837 AA.
075173; 09DN83;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-4 precursor (RC 3.4.24.) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS 4) (Aggrecanase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1- TISSUB SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED AT VERY LOW LEVEL IN PLACENTA AND SKELETAL MUSCLES.
                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-9286303; PubMed-10356395;

Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M.,
Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
Nagase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K.,
Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
Trzaskos J.M., Arner E.C.;
"Purification and cloning of aggrecanase-1: a member of the ADAMTS
family of proteins."
                                                                                                                                                                                                                                                                  MEDLINE-98403880; PubMed-9734811;
Shilkawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Olbara O.;
"Prediction of the coding sequences of unidentified human genes. X."
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertèbrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Sawaji Y.; Nagase H.; Saklatvala J., Clark A.R.;
"ADDMTS-4 genomic locus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE, AND CHARACTERIZATION. MEDLINE=20400518; PubMed~10827174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 284:1664-1666(1999).
                                                                                                                                                            ADAMTS4 OR KIAA0688
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWES-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF000130; Zn_MTpeptdse.
Pfam; PF000130; tsp_l; l.
Pfam; PF0001030; tsp_l; l.
SMART; SM00209; TSP1; l.
PROSITE; PS500142; ZINC_PROTEASE; l.
PROSITE; PS500142; ZINC_PROTEASE; l.
PROSITE; PS50012; TSP1; l.
PROSITE; PS00477; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Extracellular matrix.

SIGNAL.

1 51
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CHALTARYTY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAMTS-4.
CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> T (IN REF. 1).
R -> Q (IN REF. 3).
G -> R (IN REF. 3).
5DF9C9AC137DF41F CRC64;
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Pred. No. 9.7e-05;
0; Mismatches 0;
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1629 AA.
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CYS-RICH.
SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal;
MEDLINE-20396138; PubMed-10936055;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                      DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                     MEDINE-20181126; PubMed-10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVI.
The complete sequences of 150 new CDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000).
-I. COFACTOR: BINDS I ZINC ION (BY SIMILARITY).
-I. SUBCELLULAR LOGATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                matix (By similarity).
-i- Alternative Products: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.
EXPRESSED SLIGHTLY IN ADDLT OVARY, PANCREAS, HEART, KIDNEY, LUNG, PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECTED IN COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SW00209; TSP1; 14.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINFERIN_1; FALSE_NEG.
PROSITE; PS00142; INC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                              PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
  Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.
                  Maki R.A.;
"ADAWTS 9, a novel member of the ADAW-TS/Metallospondin gene
                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ADAMTS-9.
DISINTEGRIN-LIKE.
                                                                                  SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPACER.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001763; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000184; TSP1.
InterPro; IPR000180; Zn_WTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SWART; SM00209; TSP1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF261918; AAF89106.1; -. EMBL; AB037733; BAA92550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; M12.021; -. Genew; HGNC:13202; ADAMTS9.
                                                         Genomics 67:343-350(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; P15167; 1ATL.
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
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MIM; 605421; -
                                                                                                 TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                  THYMUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       natix (By similarity).

--- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN ADULT LUNG AND HEART AND LOW EXPRESSION DURING MOUSE DEVELOPMENT.

--- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

--- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2).
ADAMTS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                           ZINC (CATALYTIC) (L. COTENTIAL)

N-LINKED (GLCNAC. ) (POTENTIAL)

(TINKED (GLCNAC. ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
CLVTCGKGH -> VRWEGCYFP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                         CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATARITY:
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13; DB 1; Length 1629;
Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN SHORT ISOFORM).
F -> L (IN REF. 1).
W; CIC4CEFF58BB941F CRC64;
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-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 11.
POLY-SER.
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Matches 13; Conservative
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13833
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1612
1612
4334
4438
1135
1352
1352
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1629 AA;
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P57110;
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METAL
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CARBOHYD
CARBOHYD
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VARSPLIC
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                        DOMAIN
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS 5) (ADAM-TS 11)
ADAMTS OR ADAMTS11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                        HSSP; P34179; ILRG.

R HSSP; P34179; ILRG.

R MEROPS; M12.266; -

MEROPS; M12.266; -

METOPIO; IPRO01765; Dislantegrin.

R InterPro; IPR001590; Reprolysin.

R InterPro; IPR001890; Zn_MTpeptdse.

R InterPro; IPR001890; Zn_MTpeptdse.

R Ffam; PF001421; Reprolysin; 1.

SMART; SM00209; TSP1; 2.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 2.

R PROSITE; PS00144; ZINC_PROTEASE; 2.

R PROSITE; PS00144; ZINC_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99367476; PubMed=10438522;
Abbaszade I., Liu R.-Q., Yang F., Rosenfeld S.A., Ross O.H.,
Link J.R., Ellis D.M., Tortorella M.D., Pratta M.A., Hollis J.M.,
Wynn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K.,
Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H.,
Ito Y., Newton R.C., Magolda R.L., Trzaskos J.M., Hollis G.F.,
Arner E.C., Burn T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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0
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Pred. No. 0.0011;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPACER
                                                                                       EMBL; AF175282; AAF25805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98879 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%;
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905
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382
388
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A MEDLINE-20289799; PubMed-10830953;
A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Diki M., Takagi T., Sakaki Y., Taudien S., Blechachmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K., Iehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Hehrmeyer S., Borzym K., Gardiner K., Nizellc D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
T. The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Fetal brain;

MEDLINE-9395124; Pubmed-10464288;

HURSKAinen T.L., Hirohata S., Seldin M.F., Apte S.S.;

*ADAM-TS5, ADAM-TS6, and ADAM-TS7, novel members of a new family of zinc metalloproteases.";

J. Biol., Chem. 274:2555-2563(1999).

-I. FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOCLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANTATION PERIOD.

-I. CALLALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTHRITIC PATIENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX.

PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLIULAR LOCATION: Secreted, Associated with the extracellular results (By similarity).
-1- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA BUT ALSO IN OTHER TISSUES, SUCH AS HEART AND BRAIN, AND ALSO CERVIX, UTERUS, BLADDER, ESOPHAGUS, RIB CARTILAGE, CHONDROBLASTOMA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
'Cloning and characterization of ADAMTS11, an aggrecanase from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
                        ADAMTS family.";
J. Biol. Chem. 274:23443-23450(1999).
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InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF142099; AAD49577.1; -.. EMBL; AP001698; BAA95504.1; -.. EMBL; AP001697; BAA95503.1; -.. EMBL; AF141293; AAF02493.1; -.. HSSP; Q9PW35; 1BUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00090; tsp_1; 2.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:221; ADAMTS5.
                                                                                         SEQUENCE FROM N.A.
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IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR
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100.0%; Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISINTEGRIN-LIKE,
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP TYPE-1 2.
                                                                                                                                                                                                                          MGD, MGI.1346521; Adamts5.
InterPro: IPR001762; Disintegrin.
InterPro: IPR001870; Pep_MISB_propep.
InterPro: IPR001890; Reprolysin.
InterPro: IPR000884; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF001801; Esp. 12.
Pfam; PF01562; Pep_MISB_propep; 1.
SMARY; SM00209; TSP1; 2.
PROSITE; PS50215; ADAM_MBPRO; 1.
PROSITE; PS50215; ADAM_MBPRO; 1.
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POLY-ARG.
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                                                                                                                                                                                                                       1; Adamts5.
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930 AA;
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Best Local Similarity
                                                                                                                                                                                                                    MEROPS; M12.225;
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SEQUENCE
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METAL
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ATS8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIDIATE JOINTY: HITCHARG S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, novel members of a new family of
zinc metalloproteasess.";
1. Biol. Chem. 274.2555-2553(1999)
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE
INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE
DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN
PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI IMPLANTATION PERIOD.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-lala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last amontation update)
ADAMYS-5 precursor (EC 3-4.24.-1) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TSS) (Aggrecanase-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                               ADAMTS-5.
CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
TSP TYPE-1 1.
CYSTEL
                                                                 Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                              (POTENTIAL).
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100.0%; Pred. No. 0.012;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         38 A -> G (IN REF. 2).
514 R -> H (IN REF. 2).
514 P -> L (IN REF. 2).
5101715 MW; B64281502F28193B CRC64;
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 AA.
          SMART; SM00209; TSP1; 2.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS00127; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                             TSP TYPE-1 2.
POLY-ALA.
                                                                                                       POTENTIAL.
                                                                                            POTENTIAL
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Pfam; PF01562; Pep_M12B_propep; 1.
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                                                                                                                930
209
4110
4114
566
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614
692
930 AA;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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37
257
498
728
802
807
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Q9R001;
                                                                                                                                      METAL
ACT_SITE
METAL
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CARBOHYD
CARBOHYD
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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CHAIN
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                                                                                            SIGNAL
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UNDECTABLE LEVEL THRREAFTER.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PROSITE; PSO0427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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CYSTEINE SMITCH (POTENTIAL).
EXCHOCHALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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(GLCNAC. . .)
                                                                                                                                   SIMILARITY).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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us-10-009-332-1.oli.rsp

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                                                                                                                                                                                                                                                                                                                                                 Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
Lombardo M., Iruela-Arispe M.L.;
"METH-1, a human ortholog of ADAMTS-1, and METH-2 are members of a new
family of proteins with anglo-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matrix (By similarity).
TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWER
EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R InterPro; IPR00126; Disintegrin.
R InterPro; IPR0012870; Pep_M12B_propep.
R InterPro; IPR001280; Reprolysin.
R InterPro; IPR001280; Reprolysin.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01421; ADAM_MEPRO; 1.
R PR05ITE; PS500125; ADAM_MEPRO; 1.
R PR05ITE; PS500125; INC_PROTEASE; 1.
R PR05ITE; PS00427; INC_PROTEASE; 1.
R PR05ITE; PS00427; DISINTEGRIN_1; FALSE_NEG;
W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
M Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                         MEDLINE=99367466; PubMed=10438512;
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                        ADAMTS8 OR METH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
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215
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                                                                                                                                                                                                                                                                                                TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDNEY
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                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMYS-10 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
ADAMYS10.
                                                                                                                                                                                    YLTELLDGGHGDCLLDAPGAALPLPTGL -> FSGCHLQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matrix (By similarity).
-i- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombospondin type I repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                  . .) (POTENTIAL)
                                                                                                                                 (POTENTIAL)
                                                                                                                                                (POTENTIAL)
                                                                                                                                                           . .) (POTENTIAL)
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 SIMILARITY). SIMILARITY).
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                                                                                                                                                                                                                                      Match 1.1%; Score 10; DB 1; Length 890; Local Similarity 100.0%; Pred. No. 0.13; les 10; Conservative 0; Mismatches 0; Indels
                                                                                                                               N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
E -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
 (BY
(BY
                                                                                                     N-LINKED (GLCNAC.
 (CATALYTIC)
(CATALYTIC)
                        DISINTEGRIN-LIKE,
TSP TYPE-1 1,
CYS-RICH,
                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1077 AA.
                                                               SPACER.
TSP TYPE-1 2.
                                                                                           POLY-PRO.
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Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
Interpro; IPR001894; TSP1.
Interpro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                             890 AA; 96671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF163762; AAG35563.1; -.
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Genew; HGNC:13201; ADAMTS10.
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
 539 CSRTCGGGVQ 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
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Q9H324;
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16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
ADAMTS2 OR NPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cDNA cloning and expression of bovine procollagen I N-proteinase: a new member of the superfamily of zinc."metalloproteinases with binding sites for cells and other matrix components."; Proc. Calls and other matrix components."; Proc. Natl. Acad. Sci. U.S.A. 94:2374-2379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colige A., Beschin A., Samyn B., Goebels Y., Van Beeumen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 1; Length 1077; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                 TSP TYPE-1 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 3.

TSP TYPE-1 4.

TSP TYPE-1 6.

TSP TYPE-1 6.

N-LINKED (GLCNAC. ..) (POTENI N-LINKED (GLCNAC. ..)
                                                           0; Indels
                                                                                                                                                                                                                                                                                                                   DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      CYS-RICH.
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Pfam; PF00090; tsp_1; 5.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMARY; SM0209; TSPI, 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97225960; PubMed-9122202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95348096; PubMed-7622483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118072 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1077 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 RYVETLVVAD 222
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196
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P79331;
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CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
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ATS2_BOVIN
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R INTERPRO; IPR001762; Disintegrin.

R InterPro; IPR001807; Pep_M12B_propep.

R InterPro; IPR001890; Pep_M12B_propep.

R InterPro; IPR0008084; TSP1.

R InterPro; IPR000913; Zn_WTpeptdse.

R Pfam; PF00190; LSP_1; 4.

R Pfam; PF01421; Reprolysin. 1.

R Pfam; PF01421; Reprolysin. 1.

R Pfam; PF0152; Pep_M12B_propep; 1.

R PMART; SN00209; TSP1; 4.

R PROSITE; PS00142; ZTP1; 4.

R PROSITE; PS00142; ZTNC_PR0TEASE; FALSE_NEG.

R PROSITE; PS00142; ZINC_PR0TEASE; FALSE_NEG.

R PROSITE; PS00142; ZINC_PR0TEASE; ZINC; Signal; Glycoprotein; Zymogen;

W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

W Repeat; Collagen degradation; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

-:- TISSUE SPECIFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVEL.

-:- TISSUE SPECIFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVELS IN ALL TYPE I COLLAGEN-RICH TISSUES SUCH AS SKIN, BONES, TENDONS AND AORTA AND AT LOW BEYEL. IN BRAIN AND THYMUS. THE MRNA LEVELS WERE DISPROPORTIONATELY HIGH IN HEART, LIVER, RETINA AND MUSCLE.

-:- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

-:- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).

- IDISEASE: DEFECTS IN ADAMTS2 ARE THE CAUSE OF DERNATOSPARAXIS, A RECESSIVELY INHERITED DISCARDER CHARACTERIZED BY SEVERE SKIN RECESSIVELY INHERITED DISCARDER CHARACTERIZED BY SEVERE SKIN FRAGILITY AND BIOCHEMICALLY BY THE AMINO TERMINUS.

- INCOMPLETELY PROCESSED AT THE AMINO TERMINUS.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

- SIMILARITY: CONTAINS 1 DISINTEGRIN LIKE DOMAIN.

- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.

- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV.
Nusgens B.V., Laplere C.M.;
"Characterization and partial amino acid sequencing of a 107-kDa procollagen IN Proteinase purified by affinity chromatography on immobilized type XIV collagen.";
J. Biol. Chem. 270:16724-16730(1995).
- FUNCTION: CLEAVES THE PROPEPTIDES OF TYPE I AND II COLLAGEN PRIOR TO FIBRIL ASSEMBLY. DOES NOT ACT ON TYPE III COLLAGEN. MAY ALSO PLAY A ROLE IN DEVELOPMENT THAT IS INDEPENDANT OF ITS ROLE IN COLLAGEN BIOSYNTHESIS.
- COLLAGEN BIOSYNTHESIS.
- CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
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ZINC (CATALYTIC) (
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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BY SIMILARITY.
ADAMTS-2.
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ISP TYPE-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 at Ala-
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us-10-009-332-1.oli.rsp

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TISSUE SPECIFICITY: Found in cartilage and skin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                               ATS3_HUMAN STANDARD; PRT; 1205 AA.
015072; Q9BXZ8;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS3) (Procollagen II amino-propeptide processing enzyme) (Procollagen II N-proteinase) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21402912; PubMed-11408482;
Rernandes R.J., Hirohata S., Engle J.M., Colige A., Cohn D.H.,
Eyre D.R., Apte S.S.;
"Procollagen II amino propeptide processing by ADAMTS-3. Insights on
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                            D (GLCNAC. .) (POTENTIAL).
                                                                        (POTENTIAL)
                                                  (POTENTIAL)
                                                                                      (POTENTIAL)
                                                                                                                                                                                                            ;
            CELL ATTACHMENT SITE (POTENTIAL)
POLY-ALA.
POLY-GLU.
                                                                                                                                                                                 1.1%; Score 10; DB 1; Length 1205;
100.0%; Pred. No. 0.17;
cive 0; Mismatches 0; Indels
                                                                                                                                             INKED (GLCNAC. . .) (POTF 7B5B232A45320371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-!- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
                                                                      (GLCNAC. . .)
                                            N-LINED (GLCNAC.
N-LINED GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatosparaxis.";
J. Biol. Chem. 276:31502-31509(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
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Μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 5-1205 FROM N.A.
                                                                                                                                                           133887
                                                                                                                                                                                           Local Similarity 100.
Les 10; Conservative
1024
687
35
180
104
245
942
943
987
1025
1139
                                                                                                                                                           A);
                                                                                                                                                                                                                             670 DKCGVCGGDN 679
                                                                                                                                                                                                                                             704 DKCGVCGGDN 713
                                                                                                                                                                                                                                                                                                                                                                                                                            ADAMTS3 OR KIAA0366
                                                                                                                                                         1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WCBI_TaxID=9606;
                                                                                                          1025
1092
1139
                                  DOMAIN
CARBOHYD
                                                          CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                             CARBOHYD
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 DOMAIN
                        DOMAIN
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
(Procollagen I/II amino-propeptide processing enzyme).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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135570 MW; EB07B286FC85FB87 CRC64;
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
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ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1205; 0.17;
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N-LINKED (GLCNAC. . . ) (1)
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InterPro; IPR001590; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000184; TSP1.
InterPro; IPR000184; TSP1.
InterPro; IPR000184; TSP1.
InterPro; IPR000180; Zn_MTpeptdse.
Pfam; PF00160; tsp_1; Zn_MTpeptdse.
Pfam; PF0162; Pep_M12B_propep; 1.
PMOSITE; PS50012; TSP1; Z.
PROSITE; PS50012; TSP1; Z.
PROSITE; PS00042; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS00042; DISTRIGGINLD; Signal; Glycopt SIGNAL
I 20 PROFENTIAL.
PROPER Z. 21 249
PROSITERIAL Z. 22 249
PROSITERIAL Z. 22 249
PROSITERIAL Z. 23 249
PROSITERIAL Z. 250 1205
PROPENTIAL.
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TSP TYPE-1 3.
TSP TYPE-1 4.
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10;
Pred. No.
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                                                                                                                                                                                                InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.08; FIC
                                                                                                                        EMBL; AF247668; AAK28400.1; -. EMBL; AB002364; BAA20821.1; -.
                                                                                                                                                       MEROPS; M12.220; -.
Genew; HGNC:219; ADAMTS3.
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814
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813
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1205 AA;
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095450;
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ACT_SITE
METAL
METAL
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Best Local S
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ATS2_HUMAN
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SIGNAL
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ATS6_HUMAN
                                           PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                      MALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI;
ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-PROCOLLAGEN PEPTIDASE ACTIVITY.

TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON AND ACRTA AND AT LOW LEVELS IN THYMUS AND BRAIN.
DOWAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACLLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN IYPE XIV (BY SIMILARITY).
SUBGELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i. DISEASE: Defects in ADAWTS2 are the cause of Ehlers-Danlos syndrome type VIIC (EDS-VIIC), a recessively inherited connective-tissue disorder characterized clinically by severe skin fragility and joint hypermobility and biochemically by the presence in skin of procollagen incompletely processed at the N-terminus.
-i. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i. SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-i. CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                 MEDILINE—9347935; PubMed=10417273;
Colige A., Sieron A.L., Li S.-W., Schwarze U., Petty E.,
Colige A., Sieron A.L., Li S.-W., Schwarze U., Petty E.,
Wertelecki W., Wilcox W., Krakow D., Cohn D.H., Reardon W.,
Byers P.H., Lapiere C.M., Prockop D.J., Nusgens B.V.;
Byers P.H., Lapiere C.M., Prockop D.J., Nusgens B.V.;
are caused by mutations in the procollagen I N-proteinase gene.";
Am. J. Hum. Genet. 65:308-317(1999).
-I. FUNCTION: Cleaves the propeptides of type I and II collagen prior
to fibril assembly. Does not act on type III collagen. May also
play a role in development that is independent of its role in
                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(1) art Pro-+Gln and of alpha-1(II) and alpha-2(I) chains at Ala-+Gln.
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0215; ADAM_MEPRO; 1.
PROSITE; PSS0092; TSP1; 1.
PROSITE; PSS0092; TSP1; 1.
PROSITE; PSO0427; DISINTEGRIN.1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                           SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000130; Zn_WTpeptdse. Pfam; PF00090; tsp_1; 4. Ffam; PF01421; Reprolysin; 1. Pfam; PF01562; Pep_W12B_propep; 1. SWART; SW00209; TSP1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ003125; CAA05880.1; -.
                                                                                                                                                                                                                                                                                 collagen blosynthesis.
 ADAMISS OR PCINP OR PCPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:218; ADAMTS2.
                 (Human)
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                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
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MIM; 225410;
                 Homo sapiens
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Whith thrombospondin motifs 6) (ADAM-TS 6) (ADAM-TS 6).
                                                                                                                                                                                                                                                                                                                                                                                      -> FRPGAVAHACYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Repeat; Collagen degradation; Extracellular matrix; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
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                                                                 ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                 SIMILARITY). SIMILARITY).
                                                                                                                                                        CYS-RICH.
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    HCFKGHCIWLTPDILKRDGSWGA -> FRP
TLGGQGRWIA (IN ISOPORM SPNPI).
MISSING (IN ISOPORM SPNPI).
W, BECEEF25C23CAD2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1211; 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
                                                                                                 (GLCNAC.
                                                                                                                                                                                                                                                                         (GLCNAC.
                                                                                                 (CATALYTIC) (CATALYTIC)
                                                                                                              ZINC (CATALYTIC)
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC
              Ehlers-Danlos syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      860 AA
                                                                                                                                                                                                 TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. .v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 10;
                                                                                                                                                                                                                                                                         N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                    567 1211 MAS
1211 AA; 134722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                        188
112
251
949
993
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1098
1145
1150
566
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              Alternative splicing;
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                                                                                     ACT_SITE
METAL
                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS

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                                                                                                                                                                                                                                                                                                                                          R InterPro; IPR001762; Disintegrin.
R InterPro; IPR0012870; Pep_M12B_propep.
R InterPro; IPR0012870; Pep_M12B_propep.
R InterPro; IPR0018084; TSP11, InterPro; IPR0018084; TSP11, InterPro; IPR0018084; TSP11, InterPro; IPR001809; Sp11, InterPro; IPR001809; Sp11, InterPro; IPR01421; Reprolysin, InterPro; IPR01421; Reprolysin, InterPro; IPR01421; Reprolysin, InterPro; IPR01421; PS001421; ADAM_MEPRO; InterPro; IPR01421; PS001422; INTERPRO; InterPro; IPR01421; INTERPRO; InterPro; IPR01421; INTERPRO; InterPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC).

ZINC (CATALYTIC)

ZINC (CATALYTIC)

ZINC (CATALYTIC)

DISINTERRITY).

TSP TYPE-1 1.

CYS-RICH.
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(POTENTIAL)
(POTENTIAL)
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0
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E57213015DECB2C5 CRC64;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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o. 1.3;
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TSP TYPE-1 2.
POLY-ARG.
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100.0%; Pred. No. 1.3
tive 0; Mismatches
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Matches 9; Conservative
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213 FVSIPRYVETLVVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21856482; PubMed-11867212;
MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Ottin C.;
"Cloning, expression analysis, and structural characterization of seven novel human ADANTSs, a family of metalloproteinases with dishintegrin and thrombospondin-1 domains.";
EMBL, AJ315733; CAC86014.1; -.
EMBL, Protease.
SEQUENCE 950 AA: 103286 MW; 5DFBE18285CCCC3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2042; DB 4; Length 950; 100.0%; Pred. No. 1.1e-195; Live 0; Mismatches 0; Indels 0
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Q8TES8;
O1-JUN-2002 (TIEMBLE1. 21, Created)
O1-JUN-2002 (TIEMBLE1. 21, Last sequence update)
O1-JUN-2002 (TIEMBLE1. 21, Last annotation update)
Metalloprotease disintegrin 15 with thrombospondin domains.
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Matches 371; Conservative
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094134 oryctolagus
094434 drosophila
094451 drosophila
09457 homo sapien
08te56 homo sapien
08te66 homo sapien
08te56 homo sapien
08te78 homo sapien
08te59 homo sapien
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equus cabal
                                                                                                   April 29, 2003, 17:10:24; Search time 22.6233 Seconds (without alignments) 3378.970 Million cell updates/sec
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096137
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              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
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Q8VF61
Q8TE56
Q8TE56
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Q8TE59
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Q8TE59
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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Match Length
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Goad D.L., Goad M.E.;
"Molecular cloning of lapine aggrecanase-2 (ADAMTS-11) from articular
"chondrocytes.";
                                                                                                                                                                                                                                            126 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEV------FGKL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 176
                                                         67 PKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLGMADVGT
                                                                                                                                                                    173 RAN --- HMMSPTLIQIDRANPWSACSAAIITDFLDSGHG--DCLLDQPSKPISLPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 GK-.1CLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGK
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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53.8%; Pred. No. 1.7e-71;
iive 37; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317415; AAG33062.1; -.
HSSP; Q9FW35; 1BUD.
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Last annotation update)
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InterPro: IPR001590; Reprolysin.
InterPro: IPR0015094; TSP1.
InterPro: IPR001010; Zn_MTpeptdse.
Pfan: PF00421; Reprolysin; 1.
Pfan: PF00421; Reprolysin; 1.
SWART; SN00209; TSP1; 1.
PROSITE; PS500215; ADAM_WERRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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Matches 140; Conservative
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269 AA;
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                                                                                                       TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                           GVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNK 300
                                                                                                                                                                                                                                                                                                  HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R. Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Welnstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
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45.4%; Pred. No. 4.3e-83;
ive 60; Mismatches 126;
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01-NOV-1996 (TrEMBLrel. 01, C1
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01-DEC-2001 (TrEMBLrel. 19, L8
F25H8.3 protein.
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SEQUENCE FROM N.A.
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Q8SXB0
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    KS THAIN-BERKELEY;
RA Admansides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Admansides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Milklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Bonch D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Dorkova D., Botchan M.R., Bulke C., Davenport L.B., Davies P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Durbin K.J., Evangilsta C.C., Ferraz C., Ferrate S., Fleischmann W.,
RA Goon K., Doup L.E., Downes M., Dugan-Rocha S., Plasser R.,
Butsin M., Gabriellan A.E., Gary N.S., Galbart W.M., Classer R.,
Butsin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Silmel B.E., Kodire C.D., Kraft C., Kraft S., Moy M., Nuchberson D.,
RA Hurts B.M., Malush F., Rapen G.H., Re Z., Romison J.A., Ketchum K.A.,
Rabon D.K., Moy M., Murphy E., Murphy L., Muzny D.M., Nelson D.L.,
Rabon D.K., Nelson K.A., Niskon K., Nussken D. R., Pacled D. J.,
Rabon D.K., Nolson K.A., Niskon K., Nussken D. K., Pacle B.C., Shen H.,
Spitskas R., Tector C., Tunner R., Ventra S., Shu B., Shu B., Shu B., Shu B.C., Siden Klamos I., Simpson M., Stupski M.P., Smith T.,
Rabon D.K., Woyer M., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Rabon D.K., Woyer S., Woodege T., Worley R., Subne G., Shu B., 
                           237 ELAFGYGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER- 295
                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 236
                                                                                                                                                                             296 ----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 351
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG4096 protein.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTL----IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI---SLPEDLPGASYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 LSQQCELAFG-----VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.0%; Score 796; DB 5; Length 105
44.8%; Pred. No. 1e-70;
iive 52; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1: 2.
SMART; SM00209; TSP1: 2.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50012; TSP1: 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1054 AA; 118616 MW; DC15455555CB6212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                               Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSP1.
Interpro: IPR0000810; Zn_WTpeptdse.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
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                                                                                              FlyBase; FBgn0029791; CG4096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
HSSP; P15167; 1ATL. MEROPS; M12.231; -.
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Celniker S.;
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179
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milklos G.L.G.,
A Maril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Berman B.P., Bhandwar D., Bolshavo S.,
A Borkova D., Botchan M.R., Bouvk J., Brostein P., Botskein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Brosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                     15;
                                                                                                                                                                                                                           680
                                                                                                                                                                                                                                                                                              68 KV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---TCDTLGMA 121
                                                                                                                                                                                                                                                                                                                             122 DVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN---HMM 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCG-EGKLCLKGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG6107.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Bukaryota: Medazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 CVERHNLNKH----RVDGSWAKWDPYGPCSRTCGGCVQLARRQCTNPTPANGGKYCEGVR
                                                                                                                                                                                                 8 VETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLPGASYTLSQQ
                                                                                                                                                     44;
                                                                                                    Length 1688;
                                                                                            34.4%; Score 703; DB 5; Length 168
39.3%; Pred. No. 4e-61;
1ve 64; Mismatches 125; Indels
                                                   48FB8DD4DE0CA4D2 CRC64;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY094716; AAM11069.1; -. SEQUENCE 1688 AA; 189867 WW; 48FBBDD4DE0CA4D2 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 VKYRSCNLEPCPSSASGKSFREEQ 371
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                                                                                          Query Match
Best Local Similarity 39.39
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pitrman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Parle D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skropski M.P., Smith T.,
RA Stirskas R., Tector C., Stapleton M., Skropski M.P., Smith T.,
RA Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ve J., Yeh R.-F., Zaveri J. S., Zhan M., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Moodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng C.
RA Calone sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
REMEL, RECORSTOB, Reprolysin.
RELYBEAS: FBORO033340; CG6107.
RIEFERO: IPRO010844: TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 DVGTMCDFKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN---HMM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCG-EGKLCLKG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 ACVERHNINKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 KV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---TCDTLGMA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTL-IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLPGASYTLSQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Metalloprotease; 21nc.
SEQUENCE 1229 AA; 138136 MW; C1293180AB19B700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.8%; Score 670.5; DB 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1072 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF00090; tsp_1; 2.
SMART; SM00209; TSP1; 3.
PROSITE; PS50015; TSP1; 2.
PROSITE; PS50015; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||||||| || : ||:|
RKKYRSCNTHQCPPGSMDP--REQQ 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
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Q8TE57;
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Q8TE57
ID Q8TE9
AC Q8TE9
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of

12;

Gaps

35;

Length 1095;

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295 VETLVVADKKMVEKHGKGNVTTYILTVMKVSG-LFKDGTIGSDINVVVVSLILLEQEPGG 353
                                                                                                                                                                                                                                                                                                                                                                                                                   67 PKVTGNAALTLRNFCAWQKK-----LNKV--SDKHPEYWDTAILFTRQDLC--GAT 113
                                                                                                                                                                                                                                                                                                                                                                                                114 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 RSHIMSGEWVK--GRNPSDLSWSSCSRDDLENFLKSKVSTCLLVTDPRSQHTVRLPHKLP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GASYILSQQCELAFGVGSKPCPYMQY -- CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCE 344
                                                                                                                                                                                                                                                               8 VETLVVADESMYKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 LSIGHHGERSLESFCHWONEEYGGARYLGNNOVPGGKDDPPLVDAAVFVTRTDFCVHKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VETLVVADDESMVKFHG-ADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ANHMMSPTLIQIDRANP----WSACSAAIITDFLDSGHGDCLL---DQPSKPISLPEDLP
Seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";

Gene 283:49-62(2002).

EMBL: AJ315735; CAC86016.1; -.

Integrin; Protease.

SEQUENCE 1095 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21856482; PubMed=11867212; Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.; Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.; Cal S., Obaya M.J., Lamazares M., Garabaya C., Quesada V., Cloping, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ311903; CAC83612.1; -.
SEQUENCE 1081 AA; 119655 MW; 0438BF645676461E CRC64;
                                                                                                                                                                                                  31.5%; Score 643.5; DB 4; Length 36.7%; Pred. No. 2.1e-55; ive 64; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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38.0%; Pred. No. 6.6e-55;
ive 51; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 GVRVKYRSCNLEPCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | :: | | | | | GASVEHAVCENLPCPKGL--PSFRDQQ 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                    Best Local Similarity 36.79
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || || : || : || : || 463 AGRNGVFSWSPCSRQYLHKFLSTAQAICLADQP-KPVKEYKYPEKLPGELYDANTQCKWQ 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKVTGNAALTLRNFCAWQKKL-NKVSDKHPEYWDTAILFTRQDLCG--ATTCDTLGMADV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 RHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 VETLVYVDKKMMONHGHENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 LVISHHADHTLSSFCQWQSGLMGKDGTRH----DHAILLTGLDICSWKNEPCDTLGFAPI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VETLVVADESMVKFHG-ADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 FGVGSKPCPY---MQYCTKLWC--TGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                         I motif.
                                                                                                                                                                                                                                      MEDLINE-21856482; PubMed-11867212; MEDLINE-21856482; PubMed-11867212; Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.; "Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002). EMBL; AJ315734; CAC86015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1072;
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MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 654; DB 4; Length 10; Pred. No. 1.8e-56; 49; Mismatches 149; Indels
                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type
ADAMTS16.
                                                                                                                                                                                                                                                                                                                                                                                                     1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
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Last annotation update)
17, with thrombospondin
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39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 LEPCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 39.5%
Matches 149; Conservative
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                                                                                                                                                                                                          NCBI_TaxID=9606;
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10;
PKVTGNAALTLRNFCAWQKKL-NKVSDKHPEYWDTAILFTRQDLCG--ATTCDTLGMADV 123
                                    182
                                                                                                                                                                                                                 183 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSK--PISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                                                                                                                                                         GVGSKPCP---YMQYCTKLWC--TGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER 295
                                                                                                                                                                                                                                                                                                                                                                296 HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580 GELGPRPIHGOWSAWSKWSECSRTCGGGVKFQERHCNNPKPQYGGIFCPGSSRIYQLCNI 639
                                                                                                                                      524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLIERGNPSRSLEQVCRWAHSQQRQDPSHABHHDHVVFLTRQDF-----GPSGYAPVTG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                             GTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTL
                                                                                                                                                                                                                                                      : ||:|| : ||:|| 465 TGNNGVFSMSSCSRQYLKKFLSTPQAGGLVDEPKQAGQYKYPDKLPGQIYDADJQCKWQF
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
A disintegrin-like and metalloprotease with thrombospondin type
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A BOLZ H., Ramirez A., von Brederlow B., Kubisch C.;
BOLZ H., Ramirez A., von Brederlow B., Kubisch C.;

BOLZ H., Ramirez A., von Brederlow B., Kubisch C.;

Bold R., Ramily 
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133871 MW; 36394AC4D92F170F CRC64;
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5; Pred. No. 9.9e-53;
59; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMARY, SM00209; TSP1; 4.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
Signal; Integrin; Protease; Metalloprotease.
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35.9%;
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640 NPC--NENSLDFRAQQ 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 EPCPSSASGKSFREEQ 371
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Matches 134; Conservative
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Q8WXS8
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126 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD---NVKVCEEVFGKLRANHMMSPTL 182
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                183 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI-SLPEDLPGASYTLSQQCELAFG
                                                                          430 QAAFHRFHWSRCSKLELSRYLPS--YDCLLDDPFDPAWPQPPELPGINYSMDEQCRFDFG
                                                                                                                  VGSKPC---PYMQYCIKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
                                                                                                                                                                            NKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 SLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLTRQDF-----GPSGYAPVTG
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MEDLINE-21865482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization
seven novel human ADAWISs, a family of metalloproteinases with
disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
EMBL; AJ345098; CAC87943.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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607 PGTY--EDFRAQQ 617
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114 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDN-VKVCEEVFGKL 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 ASYTLSQQCELAFGVGSKPCPYMQY - - CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 WCKAGECTSRTSAPEH-LAGEWSLM---SPCSRTCSAGISSRERKC--PGLDSEARDCNG
                                                                                                                                                                                                                                                                                                            8 VETLVVADESMYKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG
                                                                                                                                                                                                                                                                                                                                                                    67 PKVTGNAALTLRNFCAWQ-KKLNKVSDKHPEY---W-----DTAILFTRQDLC--GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               286 ICLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   SEQUENCE FROM N.A.

MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
Cloning, expression analysis, and structural characterization
seven novel human ADAMTSs, a family of metalloproteinases with
disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).

EMBL; AJ311904; CAC84565.1; -.
SEQUENCE 1207 AA; 134061 MW; AF36F6BF5886FDE2 CRC64;
                                                                                                                                                                                                                                                  29.7%; Score 606; DB 4; Length 120
36.8%; Pred. No. 1.4e-51;
ive 58; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Bquus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Perissodactyla; Equidae,
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InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                   Local Similarity
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                                                Mammalia; Euther
NCBI_TaxID=9606;
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Q95N24
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MEDLINE-21839041; PubMed-11741898;
COLige A., Vandenberghe I., Thirty M., Lambert C.A., Van Beeumen J.,
Li S.W., Prockop D.J., Lapiere C.M., Nusgens B.V.;
"Cloning and Characterization of ADAMTS-14, a Novel ADAMTS Displaying High Homology with ADAMTS-2 and ADAMTS-3.";
J. Biol. Chem. 277:5756-576(2002).
EMBL; AF366351; AAL79814.1;
SEQUENCE 1159 AA; 127336 MW; A5B130149BF7FF34 CRC64;
                  909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 VGSKPC---PYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD---NVKVCEEVFGKLRANHMMSPTL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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NKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPC
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Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI-SLPEDLPGASYTLSQQCELAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.2%; Score 616; DB 4; Length 1159; 36.2%; Pred. No. 1.3e-52; ive 60; Mismatches 156; Indels 2.
                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                             1159 AA
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                                                                                                                                                                            Created)
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
ADAMTS-19.
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Best Local Similarity 36.2 Matches 135; Conservative
                                                                                                                                             PRELIMINARY;
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                                            371
                                                                      617
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PGTY--EDFRAQQ 553
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                                                           | : : || :|
PGTY--EDFRAQQ
                                          359 PSSASGKSFREEQ
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                                                                                                                RESULT 12
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ID Q8TE5
AC Q8TE5
DT 01-JU
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Tartucture of von Willebrand Factor-cleaving Protease (ADAWTS13), a
Wetalloprotease Involved in Thrombotic Thrombocytopenic Purpura.";
J. Biol. Chem. 276:41059-41063(2001).

R EMBL; AYOS376; AAL1; -.

R MEROPS; M12.241; -.

R MEROPS; M12.241; -.

InterPro; IPR001890; Reprolysin.

R InterPro; IPR001891; Zn_MTpeptdse.

R Pfam; PF01421; Reprolysin; 1.

R PROSITE; PS50015; ADAM_MEPRO; 1.

R PROSITE; PS50015; ADAM_MEPRO; 1.

R PROSITE; PS500142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                     PKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDL-CGATTCDTLGMADVGT 125
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                                                                                                                                                                                                                                                                   7 YVETLVVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKYLLLRDRDSG 66
                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,
Fujikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.4%; Score 540; DB 4; Length 1427; 32.1%; Pred. No. 7.1e-45; tive 45; Mismatches 180; Indels 4
                                                                                                                   Length 192;
                                                                                                                                                                          64; Indels
                                                      9013B0E19FCE8C56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Von Willebrand factor-cleaving protease precursor.
ADAMTS13.
                                                                                                          Query Match

27.3%; Score 558; DB 6;
Best Local Similarity 51.0%; Pred. No. 8.2e-48;
Matches 98; Conservative 26; Mismatches 64;
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                           192
20670 MW;
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Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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181 LQEFNIPQAGGW 192
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192 19
192 AA;
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236
126 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHWMSPTLIQI 185
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                                                                                                                                                            237 ELAFGVGSKPCPY----MQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGAC 292
                                                                                                                                                                                                   312 RVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRC 371
                                                                                                                                                                                                                                          293 VERHNINK-HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 351
                        DRANP-----WSACSAAIITDFLDSGHGDCLLD----QPSKPISLPEDLPGASYTLSQQC
                                                                                                                                                                                                                                                                                                                        352 SCNLEPCP------SSASGKSF 367
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Appli Appli

1, A 19, A 2, A

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Sequence 2, Application US/09130491

Fatent No. 6416974

GENERAL INFORMATION:

APPLICANT: Holtaman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT FILING DATE: 1998 08-07

EARLIER APPLICATION NUMBER: US 60/058,108

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-09-05

SERLIER FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 16

SOOTHWARE: FRAILER PAPELCATION NUMBER: US 60/054,961

SOOTHWARE: RESTERQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                   Sequence 4, p
Sequence 3, p
Sequence 3, p
Sequence 1, p
Sequence 1, p
Sequence 2, p
Sequence 2, p
Sequence 2, p
Sequence 2, p
Sequence 1, p
Sequence 1, p
Sequence 1, p
Sequence 6, p
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US-09-813-819-2
US-09-920-048-2
US-09-820-048-4
US-08-826-442-3
US-08-86-412-3
US-08-813-1288-19
US-08-09-08-790-1
US-08-313-2888-19
US-08-317-931-2
US-09-817-3838-2
US-09-817-3838-2
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US-09-817-3838-2
US-09-817-3838-2
US-09-817-3838-2
US-09-026-001A-10
US-09-026-001A-10
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US-09-026-001A-10
US-09-026-001A-10
US-09-026-001A-10
                                                                                                                                                                                                     ALIGNMENTS
  CRGANISM: Homo sapiens
US-09-130-491-2
  RESULT 1
US-09-130-491-2
  226.5
226.5
226.5
210.2
200.5
200.5
200.5
199.5
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184.5
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Sequence 2, Appli
Sequence 13, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appli
Sequence 17, Appli
Sequence 22, Appli
Sequence 5, Appli
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5, APP1
11, APP1
21, APP1
7, APP1
20, APP1
3, APP1
3, APP1
3, APP1
3, APP1
                                                                    April 29, 2003, 17:10:24; Search time 11.9712 Seconds (without alignments) 1813.869 Million cell updates/sec
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Sequence 5, Ap
Sequence 11, 2
                                                                                                                                1 FVSIPRYVETLVVADESMVK......DQCNLHRKPQELDFCVLRPC 738
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                                                                                                                                                                                                                                                                                           GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-364-9

US-09-122-126B-2

US-09-122-126B-13

US-09-122-126B-15

US-09-36-364A-15

US-09-36-364A-15

US-09-36-364A-2

US-09-130-491-16

US-09-130-491-8

US-09-36-364A-2

US-09-36-364A-2

US-09-36-364A-1

US-08-313-28BB-20

US-08-93-64-1

US-08-93-68-2
                                                                                                                                                                                                    of hits satisfying chosen parameters:
                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                             US-10-009-332-1_COPY_213_950
4043
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Maximum Match 100%
Listing first 45 summaries
                                                   protein search, using sw model
                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
Sequence:
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11;

Gaps

611

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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 FVSEARFVETLLVADASMAAFYGTDLQNHILTVMSMAARIYKHPSIRNSVNLVVKVLIV 288
                                                                                                                         790
                                                                                                                                                                                                                                                                                                                                                                                                                                                             846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER 536
                                                                                                                                                                                                                                                                                                                                                                                                  DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDK 596
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47.3%; Score 1911.5; DB 4; Length
Best Local Similarity 50.6%; Pred. No. 8.8e-156;
Matches 352; Conservative 127; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurshainen, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zir:
FILE REFERENCE: 264734007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 905
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US-09-369-364A-9
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GENERAL INC. 04103/4
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
SAFLIER FILING DATE: 1997-09-05
NUMBER OF: SEQ ID NOS: 16
SOFTWARE PASSEQ for Windows Version 3.0
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              RSCULEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRA
VERHILIN - - KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY
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llarity 49.3%; Pred. No. 4.9e-155;
Conservative 114; Mismatches 146;
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Patent No. 6416974
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Matches 339; Conserv
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US-09-130-491-13
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               CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANG 412
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                                                                     1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
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296 HNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRS
                                                                                                                                                                                                                                                                                                                   541 ---KES------FNAIPTFS-----
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53.1%; Pred. No. 7e-143;
.ive 91; Mismatches 181; Indels 1
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TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 837
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581 GGVLSHESCDPLKKPKHFIDFCTMAEC 607
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Hirstainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirchata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION UMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
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44.88; Pred. No. 4.4e-142;
wiematches 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09369364A, Patent No. 6391610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens ADAMTS-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _ Y
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LOCATION: (468)
OTHER INFORMATION: Xaa
NAME/KEY: MOD_RES
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; OTHER INFORMATION: Xaa
US-09-369-364A-13
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PatentIn Ver. 2.1
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Best Local Simi
Matches 344;
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                                                                                                                                                               RDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPRED 595
                                                                                                                                                                                                                                               628
                                                                                EPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGY 415
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 AFGVGSKPCPYMQYCTXLWC---TGKAKGOMVCQTRHFPWADGTSCGEGKLCLKGACVER 295
             2 VSIPRYVETLVVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLR 61
                                                                                                                                                                                                                                                                                                         877 PCGTGCDLRWHVASRSECSAQCGLGYRTLDIYCAKYSRLDGKTEKVDDGFCSSHPKPSNR
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48.7%; Pred. No. 1.9e-141;
tive 98; Mismatches 219; Indels
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REPERBACE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09122126B Patent No. 6451575
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Best Local Similarity 48.7
Matches 335; Conservative
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US-09-122-126B-15
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US-09-122-126B-15
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SISSH---GWWGSWGSWGSWGSKSCGGGVQFAYRHCNNPAPRNNGRYCTGKRAIYRSCSLM
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                                                                                      PEYSUCPGENDVCARLEGAVVRQGOMVCLTKKLPAVEGTPCGKGRICLQGKCVDKTKKKYY
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                                                                  LIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFG
                                                                                                                                                    VGSKPCPYMQYCTKLWCTGKAKGOMVCQTRHFPWADGTSCGEGKLCLKGACVER----H
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
TIILE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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Sequence 15, Application US/09369364A
Patent No. 6391610
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APPLICANT: HOLDMAN, Douglas A.
APPLICANT: HOLDMAN, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83;
FILE REPERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US,09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER TALING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 16
LENTH: 551
          242 VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER----H 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPT 181
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563 SISSH---GNWGSWGPWGQCSRSCGGGVQPAYRHCNNPAPRNSGRYCTGKRAIYRSCSVT
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Patent No. 6416974
GENERAL INFORMATION:
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; ORGANISM: Rattus rattus
US-09-130-491-16
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Matches 28
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                                                                                                      415 YFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVT
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                                                                         SPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-SKPISLPEDLPGASYTLSQQCE
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Best Local Similarity 47.4%; Pred. No. 8.3e-140;
Matches 327; Conservative 105; Mismatches 218;
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zin
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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591

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APPLICANT: Holtzman, Douglas A.
APPLICANT: GOGGGARI, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1990-09-05
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                        61 LPGTLYDANRQCQFTFGEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGE 120
                                                                                                                                     121 GKWCVSGKCVNKTDM-KHFATPVHGSWGPWGPWGDCSFTCGGGVQYTMRECDNPVPKNGG 179
                                                                                                                                                                                            KYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSP 400
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CASLNGVSGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSD
                                        225 LPGASYTLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE
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                                                                                                                   GKLCLKGACVERHNLNKH - - - RVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGG
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US-00-130-491-8
; Sequence 8, Application US/09130491
; Patent No. 6416974
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Matches 236; Conservative
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ORGANISM: Rattus rattus
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| 121 KLPAVEGTPCGKGRICLQGKCVDKTKKXYSTSSH---GNWGSWGGCSRGCGGGVQF
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                                                                            423 VVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMH
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APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hirohata, Satoshi
TILLE OF INVENTION: Wucleic Acids Encoding Zinc Metalloproteases
FILE REPERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT APPLICATION NUMBER: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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Sequence 22, Application US/09369364A

; Sequence 12, Application US/09369364A

; Patent No. 6391610

; GENERAL INFORMATION:
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LOCATION: (99)
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LENGTH: 518
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                                                       ----WKP-YTQVEDQDLCKLYCI
                                    ANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKS
                                                                                                          CKKVTGLFTKPMH--GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNG
                                                                                                                                                                               HFWVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFY
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APPLICANT: Apte. Suncel
APPLICANT: Hirshata, Satoshi
TILE OF INVENTION: Nucleace Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 2647344007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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SQKCPRDS - - VDFRAAQCAEHNSRRFRGRHYK - -
                                                                                                                                                                                                                                                       LPKEPREDKSSHPKDPRGPS------
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; ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7
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SEQ ID NO 7
LENGTH: 997
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Matches 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Erin
TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the SFLER REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR APPLICATION NUMBER: 05 60/225,852
PRIOR FILING DATE: 2000-08-16
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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                                416 EI---LIVQILATDPTKPLDVRYSFFVPKK-----STPK------VNSVTSHGSNKV 458
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                                                                                                                                                        507 LIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESL----QASR 561
                                                                                                                                                                                                                                PILEPLIVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSL-SNQV 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 PKVIGNAALTLRNFCAWQKKL-NKVSDKHPEYWDTAILFIRQDLCG--ATTCDTLGMADV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 LVISHHADHTLSSFCQWQSGLMGKDGTRH----DHAILLTGLDICSWKNEPCDTLGFAP1 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI---SLPEDLPGASYTLSQQCELA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 AGRNGVFSWSPCSRQYLHKFLSTAQAICLADQP-KPVKEXKXPEKLPGELYDANTQCKWQ 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 LEPCPSSASGKSFREEQC----EAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICR 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTL 182
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                                                                                   CDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKG
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US-09-930-872-4
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                                                                                                                                                                                                                                                                                                                                                                                                                 GPCSASCGSGLQKRAVDCRGS-----AGQRTVPACDAAHRPVETQACGE----PCPTW 685
                                                                                                                                                                                                                         474 TGLFTKPMH-GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ-GKYLLNGHFVV 531
                                                                                                                                                                                                                                                                                      532 SAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVL-----SVGKMTPPRVR 583
                                                                                                                                                                                                                                                                                                                                                                                                                                               863 G--QAPLGLGGWRRHLVLMGPRLPTQLLFQESNPGVHYEY-TIHREAGGHDEVPPVFSW 919
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Colige, Alain
APPLICANT: Laplere, Charles M.
APPLICANT: Laplere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
RLQYGAYSAFCEDMDNVCHTLWCSVGT----TCHSKLDAAVDGTRCGENKWCLSGECVP-
                                              584 YSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARW---VA----GSW
                                                                                             EPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGY
                                                                                                                                                          FYVLAPKVVDGTLCSP - - DSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKV
                               HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fastscop for Windows
USFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Abrams, Samuel'B
REGISTRATION UNBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-555
TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSAWSPCSKSCGRG -- FQRRSLKCVG 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-491-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 KPCPYMQY --- CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV ----E
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                                                                                                                                                                                                                                                                   LVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAFGVGS
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                                                                                                                                                                             Length 1211;
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                                                                                                                                                                          Query Match 26.2%; Score 1060; DB 4; I
Best Local Similarity 34.2%; Pred. No. 2.3e-82;
Matches 275; Conservative 109; Mismatches 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1006 DDSFGICQEERPETARTCRLGPC 1028
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                             ; TOPOLOGY: linear
US-09-491-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 KL---CLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 KYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNG-----YNHSTNRLTLAVAWVP 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 KKRFDKCGVCGGDNKSCKKVTGLFT -- KPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDD 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 NYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEV 571
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| 180 LARTEL--PALRYRFNAPIARDSLPPYSWHYAPWTKCSAQCAGGSQVQAVECRNQLDSSA 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 ---KLRANHAMSPTLIQIDRANP--WSACSAAIITDFLDSGHGDCLLDQPSK-PISLPED
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Vatosius
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                        Ouery Match 25.6%; Score 1033; DB 4; Length 1081; Best Local Similarity 31.8%; Pred. No. 4.2e-80; Matches 272; Conservative 104; Mismatches 319; Indels 160;
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                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-10
US-09-369-364A-17
                                                                                                                                                                 Patentin Ver. 2.1
GENERAL INFORMATION
                                                                                                                                                                                                   LENGIH: 1081
                                                                                                                                                                                SEQ ID NO 17
                                                                                                                                                               SOFTWARE:
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Sequence 352, Appli
                                                                                                         April 29, 2003, 17:12:21; search time 16.4049 Seconds (without alignments) 3604.758 Million cell updates/sec
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Sequence 1, Appli
Sequence 1, Appli
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Compugen Ltd.
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US-10-097-597-1
US-10-097-580-1
US-10-097-580-1
US-10-097-580-12
US-10-097-580-12
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US-10-097-580-12
US-09-321-9878-4
US-10-163-316-7
US-09-918-171A-9
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US-10-175-737-352
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  version :
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                                                                        protein search, using sw model
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GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTON: No. US20020115842Alel Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0341-USA
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR PAPLICATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
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        113 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 272
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     Sequence Seq
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Pred. No. 2.4e-287;
Mismatches 0;
 US.10-173-706 352
US.10-175-738-352
US.10-176-482-352
US.10-176-913-352
US.10-176-913-352
US.10-176-913-352
US.10-174-572-352
US.10-174-572-352
US.10-174-579-352
US.10-174-579-352
US.10-174-588-352
US.10-176-743-352
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-965-631-4
SEQ ID NO 4
LENGIH: 950
US-09-965-631-4
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                                              1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
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   SASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLA
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TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and U
TITLE OF INVENTION: Therefor
FITLE REFERENCE: MF010-025P1RNM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT APPLICATION NUMBER: US/207,863
PRIOR APPLICATION NUMBER: 60/297,863
PRIOR PILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 823
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Pred. No. 3.7e-221;
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96.28;
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Best Local Similarity 96.2
Matches 581; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Hirose, Kunitaka
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishlad, Yukako
APPLICANT: Ishlad, Yukako
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Wino, Kouji
APPLICANTON: Uparmaceutical
TITLE OF INVENTION: Uparmaceutical
TITLE OF INVENTION: Composition and method of immunologically analyzing
TITLE OF INVENTION: UNBER: US/10/097,597
CURRENT APPLICATION NUMBER: US/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-04
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFFWANDER: DATE: 1997-06-03
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Publication No. US20030022352A1
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SEQ ID NO 1
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US-10-097-597-1
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APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiji
APPLICANT: Inoguchi, Eiji
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
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                                           55.9%; Score 2260; DB 9; ilarity 54.3%; Pred. No. 3.8e-157; Conservative 129; Mismatches 172;
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     Homo sapiens
                                                        Best Local Similarity
Matches 405; Conserv
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    ; ORGANISM: Ho
US-10-097-580-1
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Best Local 8
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HDEQKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGM 132
                                                                                                                                       GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN
                                                                                             TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
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Publication No. US20030032168A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Watsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Watsushima, Kouji
APPLICANT: Wood Sequence
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT APPLICATION NUMBER: US/45,023
PRIOR APPLICATION NUMBER: US/45,023
PRIOR PILING DATE: 1997-06-03
PRIOR PILING DATE: 1997-06-03
NUMBER: OF SEQ. ID NOS: 14
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APPLICANT: Ishlada, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Human ADAMTS-1 protein, gene encoding the same, TITLE OF INVENTION: Pharmaceutical
TITLE OF INVENTION: composition and method of immunologically anal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 727;
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53.6%; Pred. No. 4.5e-157;
ive 131; Mismatches 175;
                                                                                                                                                                                                        FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,597
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: UP 9-160422
PRIOR FILING DATE: 1997-06-03
   Application US/10097597
10. US20030022352A1
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                                                               : Inoguchi, Eiji
: Hakozaki, Michinori
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SOFTWARE: Patentin version 3.0
SEQ 1D NO 12
LENGTH: 727
                                                  Kunitaka
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400; Conserv
Sequence 12, Applicat Publication No. US200 GENERAL INFORMATION:
                                                   APPLICANT: Hirose,
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; ORGANISM: Mus
US-10-097-597-12
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1.8e-157;
nes 172;
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larity 54.3%; Pred. No. 3.8e
Conservative 129; Mismatches
               CURRENT APPLICATION NUMBER: US/09/445,023A CURRENT APPLICATION NUMBER: US/09/445,023A PRIOR PILING DATE: 1999-12-03 PRIOR FILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin version 3.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                               al Similarity
405; Conserv
      TITLE OF INVENTION:
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US-10-097-597-12
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LENGTH: 727
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QY         417 YVLAPKVVDGTLCSPDSTSVCVQCKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGL 476           :     -	Over PRILITY P	Qy 241 GVGSKPCP-YMQYCTKLWCTGRAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
	RESULT 7  100-10-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-12  100-91-30-30-30-30-30-30-30-30-30-30-30-30-30-	

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61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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357 ADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNGVTGDSHLMAS 416
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Sequence 7, Application US/10163316

Publication No. US20020197703A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MPIO1-025PIRM
CURRENT FILIAN DATE: 2002-06-05

PRIOR APPLICATION NUMBER: US/10/163,316

PRIOR FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                     357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF
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                                DLVVKGSIJLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDK
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714 RLLARDQCNLHRKPQE-LDFCVLRPC 738
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           253 GEESKHCPDAASTCTTLMCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDM- 311
                                                        KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                        357 PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416
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Fatent No. US20020102210A1

GENERAL INFORMATION:

APPLICANT: Kimble Judith E

APPLICANT: Blalloch, Robert H

TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386

CURRENT APPLICATION NUMBER: US/09/321,987B

PRIOR PILING DATE: 1999-05-28

PRIOR PLING DATE: 1999-05-29

PRIOR PLING DATE: 1999-05-29

PRIOR PLING DATE: 1998-05-29

PRIOR PLING DATE: 1998-05-29
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NUMBER OF SEO ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 4
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ORGANISM: Murine
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LENGTH: 950
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Matches 4(
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APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/10/105,929
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-08
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFFWARE: FASTSEQ FOR WINDOWS Version 3.0
TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                                                  PCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416
                                                                                                                                                                                                                                                                ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                              GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                          KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                   FIKPWHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER 536
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Patent No. US20020137142A1
GENERAL INFORMATION:
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US-10-105-929-2
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                                                                                         1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
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APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TILLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REPERENCE: 26473/04193
CURRENT APPLICATION NUMBER: US/09/918,171A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/369,364
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEO ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                 Indels
Query Match 55.8%; Score 2254; DB 12; Best Local Similarity 54.0%; Pred. No. 1.5e-156; Matches 403; Conservative 131; Mismatches 172;
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941 GVLSHESCDPLKKPKHFIDFCTMAEC 966
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US-09-918-171A-9
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Matches 339;
                                                                                                                                                                      TYPE: PRT
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APPLICANT: McCarthy, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/09/803,589
CURRENT APPLICATION NUMBER: 2001-03-09
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                                                                                                     MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMS 179
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                                                                                                                                                                                                                                                238 LAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLCLKGAC
                                                                        31;
                                                     Length 905;
                                                    Query Match
47.3%; Score 1911.5; DB 10; Lengt.
Best Local Similarity 50.6%; Pred. No. 1.5e-131;
Matches 352; Conservative 127; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVDCRGSAGQRTVPACDAAHRPVETQACG-EPCP 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09803589 Patent No. US20020112251A1 GENERAL INFORMATION:
                 TYPE: PRT; ORGANISM: Mus musculus ADAMTS-8
US-09-918-171A-9
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US-09-803-589-2
Q ID NO 9
LENGTH: 905
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1larity 49.3%; Pred. No. 5.3e-131;
Conservative 114; Mismatches 146;
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PRIOR APPLICATION NUMBER: US 09/128,709
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR PLILING DATE: 1997-08-06
PRIOR PLILING DATE: 1997-08-06
PRIOR PLILING DATE: 1997-08-06
PRIOR PLILING DATE: 1997-08-06
PRIOR PLILING DATE: 1997-09-05
PRIOR FLILING DATE: 1997-09-05
PRIOR PLILING DATE: 1999-09-01
PRIOR FLILING DATE: 1999-09-01
PRIOR FLILING DATE: 1999-09-01
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENCTH: 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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652

551

712

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APPLICANT: HOLICANT: HOLICANT: Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REPERBENCE: 09404/041001
CURRENT APPLICATION NUMBER: 105/10/105,929
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: EARLIER REPLICATION NUMBER: 09/130,491
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FESTSEQ for Windows Version 3.0
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                         177 MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
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                                                                                                                                 ---KES------FNAIPTFS-----
                                                                                                                                                                                                                                                                     GRLLARDQCNLHRKPQE-LDFCVLRPC 738
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581 GGVLSHESCDPLKKPKHFIDFCTMAEC 607
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Patent No. US20020137142A1
GENERAL INFORMATION:
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US-10-105-929-13
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                                                                                                                   GENERAL INCORACTION:

APPLICANT: MCCARTLY, Sean A.

APPLICANT: HOLTZMAN, Sean A.

APPLICANT: HOLTZMAN, Douglas A.

APPLICANT: GOOGGENIL, ANGEN D.

TITLE OF INVENTION: USES

CURRENT PILIAG DATE: 2001-03-09

PRIOR APPLICATION NUMBER: US 09/128,709

PRIOR PELING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: US 60/054,645

PRIOR APPLICATION NUMBER: US 60/054,966

PRIOR APPLICATION NUMBER: US 60/054,966

PRIOR PILING DATE: 1997-08-06

PRIOR FILING DATE: 1997-08-06

PRIOR PILING DATE: 1999-09-01

PRIOR FILING DATE: 1999-09-01
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47.0%; Score 1900; DB 10;
Best Local Similarity 49.3%; Pred. No. 6.3e-131;
Matches 339; Conservative 114; Mismatches 146;
                                                             Sequence 8, Application US/09803589
Patent No. US20020112251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Mus musculus
US-09-803-589-8
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Length 608; Indels

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713 GRLLARDQCNLHRKPQE-LDFCVLRPC 738	713	ογ
AMAM	552	qq
DCRGSAGQRIVPACDAAHRPVETQACGEPCPTWELSAWSPCSKSCGRGFQRRSLKCVGHG 712	653	οy
	541	QQ
593 REDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAV 652	593	٥y
TLEQDIMYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVLTVGNALRPKIKYTYFVKKK-540	482	ਰੂ
533 AVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEP 592	533	οy
::	422	Q
473 VTGLFTKPMHGYNEVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVS 532	47	ογ
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKK 421	36,	.qq

Search completed: April 29, 2003, 17:22:03 Job time: 21.4049 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2003, 17:10:24; search time 17.07 Seconds (without alignments) 4156.253 Million cell updates/sec Run on:

US-10-009-332-1\_COPY\_213\_950 4043 1 FVSIPRYVETLVVADESMVK......DQCNLHRKPQELDFCVLRPC 738 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  $^{\circ}$  Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gene ADAMTS-1 pr	hetical r			den N	protein C37C3.6a [	hypothetical prote		angiogenesis inhib	hypothetical prote	-	-	t)	ifi	semaphorin F precu	Н	thrombospondin 1 p	a)	catrocollastatin p	u	$\overline{}$		meltrin alpha - mo	metalloproteinase	metalloproteinase	hemorrhagic protei		monocyte surface a	hypothetical prote
SUMMARIES	ΩI	T00017	T00355	T47158	T21371 ·	T18517	C89114	T34395	T16892	T18856	T00260	T15976	T22545	S24789	T00026	JC5928	TSHUP1	A40558	A59414	855270	T22836	S41607	T18900	S60257	S48169	S48160	A37877	G02390	A60385	S
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149281	A4 258/	A42972	866260	T25061	TSHUP2	A55796	HYSNFA	A30065	T13809	A59421	S05478	S71949	A39804	JC4342	S28259
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000	7/17	429	407	788	1172	616	411	480	1239	203	437	099	1178	481	789
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5.2	7.0	5.1	5.0	5.0	4.9	6.4	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.7
211.5 5.2 (									196.5 4.9	195.5 4.8	195.5 4.8	195.5 4.8	194 4.8	193.5 4.8	192 4.7

## ALIGNMENTS

	RESULT 1
_	gene ADAMIS-1 protein - mouse
	C.Species: mus musculus (incuse mouse) C.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 C.Accesion: T00017
	R;Kuno, K; Lizasa, H.; Ohno, S.; Matsushima, K. Genomina 46, 466-471 1997
	A; Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 g A; Reference number: 214055; MUID:98110583; PMID:9441751
	A:Accession: T00017 A:Status: preliminary: translated from GR/FMRL/DDBJ
	A; Molecule type: Mark A Mark
	A; Nestudes: 1-931 ANDN: A;Cross·references: EMBL:AB001735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057
	A; Experimental source: strain 129SVJ C; Genetics:
_	A,Gene: ADAMTS-1
	Aintrons: 228/1; 343/5; 388/1; 444/1; 533/5; 002/1; 000/3; /19/2 C;Superfamily: thrombospondin type 1 repeat homology F:542-598/Domain: thrombospondin type 1 repeat homology <thr3></thr3>
	Query Match 55.8%; Score 2257; DB 2; Length 951; Best Local Similarity 53.6%; Pred. No. 4.9e-147; Matches 400; Conservative 130; Mismatches 176; Indels 40; Gaps 10;
	Qy 1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
	Db 237 FVSSPRYVETMLVADQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSISLVVVKILVI 296
	Qy 61 RDRDSGPKVTGNAALTIRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
	Db 297 YEEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTAILFTRQDLCGSHTCDTLGM 356
	QY 121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
	Db 357 ADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNGVTGDSHLMAS 416
	OY 181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240 '
	Db 417 MLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLFGTLYDANRQCQFTF 476
	QY 241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
	DD 477 GEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDM- 535
	QY 300 KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYKSCNLE 356
	Db 536 KHFATPVHGSWGPWGPWGPRGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNIE 595
	Oy 357 PCPSSASGKSFREBQCEAFNGYNHSTNRLFLAVAWVPKYSGVSPRDKCKLICRANGTGYF 416

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A; Experimental source: adult melanoma (MeWo cell line); clone DKF2p762C1110 C; Genetics:
A; Note: DKF2p762C1110.1
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Cispecies: Homo sapiens (man)
Cispate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Cispate: 20-Apr-2000 #sequence_revision 20-Apr-2000
Riblum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224379
A;Reference number: 224379
A;Reference number: 224379
A;Reference number: 2250 < Aspanantary
A;Reference number: 2550 < Aspanantary
A;Residues: 1-550 < Aspanantary
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                                                                                                                                                                                                                                                                                                                                                                                 VSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SHWMASMLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANR
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                                                                                                                                                                                                                                                                                          GYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKV
                                                                                                                                                                                                                                                                                                                                                     534 VERDLVVKGSL-LRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEP
                                                                   PCPSSASGKSFREEQCEAFNGYNHSTNRLTL---AVAWVPKYSGVSPRDKCKLICRANGT
                                                                                                                                                                                             TGLETKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKFZp762C1110.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 1604; DB 2;
llarity 49.7%; Pred. No. 1.8e-102;
Conservative 106; Mismatches 142;
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Best Local Similarity
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C; Species: Homo sapiens (man)
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C; Accession: T00355
R; Ishlkawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. BNA Res. 5, 169-176, 1998
A; Title: Prediction of the coding sequences of unidentified human genes. X. The complete A; Reference number: 214142; MUID:98403880; PMID:9734811
A; Accession: T00355
A; Accession: T00355
A; Accession: T00355
A; Accession: T00355
A; Residues: 1-837 <ISH>A; Residues: 1-837 <ISH A; Residues: 1-837 <ISH>A; Residues: 1-837 <ISH A; Residues: 1-837 <IS
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A;Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 FASLSREVETLVVADDKMAAFHGAGLKRYLLTVWAAAAKAFKHPSIRNFVSLVVIRLVIL 272
                                                      832
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                                                                                                                                                        FTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVER 536
                                                                                                                                                                                                                                                    DLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDK 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGORTVPACDAAH - - RPVETQACGE - PCPTWELSAWSPCSKSCGRGFQRRSLKCVGHGG
                                                                                                                                                                                 DCPDN-NGKTFREEQCEAHNEFSKASFGNEPTVEWTPKYAGVSPKDRCKLTCEAKGIGYF
                                                                                                                                                                                                                                                                                                                                              597 SSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKRAVDCRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: KIAA0688
Superfamily: thrombospondin type 1 repeat homology
519-575/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.6%; Score 1761; DB 2; Best Local Similarity 53.1%; Pred. No. 4.8e-113; Matches 324; Conservative 91; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLLARDQCNLHRKPQE-LDFCVLRPC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein KIAA0688 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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                   969
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QY         591 EPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQKR           B         1   1   1   1   1   1   1   1   1   1	SQPDDRPPARWVAGSWGPCSASCGSGLQKR 650	Db 641 YCVGQRERYRSCNTQECPWDTOPYREVQCSEFNNKDIGIQGVASTNTHWVPKY 693  Qy 396 SGVSPRDKCKLICRANGTGYFYYLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKK 455
RESULT 4 121371 hypothetical protein F25H8.3 - Caenorhabdi. C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: T5-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 17-Oct-1999 #seconce number: 219413 A.Speciesion: T21371	litis elegans 5-Oct-1999 #text_change 29-Oct-1999 Nary 1996	
A Molecule type: DNA A Molecule type: DNA A Residues: 1-2165 <wil> A Cross-references: EMBL: 269360; PIDN: CAA9: A SExperimental source: clone F2548 R; Gajadsty, S.</wil>	93287.1; GSPDB:GN00022; CESP:F25H8.3	DD 986 VKMEGDRQTPASEHLCDRNSKPSDIASCYIDCSGRKWNYGEWTSCSETCGSNGKWHRKSY 1045  QY 708 CVCHGGRLLARDQCNLHRKPQELDFCVLRPC 738  U
submitted to the EMBL Data Library, February 1996 A;Reference number: 219949 A;Accession: T24896 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-2165 -WH2> A;Cross-references: EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022; CESP:F25H8.3 A;Experimental source: clone T13H10 A;Experimental source: clone T13H10 A;Mone position: 4 A;Map position: 4		RESULT 5 T18517 procollagen N-endopeptidase (EC 3.4.24.14) I - bovine N;Alternate names: procollagen N-proteinase C;Speciaes: Bos primigenius taurus (cattle) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18517 R;Collage, A.; Nusgens, B.V.; Lapiere, C.M. submitted to the EMBL Data Library, February 1996 A;Description: Cloning of the cDNA of the Povine procollagen I N-proteinase.
A.inclous: 31/1; 32/1; 135/2; 193/3; 215/1 Query Match Best Local Similarity 39.6%; Pred. No Matches 321; Conservative 113; Misma	/3; Zlo/l; Zbb/l; 495/2; 547/3; 584/3; 634/2; 744/l; 81 Score 1567; DB 2; Length 2165; Pred. No. 2.9e-99; 3; Mismatches 283; Indels 94; Gaps 17;	A;Reference number: 218941 A;Accession: T18517 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1205 <col/>
OY 7 YVETLVYADESMYKFHGADLEHYLLTILATAARLYRHPSILNPINIVVYKVLLLRDRDSG	ARLYRHPSILNPINIVVVKVLLLRDRDSG 66   :     :   :   :   :   :    'ASIXRHQSLRASINVVVVKLIVLKTENAG 340   WDTAILFTRQDLCGAT-TCDTLGMADVGT 125	A; Experimental source: Skin A; Experimental source: skin C; Genetics: A; Gene: PC I-NP C; Function: A; Description: catalyzes cleavage of the propeptides of type I and II collagens prior
× 1 – 1	HIDVAILLTRKDICKSOGKCDTLGLAELGT 400  MPHDNVKVCEEVFGKL 172  :   :	Query Match 25.9%; Score 1045.5; DB 2; Length 1205; Best Local Similarity 33.7%; Pred. No. 9.6e-64; Matches 260; Conservative 108; Mismatches 300; Indels 103; Gaps 31;
	DPLDSGHG-DCLLDQPSKPISLPE 223	OY 8 VETLVVADESMYKEHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66  1
QY 224 DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE		QY 67 PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDICGATTCDTLGMADVGT 125
OY 284 GKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGK		QY 126 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQ 184
OY 342 YCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYN	HSTNRLTLAVAWVPKY	OY 185 IDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSOQCELAFG 241

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A;Map position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C37C3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
C;Accession: T34395, T34394
R;Geisel, C.; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Reference number: 221518
A;Residues: 1-2167 <GEI>A;Residues: 1-2167 <GEI>A;Residues: 1-2167 <GEI>A;Residues: 1-2167 <GEI>A;Reperimental Source: Strain Bristol N2; clone C37C3
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T34394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1555, SKF' <GE2>
A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A;Residues: 1-1555, SKF' <GE2>
A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A;Residues: 1-1555, SKF' <GE2>
A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A;Reperimental source: strain Bristol N2; clone C37C3
A;Gene: CESP:C37C3.6b
A;Gene: CESP:C37C3.6b
A;Gene: CESP:C37C3.6a
A;Gene: CESP:C37C3.6a
A;Triprons: 32,72.104,7.156,7.207,7.166,7.207,7.166,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.106,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,7.207,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P--MHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERD 537
ADKVVDGTKCDSKSNDICVDGECLPVGCDGKLGSSLKFDKCGKCDGDGSTCKTIEGRFDE 232
                                                                                                                  LVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPRED-- 595
                                                                                                                                                                                                                                                                                                                                                                   ------RSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRP-----PAR 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 VEVGGTIFVYD--DAEPETLSAQGPLSEELTVALLFRKGSRDTAIKYEFSIPLEEEVDYM 344
                                                                                                                                                                                                                                                                                                                                                                                                                     YKFDNWTPCSVSCGKGVQTRNLYCIDGKNKGRVEDDLCEENNATKPEFEKSCETVDCEAE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GSWAKWDFYGPCSRICGGGVQLARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVAGSWGPCSASCG-SGLQKRAVDC-RGSAGQRTVPACD---AAHRPVETQACGE-PCPT
                                                                        P--MHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 16.8%; Score 681; DB 2; Length 2167; Best Local Similarity 33.7%; Pred. No. 2e-38; Matches 162; Conservative 63; Mismatches 176; Indels 8
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   173
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C;Species: Caenorhabditis
C;Spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                            GGDNKSCKKVTGLFTKPMH--GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQ- 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPP 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCS 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 ASCGSGLOKRAVDCRGSAGQRTVPA--CDAAHRP----VETQACGEPCPTWELSAWSP 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCGGVRVKYRSCNLEPCPSSASG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNWGPWVPENECSRSCGGGVQLEKRQCSGD------CTGASVRYISCNLNAC---ESG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSFREEQCEAFN----GYNHSTNRLTLAVAWYPKYSGVSPRDKCKLICRANGTGYFYVL 419
                                                                                                                                                                                                                                                                                                                                     SCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDKC 404
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                                                                                                                                                                                   --ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||::|| | : : | | | : : | GKFILNEENDVDPNSKTFIAMGVEWEYRDE-DGRETLQTMGPLHGTITVLVIPEG---DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KYMIHEDSLNVDDNNVLEDDSVGYEWALKKWSPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
                                      VGSKPCPYMQY - -- CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSKSCGR-GFQRRSLKCV----GHGGRLLARDQCNLHRKPQELDFCVLRPC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1558;
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16.8%; Score 681; DB 2; Length 1559
Best Local Similarity 33.7%; Pred. No. 1.4e-38;
Matches 162; Conservative 63; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     821 RISLTY-----
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C;Genetics:
A;Gene: C37C
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OY 387 LAVAWVPKYSGVSPRDKCKLICRANGTGFFYVLAPKVVDGTLCSPDSTSVCVQGKCI 443  DD 534LSGEGMQFEQAMCKIWCLISGSTNIRTVS-NFPDGAPCGPGQYCIKGECR 582  QY 444 KAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRG 503  DD 583 PLLCGSTTLAXSEAD-CPLSVLOTTTTPPPMPHSV	504 YKGLIGDDNYLALKNSQCKY:LLNGHFVVS-AVERDLVVKGSLLRYSGTGTA	QY 554 VESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHN 611	QY 612 SVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSGLQ-KRAVDCRGSAGQRTVPACDAAH 670 :	QY 671 RPVETQACGEPCPTW-ELSAWSPCSKSCGRGFQRRSLKC 708	RESULT 9 T18856 anglogenesis inhibitor homolog - Caenorhabditis elegans	C; Specials: Caendimatoris elegais C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C; Accession: T18856; T24653 R; McMurray, A R; McMurray, A	submitted to the base initially, oury 1993 A; Reference number: 219031 A; Accession: T18856 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	A; Residues: 1-1444 <wil> A;Cross-references: EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1 A;Experimental source: clone C02B4</wil>	K; McMurlay, A. submitted to the EMBL Data Library, July 1995 A; Reference number: 219917 A; Accession: 124653	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1444 <wi2> A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1</wi2>	C;Genetics: C;Genetics: A;Gene: CBSP:CO2B4.1 A;Map position: X A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3;	12.5%; Score 504; DB 2; Length 1444; 23.0%; Pred. No. 1.8e-26; vative 91; Mismatches 306; Indels 348; Gaps 43	QY 25 DLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNALT 76	QY 77 LRNFCAWQKKLNKVSD-KHPEYWDTAILFTRQDLCGATTCDTLGMADVGTWCDPKRSCSV 135	Qy 136 IEDDGLPSAFTTAHELGHVFNMPHDNVK-VCEEVFGKLRANHMMSPTLIQIDRANPWSAC 194	Qy 195 SAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSK- 245
QY 538 LVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPRED 595	345 YKFDNWTPCSVSCGKGVQTRNLYCIDGKNKGRVEDDLCEENNATKPEFEKSCETVDCEAE 4 631 WVAGSWGPCSASCG-SGLOKRAVDC-RGSAGORTVPACDAAHRPVETQACGE-PCPT 6 1	Db 405 WFTGDWESCSSTCGDQGQXRVVYCHQVFANGRRVTVEDFGNCTVERPPVKQTCNRFACPE 464  Qy 685 WELSAWSPOSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRP 737  Db 465 WALDANGSPCTANAOVESWTGESPETENT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	738 C 738	DD 524 C 524 RESULT 8	T16892    T16892	Nibenited to the EMBL Data Library, December 1995 A; Description: The sequence of C. elegans cosmid T19D2.	A, ACCESION: 1109/2 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Molecule type: DNA A, Residues: 1-860 < ABLA A, Residues: 1-860 < ABLA A, CCOSS-references: EMBL: U42846; NID: 41125809; PID: 41125810; PIDN: AAA83600.1; CESP: T19D2	:T19D2.1 5/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395	Query Match 12.6%; Score 510.5; DB 2; Length 860; Best Local Similarity 26.1%; Pred. No. 3.5e-27; Matches 198; Conservative 92; Mismatches 310; Indels 159; Gaps 40;	QY 8 VETLVVADESMVKFHGADLEHYLLTLATAARLYRHPSILNPINVVKVLL 59	QY 60 LRDRDSGPKVTGNAALTLRNPCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC 115	Qy 116 DTLGMADVGTMCDPRRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 175	176 HMMSPTLIQIDRANPWSACSAAIITDFLDSGH-GDCLLDQPSKPISLPE-D :   :	225 LPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPW 2   1   1   1   1   1   1   1   1   1	276 ADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKNDPYGPCSRTCGGGVQLAR 3 :	QY 329RQCINPIPANGGKYCEGVRVKYRSCNLEPCESSASGKSFREEQCEAFNGYNHSINRII 386

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Cispecies: Homo sapiens (man)
Cispecies: Olreeb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
CiAccession: T00260
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. Na Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: 214086; MUID:98290545; PMID:9628581
A;Accession: T00260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-951 cNAGA
A;Residues: 1-951 cNAGA
A;Cross-references: EMBL:AB011177; NID:g3043733; PIDN:BAA25531.1; PID:g3043734
A;Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSRKRIAKCDGTTENCQDKIDEETCDIACLREKHSFGPISPRRPKLI-----TSNDLRK 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                               586
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                                                                                                                                                                            |::| |: | |: | |: | | |-----QPCRVWCHLIGSELIRNKGOF------PDGTPCGFD--AYCVGGCLALSCDNK 673
                                                                                                                                                                                                                                                                      461
                                                                                                                                                                                                                                                                                      GVSPRDKCKLICRANGT-----GYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGN 450
PCP----YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE-RHNLNK 300
                                                     354
                                                                                                         LEPCPSSASGKSFREEQ-----CEAF------NGYNHSTNRLTLAVAWVPKYS 396
                                                                                                                                                                                                                                                                                                                                           194 DEWSSCSQSCGGGRRYRIRKCLDDKCDGDDLEKESCN-----TQKCISQSWGDWLPCSV
                                                                                                                                                                                                                                                                                                                                                                                                674 ALVEQPEDCPRIEGRSVHQWEEWSSWSECSVSCGLGGREVRERKCSSGRKCQGVSEESRP
                                                                                                                                                                                                                                                                                                                         -----VCGG-----VCGG------DNKSCKKVTGLFTKPMHGYNFVVAIPAGA
                                                                                                                                                                                                                                                                                                                                                                             S---SIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GIGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------DXCG--------
                                                   -- PYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCN
                                                                                                                                   ----ATSSNCLGFTREEFGNKICSSIKYDPHKPDQQLTGEGFEHST----
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hypothetical protein F08C6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change.20-Sep-1999
C;Accession: T15976
A;Bentley, D.
submitted to the EMBL Data Library, June 1995
A;Bescription: The sequence of C. elegans cosmid F08C6.
A;Reference number: 218440
A;Reference number: 218440
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-957 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      686 GPQWEMSEWSECTAKCGERSVVTRDIRCSEDEKLCDPNTRPVGEKNCTGPPCDRQWTVSD 745
                                                                                                                                                                                                                                                                                                                   GTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSC 470
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                                                                                                                                 305 GSWAKWDPYGPCSRTCGGGVQLARRQC----TNPTPANGGKYCEGVRVKYRSCNLEPCPS 360
                                                                                                                                                                                                                       SASGKSFREEQCEAFNG--YNHSTNRLTLAVAWVPKYSGVSPRD-----KCKLICRAN 411
                                                                                                                                                                                                                                                         107 -PDGRSFREEQCVSFNSHVYNGRTHQ-----WKPLY----PDDYVHISSKPCDLHC-TT 154
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                             KKVTGLFTK-PMH-GYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVVSAVERDLVVKGSLLRYSGT----GTAVESLQASRPILEPLTVEVLSV-GKMTPPRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 YKVDS-PKNFNIAGTVVKYRRPMDVYETGIEYIVAQGPINQGLNVWVWNQNGK--SPSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 FGHPGLDMELGPSQGQETNEVCEQAGGGACEGPPRGKGFRDRNVTGTPLTGDKDDEEVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 HFASQEFFSANAISDQLLGAGSDLKDFTLNETVNSIFAQGAPRSSLAESFFVDYEENEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       506 GPYLLNGSYLELSSDRVANSSSEAPFPNVSTSLLTSAGNRTHKARTRPKARKQGVSPADM
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                                                                                                                                                           Query Match
12.2%; Score 493; DB 2; Length 951;
Best Local Similarity 22.2%; Pred. No. 6.3e-26;
Matches 171; Conservative 55; Mismatches 183; Indels 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 WSPCSKSCGRGFQRRSLKCVGHGGRLLARDQCNLHRKPQELDFCVLRPC 738
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Jararhagin C precursor - jararaca (fragment)
NyAlternate names: single chain botrocetin
NyAlternate names: single chain botrocetin
NyContains disintegrin-like 20% protein; hemorrhagic proteinase (EC 3.4.24.-)
C;Species: Bothrops jararaca (jararaca)
C;Dete: 20-Feb-1995 #sequence_revision 29-Aug-1997 #text_change 09-Jun-2000
C;Accession: S24789; JC2245; A44463; A37958; JC2373
R;Paine, M.J.I.
Submitted to the EMBL Data Library, August 1992
A;Reference number: S24789
A;Accession: S24789
A;Accession: S24789
A;Accession: S24789
A;Molecule type: mRNA
A;Residues: 1-51 < Apr.
A;Cross-references: EMBL:X68251; NID:g62467; PID:g62468
B;Cami, Y.; Fujimura, Y.; Miura, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, i Bjochem: Biophys. Res. Commun. 201, 331-339, 1994
A;Title: A 28 kba-protein with disintegrin-like structure (jararhagin-C) purified frc
A;Reference number: JC2245; MUID:94256999; PMID:8198592
A;Molecule type: protein
A;Residues: 360-571 < USA>
                                            A, Reference number: 219578
A, Accession: T2545
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-1059 <WILL>
A, Cross-references: EMBL: 281086; PIDN: CAB03121.1; GSPDB: GN00019; CESP: F53B6.2
A, Experimental source: clone F53B6
C, Genetics: A, Map position: 1
A, Introns: 38/3; 92/3; 131/3; 169/1; 236/2; 282/3; 349/2; 376/2; 420/1; 576/3; 759/3,
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                                                                                                                                                                                                                                                                                                                              Length 1059;
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                             submitted to the EMBL Data Library, October 1996
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A:Gross-references: EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721.1; CESP:F08C6.
A:Experimental source: strain Bristol N2
                             A;Experimental source: strain Bristoi N2
C;Genetics:
A;Gene: CESP:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22545
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                                                                                                                                          10.2%; Score 412; DB 2; Length 957;
22.8%; Pred. No. 2.3e-20;
tive 81; Mismatches 256; Indels 292;
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Matches 186; Conservative
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N; Alternate names: BAIl protein
C; Species: Homo saplens (man)
C; Species: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Feb-1999
C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Feb-1999
C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Feb-1999
C; Date: 22-Jan-1999 #sequence_revision 700026
R; Nishimori, H; Shiratsuchi, T; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Nishimori, T00026
A; Accession; T00026
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-1584 ANIS
A; Cross-references: EMBL: AB005297; NID: d1175078; PID: d1024528
A; Cross-references: brain
C; Genetics:
A; Genetics:
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A,Map position: 8424-8424
C;Superfamily: thrombospondin type 1 repeat homology
F;408-462/Pomain: thrombospondin type 1 repeat homology <THR3>
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22.0%; Pred. No. 2.3e-09;
tive 42; Mismatches 174;
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A; Recession: A44463
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A; Accession: A44463
A; Residues: 1-23, (0', 25-92, 'G', 94-131, 'G', 133-169, 'O', 171-571 <PA2>
A; Residues: 1-23, (0', 25-92, 'G', 94-131, 'G', 133-169, 'O', 171-571 <PA2>
A; Cross-references: GB: X68251
A; Experimental source: venom gland
A; Note: sequence extracted from NCBI backbone (NCBIE: 118104)
A; Note: sequence extracted from NCBI backbone (NCBIE: 118104)
B; Fujimura, Y; Titani, K; Usami, Y: Suzuki, M; Oyama, R.; Matsui, T.; Fukui, H.; Sug B, Ochmistry 30, 1957-1964, 1991
A; Title: Isolation and chemical characterization of two structurally and functionally dispectments by Totalian and chemical characterization of two structurally and functionally A; Reference number: A37958; MUID: 91129280; PMID: 1993206
A; Accession: A37958; MUID: 91129280; PMID: 1993206
A; Mote: 361-Val was also found
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Keywords: hydrolase; metalloproteinase; venom; zinc
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Keywords: hydrolase; metalloproteinase; venom; zinc
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Keywords: hydrolase; metalloproteinase; venom; zinc
C; Superfamily: mouse meltrin alpha; disintegrin homology
F; 360-71/Prodouct: jararhagin C fistatus experimental <AAT>
F; 362-444/Domain: disintegrin homology <AIS>
F; 295, 299, 305/Binding site: zinc (His) #status predicted
F; 296/Active site: Glu #status predicted
                                                                R; Paine, M.J.; Desmond, H.P.; Theakston, R.D.; Crampton, J.M.
J. Biol. Chem. 267, 22869-22876, 1992
A; Title: Purification, cloning, and molecular characterization of a high molecular weigh
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A,Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candid A, Reference number: JC5928; MUID:9812554; PMID:9464278
A,Accession: JC528
A,Status: nucleic acid sequence not shown
A,Residues: l-1074
A,Residues: 1-1074
A,Residues: 1-1074
A,Experimental source: Drain
C;Comment: This protein disrupts normal brain development and leads to some of the featu C;Comment: This protein disrupts normal brain development and leads to some of the featu C;Comment: This protein disrupts normal brain development and leads to some of the featu C;Comment: Semaily: human semaphorin F; thrombospondin type I repeat homology
F;D-120/Domain: semaphorin #status predicted <SIG>F;D-133/Domain: semaphorin #status predicted <SIG>F;90-1993/Domain: thrombospondin type I repeat homology CHR3>
F;971-993/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%; Score 253.5; DB 2; Length 1074;
20.6%; Pred. No. 2e-09;
tive 44; Mismatches 138; Indels 257; Gaps
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Matches 114; Conservative
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Search completed: April 29, 2003, 17:13:47 Job time : 34.07 secs Human aggrecanase-Human metalloprote Human PRO153 (UNO Human PRO polypept Protein of the inv

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Murine ADAMTS-9 am Human protease #12 Human metalloprote

Human metalloprote

Human ADAMTS-9 ami Human ADAMTS-9 alt

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Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antimiflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual disfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; disorder; metabolic disorder; inflammatory disorder.
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                    AAW80285
AAY04142
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04-MAY-2001; 2001WO-US14431
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          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                       The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administring (S) which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or hann, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypotrension, psychotic disorders, neurological disorders and dysfinesias), metabolic disorders and inflammatory disorders such as those above. AAM172876-AAM172910 represent human
                                                                                                                                                                                                                                                                                                                             ö
                                                        Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS 360
                                                                                                                                                                                                                                                                                                                                                                                               RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                            Gaps
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 Caenepeel
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                                                                                                                                                                                                                                                                                                                           0;
Manning G,
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                                                                                                          Claim 28; Figure 2G; 232pp; English.
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 Sudarsanam
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                                                                                                                                                                                                                                                                                                                             Conservative
 Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SASGKSFREEQ 371
                             2002-041502/05.
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                     928 AA;
                                      N-PSDB; AAS97182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2001
 Plowman GD,
                                                                                                                                                                                                                                                                                                                             371;
                                                                                        disorders
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                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                          Query Match
          Payne V;
                                                                                                                                                                                                                                                                                                                                                                   238
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This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease with aggrecanase activity for treating joint diseases especially osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
Metalloprotease; human; aggrecanase; joint disease; osteoarthritis; osteopathic; antiarthritic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Nomura N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 950;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2042; DB 22; 100.0%; Pred. No. 1.2e-162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 56-60; 85pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                         (YAMA ) YAMANOUCHI PHARM CO LTD. (KAZU-) KAZUSA DNA RES INST.
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                                                                                                                                                                                                                                                                                11-NOV-1999; 99JP-0321740.
16-MAY-2000; 2000JP-0144020.
                                                                                                                                                                                                                                 10-NOV-2000; 2000WO-JP07917
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Best Local Similarity 100.
Matches 371; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH41003
                                                                                                                                  WO200134785-AI
                                                                                      Homo sapiens
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The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynuclectides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastriis, esophageal carcinoma and Crohn's disease, cardiovascular e.g. atherosclearosis, hypertension and myocardial infarction, autoimmunoffilammatory e.g. acquired immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g. cancer, developmental e.g. Duchenne and Becker muscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzheimer's disease and reproductive e.g. infartiity and endometriosis disorders. Numerous other examples of each disorder are given in the specification. The present protein sequence represents the human protease PRTS-11 protein of the invention.
                                                                                                                                                                                                                                                                                              cardiovascular; atherosclerosis; autolimmune disorder; dermatitis; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; cell proliferative disorder; developmental disorder; epilepsy; buchenne muscular dystrophy; epithelial disorder; neurological disorder; reproductive disorder; endometriosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful
 513 HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS 572
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                                                                                                                                                                                                                                                                                     Human; protease; PRTS; gastrointestinal; Crohn's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Twenty one human proteases (referred to as PRTS-1 to PRTS-21), in the diagnosis, treatment and prevention of gastrointestinal gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders
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                                                                                                                                                                                                                                                   Human protease PRTS-11 protein sequence.
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                                                                                                                                                     A.
                                                                                                                                                   AAU74751 standard; Protein; 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-213955P.
2000US-215396P.
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                                                                                                                                                                                                                     (first entry)
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573 SASGKSFREEQ
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                                   SASGKSFREEQ
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2000;
29-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000;
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Kallick DA;
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                                                                                                                                                                                   AAU74751;
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                                                                                                                   RESULT 4
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                                                                                                                                                   Human; novel human protein; NHP; protease; biological disorder; obesity; high blood pressure; arthritis; connective tissue disorder; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is novel human protein (NHP), human protease. NHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid encoding a human protease, useful as a hybridization for screening libraries and assessing gene expression patterns -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
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llarity 100.0%; Pred. No. 1.2e-162;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 36-38; 41pp; English.
                 AAE22541 standard; Protein; 950 AA
                                                                                                                                                                                                                                                                                                                                                                                      (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                   27-SEP-2001; 2001WO-US30350.
                                                                                                                                                                                                                                                                                                                                                     29-SEP-2000; 2000US-236689P.
                                                                                     (first entry)
                                                                                                                                                                     high blood pressure;
gene therapy; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-372123/40.
N-PSDB; AAD35569.
                                                                                                                                                                                                                                                                                                                                                                                                                   Friddle CJ, Hilbun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid
probe for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 371; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        950 AA;
                                                                                                                                                                                                                                                     WO200226949-A2.
                                                                                                                       Human protease
                                                                                   26-JUL-2002
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                     04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                   AAE22541;
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Matches
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Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                    300
                                                                                                                      240
                                                                                                                                                                                   HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS 360
                                  120
                                                                  392
                                                                                                                                     452
                                                                                                                                                                    512
                                                                                                                                                                                                  572
                                                                                                                                                                                                                                                                                                                                          a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis;
           Gaps
                          9
                                                                                                                                                                                            GVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNK
                                                                                                                                                            FVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                         RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM
                                                                                        ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP
                                                                                                                      TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is rat metalloproteinase ADAMTS-5. The
           Indels
    1.2e-162;
nes 0;
                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; brain tumour; brain injury.
     Pred. No. 1.3
Mismatches
                                                                                                                                                                                                                                                                                                                                      ADAMTS-5; metalloproteinase; ADAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 14; 129pp; English
100.08; F.
                                                                                                                                                                                                                                                                         AAB21257 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                      Rat metalloproteinase ADAMTS-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEUR-) NEUROCRINE BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maki RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US06237.
                                                                                                                                                                                                                                                                                                        (first entry)
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kelner GS, Clark M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-594326/56.
N-PSDB; AAA95827.
                                                                                                                                                                                                                    SASGKSFREEQ 371
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                          WO200053774-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12;
                                                                                                                                                                                                                                                                                       AAB21257;
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              Matches
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and Metalloproteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRVDGSWAKWDPYGPCSRTCGGGVQLARR--QCTNPTPANGGKYCEGVRVKYRSCNLEPC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ADAMTS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheinmer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNK
                                                                                                                                                                                                                                                                                                                                   505;
                                                                                                                                                                                                                                                                                                                                      21; Length
                                                                                                                                                                                                                                                                                                                                 Score 1920.5; DB 21; Lengt
Pred. No. 8.5e-153;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Xaa= any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Xaa= any amino acid"
Misc-difference 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid"
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Misc-difference 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human metalloproteinase ADAMTS-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21261 standard; Protein; 381
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                                                                                                                                                                                                                                                                                                                                      94.0%;
llarity 95.1%;
Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSSASGKSFR 368
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Matches 352; Conserv
                                                                                                                                                                                                                                                                                               505 AA;
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(first entry)

11-MAY-1999

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                                                                                                                                                                                                                                                         Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                   present sequence is human metalloproteinase ADAMTS-5. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1767; DB 21;
Pred. No. 4.6e-140;
3; Mismatches 18;
               "Xaa= any amino acid"
                                                                                                                                                          (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 23; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.5%;
93.3%;
                                                                                                 2000WO-US06237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 322; Conservative
                /note=
                                                                                                                                                                                     Clark M,
                                                                                                                                                                                                               WPI; 2000-594326/56.
Misc-difference 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                N-PSDB; AAA95831
                                         WO200053774-A2
                                                                                                08-MAR-2000;
                                                                                                                             08-MAR-1999;
                                                                                                                                                                                     Kelner GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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ID AAW7
XX
AC AAW7
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4;
                                                             Metalloproteinase-disintegrin protein with a thrombospondin domain; ARDS; ADAMTS-1; drug composition; foodstuff; leukocyte; thrombocyte; hepatitis; blood; erythrocyte; inflammatory disease; rheumatoid arthritis; asthma; nephritis; Crohn's disease; acute respiratory disease syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein with a thrombospondin domain (ADAWTS-1). The protein may be in drug compositions and foodstuffs, as an agent for decreasing the leukocyte and thromboyte blood count and increasing the erythrocyte blood count, e.g. for treatment of inflammatory diseases such as rheumatoid arthritis, hepatitis, nephritis, crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a novel human metalloproteinase-disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                                                                                                                                                                                                                                                                                                                                                                          Human metalloproteinase-disintegrin protein with thrombospondin domain - useful as leukocyte and thrombocyte decreasing and erythrocyte increasing agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 727;
                                                                                                                                                                                                                                                                                              Ishioka K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.5%; Score 1337; DB 20; 63.5%; Pred. No. 1.3e-103;
                                                                                                                                                                                                                                                                                              Ishida Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                              Inoguchi E,
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 51-52; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                  (KURE ) KUREHA CHEM IND CO LTD.
                                                                                                                                                                                                                                       97JP-0160422.
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                                     Human ADAMTS-1 protein.
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Kuno K, Matsushima
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070277/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                727 AA;
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                                                                                                                                 Homo sapiens
                                                                                                                                                          W09855643-A1
                                                                                                                                                                                                             03-JUN-1998;
                                                                                                                                                                                                                                       3-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Matches
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29-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is mouse metalloproteinase ADAMTS-1. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FVSIPRYVETLVVVADESMVKFHGADLEHYLLTLLTATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                       Mouse; ADAWTS-1; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; optostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.5%; Score 1337; DB 21; Length 896; 63.2%; Pred. No. 1.7e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 17; 129pp; English.
                                                                                            AAB21265 standard; Protein; 896 AA.
                                                                                                                                                                                             Mouse metalloproteinase ADAMTS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maki RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0264585.
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US06237
                                                                                                                                                             (first entry)
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| | : :||:||||| 372 DCPDN-NGKTFREEQ 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-594326/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 AA;
                                                                                                                                                                                                                                                                                                                                                                          WO200053774-A2.
                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                             23-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelner GS,
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                                                                                                                            AAB21265;
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metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH2 have been found to be potent inhibitors of anglogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to anglogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemandjomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency.
                               595
                                                                                                                                GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN
TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                 300 KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                                                                                                                                                                       GEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY49501 standard; Protein; 950 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US01313
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596 DCPDN-NGKTFREEQ 609
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                                                                                                                                                                                                                                                                                                                                                                                                             357 PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-590684/50.
N-PSDB; AAZ32000.
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Claim 1; Page 12-14; 22pp; Japanese.
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                                                                                                               Sequence
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cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diapnosis. AA2137012 to AA232080, and AAY49503 to AAY49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an anti-cancer and
                                                                                                                                RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                               ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                         GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                      Gaps
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                                                                                                                                                                     1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                                                                                                                                                                         181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                              GEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTD-R
                                                                                                                                                                                                                                                                                                                       KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
                                                                                                     9
                                                                                   Length 950;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   And Metalloprotease; cancer; arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metal protease and its preparation for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ADAM-type metalloprotease MDTS4, SEQ ID NO:4.
                                                                                 Score 1334; DB 20;
Pred. No. 3.2e-103;
0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; MDTS4; ADAM-type metalloprotease; drug
                                                                                                   50; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                AAB73549 standard; Protein; 950
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                                                                                  65.3%;
63.5%;
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                                                                                          Best_Local Similarity 63.5
Matches 238; Conservative
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595 DCPDN-NGKTFREEQ 608
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                                                                950 AA;
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                                                invention.
                                                                 Seguence
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                                                                                  Query Match
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The invention relates to the novel human ADAM (A Disintegrin And Metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 specific for MDTS4 or MDTS5, and antibody specific for MDTS4 or MDTS5, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; METH1; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular anglogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb anglogenesis; Osler Webber syndrome; plaque neovascularisation; telangiectasia; haemophiliac joint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                               Length 950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiofibroma; fibromuscular dysplasia; wound granulation;
Crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                               65.3%; Score 1334; DB 22;
63.5%; Pred. No. 3.2e-103;
ive 50; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB50002 standard; Protein; 950 AA.
                                                                                                                                                                                                                                                           sequence represents human MDTS4.
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Matches 238; Conservative
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595 DCPDN-NGKTFREEQ
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                                                                                                                                                                                                                                                                                                                       950 AA;
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(HUMA-) HUMAN GENOME SCI INC.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
                                                                                                                                                     AAW80285 standard; Protein; 967
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                                                                                                                                                                                                                 (first entry)
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238; Conservative
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ITGL-TSP polypeptide.
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595 DCPDN-NGKTFREEQ
                                                PCPSSASGKSFREEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fronwald JA,
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                    535
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                                                                                                                            RESULT 12
                                                                                                                                           AAW80285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human METH1 (ME for metalloprotease and TH for thrombospondin). METH1 can be used for inhibiting anglogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque meovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH1 can also be used in birth control. METH1 can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 HDEOKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQTCDTLGM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used in diagnostic methods for the prognosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                          Jonak ZL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%; Score 1334; DB 22; 63.5%; Pred. No. 3.2e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Mismatches
                                                                                                                                                                     SMITHKLINE BEECHAM CORP.
BETH ISRAEL DEACONESS MEDICAL CENT.
ITURELA ARISPE L.
HASTINGS G A.
                                                                                                                                                                                                                                                                                                                          Hastings GA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Fig 1; 768pp; English
                                                                99US-0144882.
99US-0147823.
99US-0373658.
99US-0171503.
                                                                                                                                                             HUMAN GENOME SCI INC
                                                                                                                             2000US-0183792
                      2000WO-US14462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                                                                                                                                                          Terrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
238; Conserva
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-025136/03.
N-PSDB; AAC90057.
                                                                                                                                                                                                                                                                                            TERRETI J A.
                                                                                                                                                                                                                                   RUBEN S M.
JONAK Z L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950 AA;
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Fornwald JA, Ter
                    25-MAY-2000;
                                                                                                                             22-FEB-2000;
                                                                                               13-AUG-1999;
22-DEC-1999;
                                                                                 10-AUG-1999;
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Best Local
                                                                                                                                                                        (SMIK)
(BETH-)
(IRUE/)
(HAST/)
                                                                                                                                                                                                                                                                 TRUL/)
FORN/)
                                                                                                                                                             HUMA-)
                                                                                                                                                                                                                                                   JONA/)
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This represents a human integrin ligand polypeptide ITGL-TSP. ITGL-TSP polypeptides can be used in the treatment of angiogenic diseases such as cancer. cancer metastasis, chronic inflammatory disorders, rheumatoid arthritis, atherosclerosis, macular degeneration or diabetic retinopathy restenosis, Alzheimer's disease and tissue remodeling. They can be used to treat a subject in need of enhanced activity or expression of the
                                                                                                                                                                                                                                                                 ITGL-TSP; integrin ligand; angiogenic disease; cancer; atherosclerosis; chronic inflammatory disorder; rheumatoid arthritis; tissue remodeling; macular degeneration; diabetic retinopathy; Alzhelmer's disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding integrin ligand polypeptide ITGL-TSP - used to treat anglogenic diseases; restenosis, Alzheimer's disease and in tissue remodeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 967;
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63.5%; Pred. No. 3.3e-103.
ive 50; Mismatches 81.
                                                                                                                                                                                                       Human integrin ligand polypeptide ITGL-TSP.
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Human; METH1; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; Osler-Webber syndrome; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                                               181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                                                                                                                                                                                                    RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                              ADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                                                                                                                                                                                                                                                                                                                           300 KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE
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1) BETH ISRAEL DEACONESS MEDICAL CENT.

1) INGELA-ARISPE L.

1) HASTINGS G A.

1) RUBEN S M.

1) JOHEN S H.
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99US-0147823.
99US-0373658.
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2000US-0183792.
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|DCPDN-NGKTFREEQ 625
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22-FEB-2000;
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10-AUG-1999;
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(SMIK)
(BETH-)
(IRUE/)
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RUBE/)
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(TRUL/)
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                                181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
                                                                                                     241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                493 GEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTD-R 551
                                                                                                                                                                        300 KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
                                                    as
373 ADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMAS
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                                                                                                                          65.3%; Score 1334; DB 20;
63.5%; Pred. No. 3.3e-103;
iive 50; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
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97US-0054966
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Best Local Similarity 63.5
Matches 238; Conservative
                                                                                                                                                                                                                                                                612 DCPDN-NGKTFREEQ 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Tango-71 protein
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N-PSDB; AAX19955.
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4;
                                                                                                                                                             metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

METH can be used for Inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocultar angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, soleroderma, trachoma, vascular adhesions, myocardial angiogenesis, soleroderma, trachoma, vascular adhesions, myocardial angiogenesis, is cheemed limb angiogenesis, osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, thorowascularisation, telangiectasia, haemophiliac joints, angiofibroma, thorowascularisation, methods promised in birth control. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer. The present sequence is a protein isolated in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                        used to
                                  Trulli SH;
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9
                                                                                                                                                      present invention relates to human METH1 and METH2 (ME for
                                                                                                                                                                                                                                                                                                                                            65.3%; Score 1334; DB 22; Length 968; 63.5%; Pred. No. 3.3e-103; ive 50; Mismatches 81; Indels 6
                                                                                       METH1 and METH2 polynucleotides and encoded polypeptides, inhibit angiogensis in the treatment of disorders such as rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein encoded by gene 64 clone HOUCQ17.
                                   Jonak ZL,
                                  Hastings GA, Ruben SM,
                                                                                                                                   Claim 15; Pages 759-763; 768pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW78189 standard; Protein; 967 AA.
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613 DCPDN-NGKTFREEQ 626
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                                    Iruela-Arispe L, Hasting
Fornwald JA, Terrett JA;
    (FORN/) FORNWALD J A.
              (TERR/) TERRETT J A.
                                                                   WPI; 2001-025136/03.
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                          968 AA;
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                                               Fornwald JA,
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                                                                                                                                                                                                                                                                                                                           Sequence
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AAW78189
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; ospitity edisorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lafleur DW;
Y, Young F
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                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label- unknown
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97US-0050566.
97US-0050901.
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9705-0051919.
9705-0055984.
9705-0058665.
9705-0058668.
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970S-0058972.
970S-0058975.
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N-PSDB; AAX04374.
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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX04311-X04410; amino acid sequences AAX04311-X04410; amino acid sequences AAX04311-C04410; amino acid sequences AAX04311-C0410; and be aminorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).
                  Claim 11; Page 297-300; 380pp; English
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967 AA; Sequence

4; Gaps 9; Query Match 64.7%; Score 1321; DB 20; Length 967;. Best Local Similarity 62.9%; Pred. No. 4e-102; Matches 236; Conservative 50; Mismatches 83; Indels 6; ò

1 FVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60

RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120 61

> ò g

121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180

181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240

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| :|: ||| ||| :||: || || 433 MLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQL.PGDL.PGTSYDANRQCQFTF 492 241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299 g ď

300 KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356 g δλ

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357 PCPSSASGKSFREEQ 371

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Search completed: April 29, 2003, 17:20:31 Job time: 22.0541 secs

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April 29, 2003, 17:10:24; Search time 6.01802 Seconds (without alignments) 1813.869 Million cell updates/sec
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2042
1 FVSIPRYVETLVVADESMVK......SCNLEPCPSSASGKSFREEQ 371
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcrVB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 13, Appli Sequence 13, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 2, Appli Sequence 3, Appli
SUMMARIES	US-09-130-491-2 US-09-122-1268-2 US-09-360-3648-2 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-13 US-09-360-3648-17 US-09-360-3648-17 US-09-360-3648-17 US-09-360-3648-17 US-09-360-3648-17 US-09-360-3648-17 US-09-360-3648-17 US-09-310-322-5 US-09-310-322-5 US-09-310-322-7 US-09-310-322-7 US-09-310-322-7 US-09-310-322-7 US-09-310-322-7 US-08-313-2888-20 US-08-313-2888-20 US-08-313-2888-20 US-08-313-2888-20 US-08-313-288-3 US-08-313-383-3443-3 US-08-385-526-3 US-08-836-442-3
DB	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Length	967 608 937 930 930 930 937 1022 1024 1024 1024 1024 1024 1024 1024
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Score	11834 11136 11123 11112 11112 11112 1019:5 654 6654 6814 6814 6813 625 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 618:5 6
Result No.	10845949999999999999999999999999999999999

181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240 | :| :| || || || :|| :|| :|| || 433 MLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANRQCQFTF 492

GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299 KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356 

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1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60

65.3%; Score 1334; DB 4; 63.5%; Pred. No. 6.2e-113; live 50; Mismatches 81;

Conservative

Query Match Best Local Similarity Matches 238; Conserv

ORGANISM: Homo sapiens US-09-130-491-2

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Gaps

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Length 967; 81; Indels

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29	196.5	9.6	852	4	US-09-813-819-2	Sequence 2, Appli
30	196.5	9.6	855	4	US-09-920-048-2	Sequence 2, Appli
31	193.5	9.5	239	Ŋ	PCT-US93-01652-1	Sequence 1, Appli
32	184	9.0	201	4	US-09-411-329C-1	'n
33	184	0.6	201	4	US-09-411-335-1	7
34	184	9.0	201	4	US-09-466-276-1	1
35	184	9.0	462	4	US-09-411-329C-3	'n
36	184	0.6	462	4	US-09-411-329C-17	17,
37	183.5	9.0	202	4	US-09-411-329C-16	16,
38	183.5	9.0	203	4	US-09-411-329C-5	2, 7
39	183.5	0.6	203	4	US-09-411-329C-15	15,
40	183.5	0.6	203	4	US-09-411-335-3	m
41	183.5	0.6	203	4	US-09-466-276-3	3, 4
42	183.5	9.0	464	4	-09-411-329C	14,
43	183	0.6	462	4	-09-026-001A-1	16,
44	179	8.8	285	4	-09-026-0	14,
45	178.5	8.7	200	N	US-08-836-442-4	4, 7
RESULT 1 US-09-130-4; Sequence; Sequence; Patent OF GENERAL II APPLICAN TITLE OF FILE REF; CURRENT I EARLIER I	RESULT 1  105-09-130-491-2  Sequence 2, Application US/09130-1  Patent No. 6416974  GENERAL INFORMATION:  APPLICANT: HOLTAMAN.  APPLICANT: Goodearl, Andrew D.J.  TITLE OF INVENTION: TANGO-71, TITLE OF INVENTION: TANGO-71, TITLE OF ERRENCE: 09404/041001  CURRENT FILING DATE: 1998-08-07  EARLIER FILING DATE: 1997-08-06  EARLIER FILING DATE: 1997-08-06  NUMBER OF SEQ ID NOS: 16  SOFTWARE: FASLIGATION NUMBER: US  EARLIER FILING DATE: 1997-08-06  NUMBER OF SEQ ID NOS: 16	91-2 6416974 NFORMATION: T: Goodearl, Andrew D.J. INVERNUES, 944/041001 APPLICATION NUMBER: US/09/APPLICATION NUMBER: US/09/APPLICATION NUMBER: US 60/APPLICATION NUMBER: US 6	Con US/09130 Douglas A. Andrew D.J. TANGO-71, TANGO-71, US/041001 NUMBER: US/NUMBER: US/NUMBER: US/1997-08-06 1997-08-06 S: 16	091 8	491 ANGO-73, TANGO-74, 09/130,491 60/058,108 60/054,961	TANGO-76, AND TANGO-83
; LENC	LENGTH: 967					
TYP:	TYPE: PRT	7				

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SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 608
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Patent No. 6416974
Patent No. 6416974
Barrard. Information: Douglas A. APPLICANT: Holtzman, Douglas A. APPLICANT: Holtzman, Douglas A. APPLICANT: Goodearl, Andrew D.J. APPLICANT: Goodearl, Andrew D.J. TANGO-74, TANGO-76, AND TANGO-83 FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 FGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 GSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSDPDHFDTAILFTRQDLCGVSTCDTLGM 332
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                     57.9%; Score 1182.5; 55.5%; Pred. No. 3.1e
                                                                                                                                                                                                                                                                                                                                                                                                  56; Mismatches
                                                                                                                         Sequence 2, Application US/09122126B
Patent No. 6451575
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573 DCP-TGSALTFREEQ 586
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| 512 DCPDN-NGKTFREEQ 625
                       371
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ORGANISM: Homo sapiens
                         357 PCPSSASGKSFREEQ
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US-09-130-491-13
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US-09-122-126B-2
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-09-122-126B-2
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Best Local
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satohata, Satohata,
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53.8%; Pred. No. 3e-94;
:ive 64; Mismatches 100; Indels
                                                                                                                            Score 1136; DB 4;
Pred. No. 3.5e-95;
9; Mismatches 73;
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                                                                                                                                Query Match 55.6%; Sox
Best Local Similarity 63.0%; Pro
Matches 201; Conservative 39;
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Matches 205; Conservative
ORGANISM: Mus musculus US-09-130-491-13
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Gaps

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LISIDASKPWSKCTSATITEFLDDGHGNCLLDLPRKQILGPEELPGQTYDATQQCNLTPG 502
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             APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 930
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LOCATION: (468)
COTHER INFORMATION: Xaa = C
NAME/KEY: MOD_RES
LOCATION: (521)
COTHER INFORMATION: Xaa = Y
US-09-369-364A-13
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PCP--PNGKSFRHEO 632
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ORGANISM: Homo sapiens
US-09-122-126B-15
 GENERAL INFORMATION:
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409 PFFIHVNKTLPWSPCSAVXLTELLDDGHGDCLLDAPTSVLPLPTGLPGHSTLYELDQQCK 468
                                                 238 LAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLCLKGAC 292
                                                                                                                                          62 DRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMA 121
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurshain, Sancshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CORRENT APPLICATION NUMBER: US/09/369,364A
CORRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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53.3%; Pred. No. 9e-93;
iive 59; Mismatches 106; Indels 10;
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Patent No. 6451575
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
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QSCNTEECP--PNGKSFREQQ 607
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Matches 200; Conservative
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US-09-122-126B-15
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-09-369-364A-2
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                                                                                                                            Sequence 15, Application US/09369364A

Sequence 15, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hirohata, Satoshi
TITLE OF INFORTION: Nucleic Acids Encoding 2inc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00

CURRENT FILING DATE: 1999-08-06

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 15: SEQ ID NOS: 31

SEQ ID NO 15: SEQ ID NOS: 31
                             Gaps
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                                                      1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
50.4%; Score 1030; DB 4; Length 1882;
51.3%; Pred. No. 6.2e-85;
ive 58; Mismatches 109; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.9%; Score 1019.5; DB 4; Length 874; 50.9%; Pred. No. 2.1e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Mus musculus ADAMTS-9
US-09-369-364A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 49.9%
Best Local Similarity 50.9%
Matches 192; Conservative
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                Best_Local Similarity 51.3
Matches 193; Conservative
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US-09-369-364A-15
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 HNLNKHRVDGSWAKWDPYGPCSRICGGGVQLARRQCINPIPANGGKYCEGVRVKYRSCNL 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354
                                                                              477
                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.9%; Score 814; DB 4; Length 997;
11arity 46.8%; Pred. No. 1.2e-65;
Conservative 43; Mismatches 141; Indels 16; Gaps
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                                                                                                                                                                                                                                                                                         Zinc Metalloproteases
                                                                                                                                                                                                                                               APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zii
TITLE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09130491; Patent No. 641694
GENERAL INFORMATION: APPLICANT: HOLTZMAN, DOUGLAS A.
                                                                                                                                                                                                        Sequence 7, Application US/09369364A; Patent No. 6391610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7
                                                                                                                              356 EPCPSSASGKSFREEQ 371
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                                                                                                              355 LEPCPSSASGKSFREEQ
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Best Local Similarity
Matches 176; Conserv
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US-09-130-491-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLG 119
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                                                                                                                                                                                                                       295 RHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCN 354
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GENERAL INFORMATION:

APPLICANT: Apte, Suneel

APPLICANT: Hirohata, Satoshi

TILLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

FILE REPERRNE: 26473/4007/10-30-00

CURRENT FILING DATE: 1999-08-06

CURRENT FILING DATE: 1999-08-06

SOFTWARE: PACENTIN Ver. 2.1

SECTION O11
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APPLICANT: Apte, Suneal
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
TITLE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
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Best Local Similarity 57.9%; Pred. No. 3.5e-51;
Matches 114; Conservative 41; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09369364A Patent No. 6391610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT (CRANISM: Homo sapiens ADAMTS-8 US-09-369-364A-11)
                                                                                                                                                                                                                                                                                                      355 LEPCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                           SOKCPRDS -- VDFRAAQ 651
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201 PLFVHLNQTLPWSPCSA 217
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US-09-369-364A-11
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TITLE OF INVENTION: 0.6448388el Human Proteases and Polynucleotides Encoding the SFILE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the SFILE REFERENCE: LEX. 0219-038
CURRENT APPLICATION NUMBER: US/09/930,872
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTHARE: FASTSEQ for Windows Version 4.0
APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT APPLICATION NUMBER: US/09/130,491

CURRENT FILING DATE: 1998-08-07

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTEEQ for Windows Version 3.0

SEQ ID NO 16

LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 VETLVVVDKKMMQNHGHENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPG 351
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                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 687; DB 4; Length 551; 56.4%; Pred. No. 2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09930872
Patent No. 6448388
GENERAL INFORMATION:
APPLICANT: Friddie, Carl Johan
APPLICANT: Hilbun, Erin
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                                                                                                                                                                                                                                                                                           ; ORGANISM: Rattus rattus
US-09-130-491-16
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LENGTH: 1224
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Matches 119;
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US-09-930-872-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 PKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQIDR 187
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                                                                              11 LVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKV 69
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                          327 ARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.6%; Score 625.5; DB 4; Best Local Similarity 38.5%; Pred. No. 2.1e-48; Matches 145; Conservative 54; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUMPUTER: IBM Compatible
ODERATING SYSTEM: Windows
SOFTRARE: Fast5EQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE:
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STREET: 1155 Avenue of the Americas
CITY: New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFRENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                            Sequence 5, Application US/09491522 Patent No. 6428998 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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10036-2811
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hiohate, Satoshi
TIILE APPLICANT: Hiohate, Satoshi
TILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT PILLING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 518
TYPE: PRT
OWGANISM: Homo sapiens ADAMTS-5
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                                                                                                                                              Query Match 30.9%; Score 631.5; DB 4; Best Local Similarity 37.1%; Pred. No. 5.3e-49; Matches 145; Conservative 57; Mismatches 154;
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48.9%; Pred. No. 3.5e-49;
tive 31; Mismatches 74
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                                                                                        ORGANISM: Homo sapiens ADAMTS-10
US-09-369-364A-17
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US-09-369-364A-22
              Patentin Ver. 2.1
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Matches 110; Conserv
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LOCATION: (99)
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                                                     1081
                                   SEQ ID NO 17
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                                                                        TYPE: PRT
                SOFTWARE:
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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10: 'cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
11: 'cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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237; Conserv
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LENGTH: 727
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Best Local Si
Matches 237;
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                                              213 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 272
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                                                                                                                                                                                               Sequence 2, Application US/10163316

Publication No. US20020197703A1

GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVERMION: 65552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVERMION: Therefor 10/10/16/3/316

FILE REPERENCE: MPI01-025PIRMM
CURRENT APPLICATION NUMBER: US/10/163/316

PRIOR APPLICATION NUMBER: 60/297, 863
PRIOR FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FASTERO for Windows Version 4.0
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                              HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-10-163-316-2
                                                                                          361 SASGKSFREEQ 371
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573 SASGKSFREEQ 583
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US-10-097-597-12
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US-10-163-316-2
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APPLICANT: 19h10ca, Keiko

APPLICANT: 19h10ca, Keiko

APPLICANT: 19h10ca, Keiko

APPLICANT: 18h10ca, Keiko

APPLICANT: 18h10ca, Kouji

APPLICANT: Kuno, Kouji

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,

TITLE OF INVENTION: composition and method of immunologically analyzing human ADA

TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA

TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA

FILE REFERENCE: 057092

CURRENT APPLICATION NUMBER: 05/445,023

PRIOR PELING DATE: 1999-12-03

PRIOR PELING DATE: 1999-12-03

PRIOR PELING DATE: 1997-06-03

WUMBER OF SEQ ID NOS: 14

SOFTMARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
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63.2%; Pred. No. 2e-108;
iive 52; Mismatches 80;
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APPLICANT: Hirose, Kunitaka
APPLICANT: Infoguchi, Biji
APPLICANT: Infoguchi, Biji
APPLICANT: Tahloka, Keiko
APPLICANT: Ishloka, Keiko
APPLICANT: Ishloka, Keiko
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
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composition and method of immunologically analyzing human AD!
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APPLICANT: Inoquchl, Eiji
APPLICANT: Inoquchl, Eiji
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishida, Kelko
APPLICANT: Ishida, Yukako
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human AbanTS-1 protein, gene encoding the same,
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzin,
TITLE OF INVENTION: 1990-12-03
TITLE OF INVENTION: 1990-12-03
FRIOR APPLICATION NUMBER: US/10/097,597
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DP 9-160422
PRIOR FILING DATE: 1997-06-03
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                                                                                           13 FVSSPRYVETMLVADQSWADFHGSGLKHYLLTLFSVAARFYKHPSIRNSISLVVVKILVI 72
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Best Local Similarity 63.5%; Pred. No. 3e-108;
Matches 238; Conservative 50; Mismatches 81; Indels
                                  Indels
            Local Similarity 63.2%; Pred. No. 2e-108;
hes 237; Conservative 52; Mismatches 80;
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Publication No. US20030022352A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
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|DCPDN-NGKTFREEQ 385
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SOFTWARE: PatentIn versic
SEQ ID NO 1
LENĞTH: 727
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US-10-097-597-1
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APPLICANT: Higose, Kunitaka
APPLICANT: Inoguchi, Eiji
APPLICANT: Hakozaki, Michinori
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT APPLICATION NUMBER: UP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VETSION 3.0
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; Pred. No. 2e-108;
52; Mismatches 80; Indels
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; PRIOR APPLICATION NUMBER: 09/445,023
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1997-06-03
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SCGTWARE: Patentin version 3.0
; SEQ ID NO 12
; LENGTH: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09445023A Patent No. US20020119167A1 GENERAL INFORMATION:
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Best Local Similarity 63.2%
Matches 237; Conservative
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372 DCPDN-NGKTFREEQ 385
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                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-097-580-12
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ORGANISM: Mus
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US-09-445-023A-12
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LENGTH: 727
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Sequence 1, Application US/09445023A

Sequence 1, Application US/09445023A

Sequence 1, Application US/09445023A

Sequence 1, Application US/09445023A

Setent No. Us20020119167A1

APPLICANT: Hirose, Kunitaka

APPLICANT: Ishioka, Kelko

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

APPLICANT: Matsushima, Kouji

TITLE OF INVENTION: Gomposition and method of immunologically analyzing human ADA

FILE REFERENCE: 057092

CURRENT APPLICATION NUMBER: US/09/445,023A

FILE REFERENCE: 1999-12-03

FRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 1

LENGTH: 727
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                                                                   Length 727;
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Llarity 63.5%; Pred. No. 3e-108;
Conservative 50; Mismatches 81;
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|DCPDN-NGKTFREEQ 385
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372 DCPDN-NGKTFREEQ 385
                                                                                                                                    357 PCPSSASGKSFREEQ 371
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ORGANISM: Homo sapiens
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US-09-321-987B-4
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Matches 23
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                                                     133 ADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMAS 192
                                                                                                                  TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
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                                 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
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63.5%; Pred. No. 3e-108;
.ive 50; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIAL INFORMATION:
APPLICANT: HITOSE, Kunitaka
APPLICANT: HOGUCHI, Eiji
APPLICANT: Hakozaki, Michinori
APPLICANT: Hakozaki, Michinori
APPLICANT: Hakozaki, Michinori
APPLICANT: Hahloka, Keiko
APPLICANT: Hahloka, Kukako
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Muno, Kouji
TITLE OF INVENTION: Composition and method of FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/445,023
PRIOR FILING DATE: 1999-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ADAMTS-1 protein, composition and method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10097580 publication No. US20030032168A1 GENERAL INFORMATION:
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Matches 238; Conservative
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ORGANISM: Homo sapiens
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SEQ ID NO 1
LENGTH: 727
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APPLICANT: Mimble, Robert H

TITLE OF INVENTION: ABOLIACH, Robert H

TITLE OF INVENTION: ABOLIACH, ROBERT AND METHOD FOR MODULATING Cell Migration
FILE REFERENCE: 960296, 95386

CURRENT APPLICATION NUMBER: US/09/321,987B

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 60/189,023

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 4

LENGTH: 950
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TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
CURRENCE: MITOL-0.55P.RNM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR PPLICATION NUMBER: 60/297,863
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                           65.5%; Score 1337; DB 10; Length 950; 63.2%; Pred. No. 4.2e-108; 1ive 51; Mismatches 81; Indels 6
Sequence 4, Application US/09321987B
Patent No. US20020102210A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/10163316; Publication No. US20020197703A1; GENERAL INFORMATION:
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596 DCPDN-NGKTFREEQ 609
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                       ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                       US-09-321-987B-4
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LENGTH: 968
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Sequence 2, Application US/10105929
Fatent No. US20020137142A1
Fatent No. US20020137142A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REPERENCE: 094.04/041001
CURRENT ELLING DATE: 2002-03-25
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
PRIOR APPLICATION NUMBER: EARLIER PRING DATE: 1998-08-07
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-05
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-06
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-06
PRIOR PRILING DATE: EARLIER FILING DATE: 1997-09-06
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                                                                              1 FVSIPRYVETLVVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
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        Length 968;
                                              Indels
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  65.5%; Score 1337; DB 9;
63.2%; Pred. No. 4.3e-108;
11ve 51; Mismatches 81;
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Best Local Similarity 63.5%; Pred. No. 7.8e-108;
Matches 238; Conservative 50; Mismatches 81;
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SOFTWARE: FastSEQ for Windows Version 3.0
Query Match
Best Local Similarity 63.2
Matches 237; Conservative
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613 DCPDN-NGKTEREEQ 626
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US-10-105-929-2
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LENGTH: 967
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NKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                              Sequence 352, Applic
Publication No. US2
GENERAL INFORMATION
                                                                                                                                  RESULT 13
US-10-176-758-352
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US-10-175-737-352
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APPLICANT: Pan, James
APPLICANT: Watanabe, Colin K.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P4430RLC42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
PLIOR application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
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                                                                                                    GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                              300 KH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCNLE 356
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                                                        181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
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                                                                                                                                                                                                                                                                                                                         Sequence 352, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin P.
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Best Local Similarity 55.5
Matches 208; Conservative
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US-10-174-590-352
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RIC104 CURRENT APPLICATION NUMBER: US/10/176,758 FILING DATE: 2002-06-21 Prior Application Formoved - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
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55.5%; Pred. No. 1.2e-94;
ive 56; Mismatches 106;
                                                                                                                                                                                                                                     Application US/10176758 US20030008353A1
                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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Best Local Similarity 55.5%
Matches 208; Conservative
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| DCP-TGSALTFREEQ 586
                                                                  PCPSSASGKSFREEQ 371
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DCP-TGSALTFREEQ
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US-10-176-758-352
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Gaps

Length 837;

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APPLICANT: WOOD, William I.

APPLICANT: WOOD, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: 93430RLC/7

CURRENT APPLICATION NUMBER: US/10/173,706

CURRENT FILING DATE: 2002-06-17

FILIO APPLICATION TO SECRETE SOURCE SECRETE SECRETE SOURCE SECRETE SEC
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Job time : 12.2469 secs
             Watanabe, Colin K.
Wood, William I.
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Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-352
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PAJ 301ACO
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
PILOT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Publication No. US20030022293A1
GENERAL INFORMATION:
Sequence 352, Application US/10175737 Publication No. US20030013153A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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573 DCP-TGSALTFREEQ 586
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Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 PCPSSASGKSFREEQ 371
                                                                                               APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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US-10-175-737-352
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April 29, 2003, 17:10:24; Search time 8.58125 Seconds (without alignments) 4156.253 Million cell updates/sec
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2042
1 FVSIPRYVETLVYADESMVK.....SCNLEPCPSSASGKSFREEQ 371
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
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283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tora 1-2 MADA enep	hetical n			2	٠,		-	ď	Ω	•	- 1	٤.		metalloproteinase	metalloproteinase	hemorrhagic protei	metalloproteinase	catrocollastatin p	metalloproteinase	monocyte surface a	fibrolase (EC 3.4.	trigramin precurso	disintegrin-like m	metalloproteinase	Semaphorin F precu			fibrinolytic metal	
SUMMARIES	CI.		T00355	T21371	T47158	T18517	T16892	T18856	T15976	S60257	T22836	TSHUP1	A40558	S24789	S41607	A59414	S48169	A37877	S48160	S55270	866260	A60385	HYSNFA	A30065	G02390	A59421	JC5928	JC4342	JC2550	JC4880	
	DB	~	7	7	N	7	~	7	~	7	~	Н	7	7	~	7	7	~	7	7	~1	7	Н	Н	7	~	N	~	7	7	ı
	Query Match Length	951	837	2165	550	1205	860	1444	957	903	208	1170	1170	571	419	419	549	416	617	609	407	826	411	480	814	203	1074	481	202	478	
dР	Query	65.5	57.9	45.2	33.5	30.8	19.2	18.5	14.6	11.4	11.3	11.2	11.0	10.8	10.7	10.7	10.4	10.3		10.2	6.6	7.6	7.6	9.6	9.6	9.6	9.5	9.5	9.4	9.4	
	Score	1337	1182.5	923.5	684	628.5	393	377.5	297.5	233.5	231.5	229.5	224.5	220	218.5	217.5	213	210	209.5	208.5	201.5	199	197.5	197	196.5	195.5	194	193.5	191.5	191	
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357 PCPSSASGKSFREEQ 371

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30	189	6.3	429	7		l factor
31	187.5	9.5	414	~	S41609 atrolysin C	: (EC 3.
32	184.5	0.6	481	7	S43125 trimucin precursor	ecursor
33	181.5	8.9	414	Н	HYRSAC atrolysin C (EC 3.	(EC 3.
34	181	8.9	009	~	149281 fertilin alpha pre	pha pre
35	180.5	8.8	952	7		and me
36	180	8.8	1172	~	A42587 thrombospondin 2 p	din 2 p
37	179.5	8.8	200	~	S15111 hemorrhadic factor	factor
38	177	8.7	1572	7	T00027 brain-specific and	fic and
39	174.5	8.5	1178	П	A39804 thrombospondin pre	din pre
40	173	8.5	478	7	A43296 atrolysin E (EC 3.	: (EC 3.
41	170.5	8.3	469	٦		recurso
42	170.5	8.3	1172	Н	TSHUP2 thrombospon	din 2 p
43	170	8.3	202	Н	HYRSR ruberlysin (EC 3.4	(EC 3.4
44	170	8.3	437	~	S05478 properdin - mouse	mouse
45	169.5	8.3	1584	Ģ	T00026 brain-specific and	fic and
					ALIGNMENTS	
RESULT	1					
gene AD	TOUGL/ gene ADAMTS-1 protein		9811011			
C; Speci	C; Species: Mus musculus (house mouse)	usculus	snou)	ĕ	onse)	
C;Date:	C; Date: 22-Jan-1999	98# 666	#sequence_revision	re	/ision 22-Jan-1999 #text_change 21-Jul-2000	-2000
C; Acces	C;Accession: T00017	017				
R; Kuno,	K.; Liza	sa, H.,	Ohno,	ŝ	R; Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K.	
Genomic	Genomics 46, 466-4/1, 1997	-4/1,	7.661			
A; Title A; Refer	A;Title: The exon/in A;Reference number:	n/intro er: 214	on orga 1055; M	niză UID	A;ILLLe: The exon/Intron organization and chromosomal mapping of the m A;Reference number: 214055; MUID:98110583; PMID:9441751	the mouse ADAMTS-1 g
A; Acces	sion: IOO	017				
A; Statu	s: prelim	inary;	transl	ate	A;Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molec	A;Molecule type: DNA A;Residues: 1-951 <kun></kun>	DNA 1 <kun3< td=""><td></td><td></td><td></td><td></td></kun3<>				
A; Cross	-referenc	es: EME	3L:AB00	173	A; Cross-references: EMBL: AB001735; NID: q2809056; PIDN: BAA24501.1; PID: q2809057	g2809057
A: Exper	A:Experimental source: strain 129sv.	on rob.	atrain	12	SQV.T	

RESULT TOOO17	SULT 1	
gene C; Spe C; Dat	gene ADAMTS-1 protein - mouse C:Species: Mus musculus (house mouse) C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000	
C; Ac		
A; Ti	endomics vo, 400-4/1/, 1997 A; Title: The exon/intron organization and chromosomal mapping of the mouse ADAWTS-A; Reference number: 214055; MUID:98110583; PMID:9441751	'n
A; St.	A;Accession: 10001/ Status: preliminary; translated from GB/EMBL/DDBJ A:Wolenile troe: DNA	
A; Re	A. Residues: 1-951 CMU> A. Cross-references: EMBL: AB001735: NID: 02809056: PIDN: RAA24501 1: PID: 02809057	
A; Exi	A:Experimental source: strain 129SVJ C:Genetics:	
A; Ger	A;Gene: ADAWTS-1 A:Introns: 278/1: 343/3: 388/1: 444/1: 526/2: 602/1: 660/2: 716/2	
C; Sul F; 54	C:Superfamily: thrombospondin type 1 repeat homology F:542-598/Domain: thrombospondin type 1 repeat homology <pre></pre>	
ŏnŎ	Luery Match 65.5%; Score 1337; DB 2; Length 951;	
Ber	Best Local Similarity 63.2%; Pred. No. 3.9e-97; Matches 237; Conservative 51; Mismatches 81; Indels 6; Gaps 4;	
ΟŊ	1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLTATAARLYRHPSILNPINIVVVKVLLL 60	
qq	237 FVSSPRYVETMLVADQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSISLVVVXILVI 296	
Qy	61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120	
qq	297 YEEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTALLFTRQDLCGSHTCDTLGM 356	
Qγ	121 ADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180	
qq	357 ADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNGVTCDSHLMAS 416	
Qy	181 TLIQIDRANPWSACSAAIIIDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240	
qq	417 MLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLYDANRQCQFTF 476	
δλ	241 GVGSKPCP-YMQYCTKLWCIGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299	
qq	477 GEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDM- 535	
οy	300 KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSCNLE 356	
QQ	536 KHFATPVHGSWGPWGPWGDCSRTCGGGVQYIMRECDNPVPKNGGKYCEGKRVRYRSCNIE 595	
Qy	357 PCPSSASGKSFREEQ 371	

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A;Gene: CESP:F25H8.3
A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
submitted to the EMBL Data Library, February 1996
A; Reference number: 219949
A; Accession: T24896
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Redidues: 1-2165 AWI2>
A; Cross-references: EMBL: 269361; PIDN: CAA93288.1; GSPDB: GN00022; CESP: F25H8.3
A; Experimental source: clone T13H10
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Experimental source: adult melanoma (MeWo cell line); clone DKF2p762C11110
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 QCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE 283
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                                                                                                                                                                                                                                                                                                                                                                            PKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLGMADVGT 125
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                                                                                                                                                                                                                                                                        Length 2165;
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R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, submitted to the Protein Sequence Database, March 2000
A; Reference number: 224379
A; Accession: T47158
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-550 < AAA>
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                                                                                                                                                                                                                                                                      Query Match
45.2%; Score 923.5; DB 2;
Best Local Similarity 45.4%; Pred. No. 2.9e-64;
Matches 177; Conservative 60; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
33.5%; Score 684; DB 2;
Best Local Similarity 59.2%; Pred. No. 4.4e-46;
Matches 119; Conservative 25; Mismatches 51.
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                                                                                                                              hypothetical protein F25H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T21371; T24896
R;Gajadsty, S.
Submitted to the EMBL Data Library, February 1996
A;Reference number: 219413
A;Accession: T21371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2165 <WIL>
A;Cross-references: EMBL: 269360; PIDN: CAA93287.1; GSPDB: GN00022; CESP: F25H8.3
A;Experimental source: clone F25H8
R;Gajadsty, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 FASLSREVETLVVADDKWAAFHGAGLKRYLLIVWAAAAKAFKHPSIRNPVSLVVTRLVIL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKL-RANHMMS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 FGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: KTAA0688
C;Superfamily: thrombospondin type 1 repeat homology
F;519-575/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1182.5; DB Pred. No. 4.7e-85;
                                                                                                                        hypothetical protein KIAA0688 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%;
55.5%;
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573 DCP-TGSALTFREEQ 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCPSSASGKSFREEQ 371
                          DCPDN-NGKTFREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Matches 208;
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60; Gaps

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A; Cross-references: EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CESP:T1 C; Genetics: A; Genee: CESP:T19D2.1 A; Genee: CESP:T19D2.1 A; Cross: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tibeson in this inhibitor homolog - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 12: Oct-1999 #text_change 18-Feb-2000 C; Accession: T18865; T24653
R; McMurray, A. Submitted to the EMBL Data Library, July 1995
A; Reference number: 219031
A; Reference number: 219031
A; Reference number: 219031
A; Residues: 1-1444 <WIL>
A; Cross references: EMBL: 250004; PIDN: CAA90293.1; GSPDB: GN00028; CESP: C02B4.1
A; Experimental source: Clone C02B4
R; McMurray, A. Submitted to the EMBL Data Library, July 1995
A; Reference number: 219917
A; Accession: T24653
A; Residues: 1-1444 <WIL>
A; McOlecule type: DNA
A; Residues: 1-1444 <WIL>
A; Residues: 1-1444 <WIL>
A; Residues: 1-1444 <WIC>
A; Residues: 1-1444 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 DILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 LPGASYTLSQQCELAFGVGSKPC-----PYMQYCTKLWCTGKAKGQMVCQTRHFPW 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 ADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWD--PYGPCSRTCG-----GGVQLAR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 LRD----RDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 HMMSPTLIQIDRANPWSACSAAIITDFLDSGH-GD-----CLLD---QPSKPISLPE-D 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 VETLVVADESM ---- VKFHGADLEHYLLTLLATAAR ----LYRHPSILNPINIVVVKVLL 59
                                                                                                                                                                                                                                                                                                                                                                                                Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                  elegans cosmid T19D2.
                                                                                                                                                                                                                                                                                                                                                                                             19.2%; Score 393; DB 2; Lv 29.8%; Pred. No. 5.2e-23; ive 54; Mismatches 161;
                                                                               A; Description: The sequence of C. elegans cosmid T1:
A; Reference number: 218599
A; Accession: T16892
A; Status: Pranslated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-860 < EBN>
C;Accession: T16892
R;Bentley, D.
submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 -- RQCINPIPANGGKYCEGVRVKYRSCNLEPC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIRQCNNPSSNNGGAPCQGDEARGMYCHRDVC 507
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.89
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476
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                                                                                                                                                                                                                                                                                                                                                                              procollagen N-endopeptidase (EC 3.4.24.14) I - bovine
N;Alternate names: procollagen N-proteinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18517
R;Codiage, A.; Nusgens, B.V.; Laplere, C.M.
Submitted to the EMBL Data Library, February 1996
A;Description: Cloning of the CDNA of the bovine procollagen I N-proteinase.
A;Reference number: 218941
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: T18517
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residuses: 1-1205 <COL>
A;Residuses: 1-1205 <COL>
A;Residuses: 1-1205 <COL>
A;Cross-references: EMBL:X96389; NID:e990769; PID:e228215; PIDN:CAA65253.1
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Description: catalyzes cleavage of the propeptides of type I and II collagens prior tc
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ζţ
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hypothetical protein T19D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLIEIGNPSQSLENVCRWAYLQQKPDTDHDEYHDHAIFLTRQDF-GPSGMQ--GYAPVTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AFHRFHWSRCSQQELSRYLHS--YDCLRDDPFTHDWP-ALPQ-LPGLHYSMNEQCRFDFG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293
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294 ERHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY 350
                                                                                                                MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 IDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ERHNLNKHRVDGSWÄKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSKPCPYMQY - - - CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 LGYMMCTAFRTFDPCKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHCFKGHCIWLTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                           RSCNLEPCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 SCNLEPCPSSASGKSFREEQ 371
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LCNSQDCPDALA--DFREEQ 620
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Db 384 DTLETGTFCGPSKWCQLGRCVPWTGTNEIQPTVQHVAPVVTTLPSRIDGSWSGWGATICS 443	OY 214 Q	282 561 321 621	RESULT 9 S60257 meltrin alpha - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000 A; Title: A metalloprotease-disintegrin participating in myoblast fusion. A; Reference number: \$60257; MUID: 96026308; PMID: 7566181 A; Accession: \$60257 A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-903 < YAG> A; Residues: 1-903 < YAG> A; Cross_references: EMBL: D50411; NID: 91054586; PIDN: BAA08912.1; PID: 91054587	jth 903; els 203; Ga [NIVVVKVLLR     :	PARTICINECONDITIONS   PARTICIPATOR   PARTICION   PARTICINE   PAR	Db 378 MNPSTGFPFPMVFSSCSRKDLEASLEKGMGMCLFNLPEVKQAFGGRKCGNGYVEE 432  Qy 216SKPISLPED 224  Db 433 GEECDCGEPEECTNRCCNATTCTLKPDAVCAHGQCCEDCQLKPPGTACRGSSNSCDLPEF 492  Qy 225 LPGAS
A;Map position: X A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566	Query Match 18.5%; Score 377.5; DB 2; Length 1444; Best Local Similarity 30.5%; Pred. No. 1.5e-21; Matches 115; Conservative 45; Mismatches 170; Indels 47; Gaps 15;  Qy 25 DLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPRVTGNAALT 76  D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		QY 195 SAAIITDELDSGHGDCLLDQPSRPISLPEDLPGASYTLSQQCELAFGVGSK- 245	RESULT 8 T15976 hypothetical protein F08C6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15976 R;Bentley, D. R;Bentley, D. R;Bentley, D. R;Description: The sequence of C. elegans cosmid F08C6.	ry; translate BEN5 BEN5:U29378; ce: strain Br 1 5/3; 220/3; 2	

Fujisawa-

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95; Conservative
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                                                                                                       A; Accession: A3427
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TSHUPI

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TSHUPI

Thrombospondin 1 precursor - human

C; Species: Homo sapiens (man)

C; Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 17-Nov-2000

C; Accession: A2615; A4274; A30140; A25812; A05172; A42927

R; Lawler: J: Hynes, R.O.

J. Cell Biol. 103, 1635-1648, 1986

A; Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple of A; Reference number: A26155; MUD:87057617; PMID:2430973

A; Residues: 1-1170 < LAMA

A; Residues: 1-1170 < LAMA

A; Cross-references: GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138

A; Note: parts of this sequence, including the amino end of the mature protein, were dete B:Laherty, C.D.; Giernan, T.M.; Dixit, V.M.

Biol. Chem. 264, 11222-11227, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                          12630

hypothetical protein F57B7.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999

C;Accession: T22836

A;Reference number: 219623

A;Residues: 1-508 <WIL>
A;Residues: 1-509 <WIL>
A;Residues: 1-509 <WIL>
A;Residues: 1-509 <WIL>
A;Residues: 1-509 <WIL>
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SACSAAIITDFLDSGHGDCL---LDQPSKPISLPEDL--PGASYTLSQQCELAFGVGSKP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 FCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-TCDTLGMADVGTMCDPKRSCSVIED 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 IGAGLTSLIMAHEIGHSLGALHDGAXETAEC--DSNDNYLMAVSVSGSADRQSFLNSRRM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPYMQY-----CTKLWCTGKAKGQMVCQT-RHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLP-SAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLI-QIDR-----ANPW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 SNCSINSIIENLKEPTANCVKKWKTKKGKDVSQKDFIKKPGELVKITRQCQVAFGPTFIP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KHRVDGSWAKW-DPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEP- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KYSTSKLKHY 487
                        --CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 231.5; DB 2; Length 27.2%; Pred. No. 1.4e-10; Live 43; Mismatches 111; Indels
    613 CRGTHVYLGDDMPDPGLVLAGTKCAEGKICLNRRCQNISVFGVHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A:Introns: 45/3; 137/2; 221/2; 256/2; 306/2; 409/3; 451/3
                                                                          318 RTC-GGGVQLARRQCINPTPANGGKYCE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NTKKWMDCKDINSKTCS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 27.28
Matches 85; Conservative
                                                                                                                               CKS----KDFRE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 CPSSASGKSFRE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F57B7.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
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                                                                                                                           A; Molecule type: DNA
A; Residues: 1-166 <LAB:
A; Cross-references: GB:J04835
B; Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwen
J. Cell Biol. 108, 729-736, 1989
A; Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in
A; Reference number: A30140; MUID:89139590; PMID:2918029
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-83, A', 85-522, A', 524-1170 <HEN>
A; Cross-references: EMBL:X14787; NID:937464; PIDN:CAA32889.1; PID:937465
A; Note: parts of this sequence, including the amino end of the mature protein, were d
B; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysian A; Reference number: A25812; MUID:87157592; PMID:3030396
A; Accession: A55812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: mRNA
A; Residues: 1-83, 74, 85-374, 78C' CDIX>
A; Residues: 1-83, 74, 85-374, 78C' CDIX>
A; Cross-references: GB-M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801
A; Note: parts of this sequence, including the amino end of the mature protein, were d
B; Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A; Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin
A; Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Description: participates in cell migration and adhesion, and in platelet aggregati C Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; C; Keywords: beta-hydroxyasparagine; calcium bluding; cell adhesion; glycoprotein; tri F; 1-18/Domain: signal sequence #status predicted <SIG> F; 19-1170/Product: thrombospondin 1 #status predicted <MAT> F; 378-429/Domain: whilebrand factor type C repeat homology <WWC> F; 378-429/Domain: thrombospondin type 1 repeat homology <THR1> F; 434-490/Domain: thrombospondin type 1 repeat homology <THR2> F; 551-586/Domain: EGF homology <EGF2> F; 550-689/Domain: EGF homology <EGF2> F; 520-586/Domain: EGF homology <EGF2> F; 520-580/Bomain: Cell attachment (R-G-D) motif
A;Title: Characterization of the promoter region of the human thrombospondin gene.
A;Reference number: A34274; MUID:89291870; PMID:2544587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA

A; Residues: 1-83, A', 85-397 <KOB>

A; Cross-references: GB:MZ5631; NID:9538353; PIDN:AAA36741.1; PID:9538354

R; Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwell, P.; Frazler, W.A.

Proc. NBLI. Acad. Sci. U.S.A. 83, 5449-5453, 1986

A; Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 229.5; DB 1; Length 1170; 24.8%; Pred. No. 5:1e-10; Live 34; Mismatches 105; Indels 149;
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F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent
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A; Residues: 987-1003 <50N>
A; Note: Cys-992 is shown to have a free sulfhydryl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
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A;Cross-references: GDB:124438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1
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A;Molecule type: mRNA
A;Residues: 1-571 <PAI>
A;Residues: 1-571 <PAI>
A;Cross-references: RMBL:X68251; NID:962467; PID:962468
A;Cross-references: RMBL:X68251; Nid:A; S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K
B;Usami, Y.; Fujimura, Y.; Miura, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K
B;Ochem. Biophys: Res. Commun. 201, 331-339, 1994
A;Title A 28 kDa-protein with disintegrin-like structure (jararhagin-C) purified fro
A;Reference number: JC2245; MUID:94256999; PMID:8198892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Purification, cloning, and molecular characterization of a high molecular
                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jararhagin C precursor - jararaca (fragment)
NyAlternate names: single chain botrocetin
NyContains: disintegrin-like 28k protein; hemorrhagic proteinase (EC 3.4.24.-)
C;Species: Bothrops jararaca (jararaca)
C;Date: 20-Feb-1995 #sequence_revision 29-Aug-1997 #text_change 09-Jun-2000
C;Accession: S24789; JC2245; A44463; A37958; JC2373
Submitted to the EMBL Data Library, August 1992
A;Reference number: S24789
A;Accession: S24789
                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-----PRCWPSDSADDGWSPWSEWTSCSATCGNGIQQRGRSCDSLNNRCE-GSSVQT 420
                                                                                                                                                                                                                                                                                                                                         63 RDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDL---CGATTCDTLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 RPPLCFHNGVQYKNNEEWTVDSCTECHCQNSVTICKKVSCPIMPCSNATVPD-----GE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLDQPSKPISLPED-----LPGASYT------LSQQCELAFGVGS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SSMVLELKGLRIVTL------QDSIRKVTEE--NRELVSELK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CSAAIITDFLDSGHGD 209
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-47/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF>
F;551-586/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149;
                                                                                                                                                                                                        Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-23,'Q',25-92,'G',94-131,'G',133-169,'Q',171-571
A;Cross-references: GB:X68251
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: venom gland
A;Note: sequence inconsistent with the nucleotide translation
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R;Paine, M.J.; Desmond, H.P.; Theakston, R.D.; Crampton, J.M.
J. Biol. Chem. 267, 22869-22876, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ily.
A;Reference number: A44463; MUID:93054601; PMID:1385408
                                                                                                                                                                                                            11.0%; Score 224.5; DB 2; 24.3%; Pred. No. 1.3e-09; ive 35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWAD-GTSCGEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 SPTL ----IQIDRANPWSA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 ANGGKYCEGVRVKYRSCNLEPCP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 QFGGKDCVGDVTENQVCNKQDCP 547
                                                                                                                                                                                                                                                                                       Matches 93; Conservative
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A; Residues: 360-571 <USA>
                                                                                                                                                                                                                                                   Similarity
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Best Local
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
B;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
A;Accession: B42587
A;Accession: Dreliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Across-references: GB:M87276
A;Across-ref
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R; Chen, H; Aeschlimann, D; Nowlen, J; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A; Title: Expression and initial characterization of recombinant mouse thrombospondin 1
A; Reference number: S68787; MUID:96234006; PMID:8654563
A; Accession: S68787
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A; Residues: 19-26, 7%, 7, 28-37 < CHE>
C; Complex: homotrimer, disulfide linked
C; Complex: homotrimer, disulfide linked
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; V; Keywords: calcium binding; glycoprotein; homotrimer
E; 1-18-20main: signal sequence #status predicted < SIGS
F; 19-1170/Product: thrombospondin 1 #status predicted < VMC>
F; 317-375/Domain: von Willebrand factor type C repeat homology < VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999
C;Accession: A40558; A37905; B42587; S68787
E;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkin A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
A;Accession: A40558
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                                                                                                                                                                                                                                                                                           ---- LSQQCELAFGVGS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 CEGEARETKACKKDAC-----PINGGWGPWSPWDICSVTCGGGVOKRSRLCNNPTP 524
                 120 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMM 178
                                                                ----CSAAIITDFLDSGHGD
                                                                                                                                                                                                                                                                                                                                      314 RPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKKVSCPIMPCSNATVPD-----GE
                                                                                                                                                                                                                                                                                                                                                                                                                                   245 KPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWAD-GTSCGEG----------
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                                                                                      ----SSMVLELRGLRIVTTL---
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A: Title Inchmistry 30, 1957-1964, 1991 A: Title Inchmistry 30, 1957-1964, 1991 A: Title Isolation and chemical characterization of two structurally and functionally discrete number: A37958, MUID: 91129280; PMID: 1993206 A: Reference number: A37958, MUID: 91129280; PMID: 1993206 A: Residues: A37958 A: Molecule type: protein A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Note: 361-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> A: Residues: 360-372, E', 374-378, 'X', 380-384 < FUJ> C: Comment: Inhibits collager- and ADP-induced platelet aggregation. C: Superfamily: mouse meltrin alpha; dishtegrin homology C: Reywords: hydrolase: metalloproteinase; veore: war- F: 360-244/Domain: dishtegrin homology < FUJS> FI HI	### Conserver
Db 264 AYIGAWGHRENGYGYSFILINDYMAHAMEMGHNLGIHHPTGSCGCDY 315  OY 177MASPTLIODORANGYSFILINDYMAHAMEMGHNLGIHHPTGSCGCGDY 315  Db 316 FCIMCPT-ISNERSKFENGSATITDFLDSGHGCTLDOPSKPISLEDDPGA 228  1	QY 282 GECKLCLKGARCVE 294  DD 393 ADGRYCKNRGCVD 405  RESULT 15 A5914  metalloproteinse (EC 3.4.24) (brevilysin) H6, venom - Gloydius halys brevicaudus disintegrin.  C. Species: Gloydius halys brevicaudus C. Date: 01-Mar-2002 floodius halys brevicaudus contains: 01-Mar-2002 seaquence_revision 01-Mar-2002 floodius halys brevicaudus c. Species: Gloydius halys brevicaudus c. Streads. S. Date: 01-Mar-2002 seaquence_revision 01-Mar-2002 floodius halys brevicaudus c. Streads. S. Date: 01-Mar-2002 floodius halys brevilysin H6 from the Venom of Glo A/Reference number: A59414 A/Reference number: A59414 A/Reference number: A59414 A/Rodecule type: protein A/Rodecule type:

171 ISHEPSTFFSNCSYIQCWDFIMDHNPECIVNEPLGTDIVSPEVGNELLEVGE 223 220	
	643
	231
224 ECDCGTPENCQNECCDAATCKLKSGSQCGHGDCCEQCKFSKSGTECRESMPECDPAEHCT 283	283
-AF	248
- QA	343
	275
ENGIKIPCAPEDVKCGRLYCKDNSPGQNNPCKMFYSNEDEHKGWV	395
276 ADGTSCGECKLCLKGACVE 294	
396 LPGTKCGDGKVCSNGHCVD 414	
Search completed: April 29, 2003, 17:13:21 Job time : 12.5813 secs	
· 0 >1->1 4 1 14	MYHQCYALMCADVYDAEDSCFESNTKGN 3QMVCQTRHFPW

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April 29, 2003, 17:10:24; search time 4.56924 Seconds (without alignments) 3367.676 Million cell updates/sec
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                   OM protein - protein search, using sw model
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US-10-009-332-1\_COPY\_213\_583
2042
1 FVSIPRYVETLUVADESMVK.....SCNLEPCPSSASGKSFREEQ 371 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	mus	Q9uhi8 homo sapien				_		mus m	homo	homo	homo	рошо	homo	h ada								homo	mus m	P07996 homo sapien	mus m	P78325 homo sapien	3 bos t	both	9	Q9bz11 homo sapien	4 mus m	<b>-</b> *	Q9h013 homo sapien
SUMMARTES	;	ID	ATS1_MOUSE	ATS1_HUMAN	ATS1_RAT	ATS4_HUMAN	ATS4_RAT	ATS8_MOUSE	ATS8_HUMAN	ATS5_MOUSE	ATS5_HUMAN	ATS9_HUMAN	ATS7_HUMAN	AT12_HUMAN	AT10_HUMAN	ATS2_HUMAN	ATS3_HUMAN	ATS2_BOVIN	ATS6_HUMAN	ATS5_BOVIN	ATS4_BOVIN	AD28_MACFA	AD12_HUMAN	AD28_HUMAN	AD12_MOUSE	TSP1_HUMAN	TSP1_MOUSE	AD08_HUMAN	TSP1_BOVIN	DISJ_BOTJA	AD28_MOUSE	AD33_HUMAN		HR1B_TRIFL	AD19_HUMAN
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dР	Query	Match	65.5	65,3	65.0	57.9	56.5	55.2	55.2	54.6	54.4	51.2	40.1	38.5	36.8	31.0	30.9	30.8	30.4	29.3	29.3	12.1	11.6	11.5	11.4	11.2	11.0	10.9	10.9	10.8	10.7	10.5	10.3	10.3	10.1
		score	1337	1334	1327	1182.5	1153.5	1128	1126.5	1114	1110	1046.5	819	786	751	633.5	631.5	628.5	620	599	599	246.5	236.5	234	233.5	229.5	224.5	223.5	222.5	220	219.5	214	210.5	210	205.5
	Result	. I	Н.	010	m ·	4	'n	9	7	Φ,	, סי	10	1;	12	13	14	15	16	17	18	19	50	$\frac{21}{20}$	22	23	77	25	526	27	28	29	30	31	3.5	2,5

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                    CELLS OF PRECOULATORY FOLLICLES.

CELLS OF PRECOULATORY FOLLICLES.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.

CAUTION: REP. 2 SEQUENCE ELFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 7.
                                                        SITE, WITHIN THE CHONROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
                                                                                                                     INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER
                                           CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-|-LEU-1692
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS000427; TSP1, 3.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
           CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (BY SIMILARITY)
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SIMILARITY)
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E->Q: LOSS OF ACTIVITY.
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ZINC (CATALYTIC) (1
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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TSP TYPE-1 3.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF00409; tsp_1; 3, Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB001735; BAA24501.1; ALT_INIT.
EMBL; D67076; BAA11088.1; ALT_FRAME.
MEROPS; M12.222; -
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968 AA;
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Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Olkemus S.,
Lombardo M., Iruela-Arispe M.L.;
Is a man ortholog of AbANTS-1, and METH-2 are members of a new
family of proteins with angio-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATS1 HUMAN STANDARD; PRT; 967 AA. 69UH18; Q9UP80; Q9UH83; Q9PR0; Q9NSJ8; 30-MAY-2000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ADAMTS-1 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1) (METH-1). ADAMTS1 OR METH1 OR KIAA1346.
                                                                                                                                                                                                                                                  GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
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                                                                                                                                         121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Casas C., Pritchard M.A., Estivill X., Arbones M.L.; Casas C., Pritchard M.A., Estivill X., Arbones M.L.; "Cloning, characterization and mapping on human chromosome 21 of orthologue of murine Adamts-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20247184; PubMed=10785405; Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B., Rosenthal A., Thierauch K.H.; "Differential gene expression by endothelial cells in distinct and foodends states."
                                ;
6
Length 968;
                                81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
 DB 1;
Score 1337; DB 1
Pred. No. 2e-103;
                                51; Mismatches
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TISSUE=Endothelial cells;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCPDN-NGKTFREEQ 626
                                                                                                                                                                                                                                                                                                                                                                                                                                            357 PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Heart
                                    237;
    Query Match
Best Local S
                                     Matches
                                                                                                                               61
                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                              WEDLINE-20289799; PubMed-10830953;
WADLINE-20289799; PubMed-10830953;
WA MEDLINE-20289799; PubMed-10830953;
WA Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Yada T.,
A Park H.-S., Toyoda A., Tishii K., Totcki Y., Choi D. K., Soeda E.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schlilhabel M., Schudy A., Zimmermann W.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLOSUE SETERATIONS:

Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER (BY SIMILARITY). HAS ANGIOGENIC INHIBITOR ACTIVITY. ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED MITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE.

- CATALTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLU-1-LEU-1939

SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN.

-- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix (By similarity).

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                MEDLINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 6
Pfam; PF01421; Reprolysin; 2.
Pfam; PF0152; Pep_M12B_propep; 2.
SMART; SM00209; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF170084; AAF15317.1; -
EMBL, AF060152; AAA8080.1; ALT_INIT.
EMBL, AF207664; AAF23772.1; -
EMBL, AB037767; BAA92584.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL162080; CAB82413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 418-967 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001697; BAA95502.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; M12.222; -.
Genew; HGNC:217; ADAMTS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: THE PARE SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Melanoma;
     TISSUE=Brain:
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ATSL_RAT STANDARD; PRT; 967 AA.
OSWUG1; Q9ER11;
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 KH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLTATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747 N-LINKED (GLCNAC. . .) (POTENTIAL).
720 N-LINKED (GLCNAC. . .) (POTENTIAL).
764 N-LINKED (GLCNAC. . .) (POTENTIAL).
727 P -> A (IN REF. 4 AND 5).
768 Q -> H (IN REF. 1).
761 S -> N (IN REF. 1).
761 S -> N (IN REF. 1).
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS0617; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS06092; TSP; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; extracellular matrix; Heparin-binding.
SIGNAL
PROSITE; PS00215; PS00215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                        CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 1334; DB 1;
63.5%; Pred. No. 3.5e-103;
live 50; Mismatches '81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISINTEGRIN-LIKE,
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP TYPE-1 2.
TSP TYPE-1 3.
POLY-LYS.
                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                ADAMTS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 238; Conservative
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|DCPDN-NGKTFREEQ 625
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843
547
720
764
764
77
227
468
468
967 AA;
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SITE
METAL
ACT_SITE
METAL
METAL
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CARBOHYD
CARBOHYD
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                            PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY STRILARTY). ACTIVE METALLOPROTESE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1683-GLU-1-LEU-1684 STE, WITHIN THE CHONDROITH SULFARE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                    J.A.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Zymogen;
                                                                                                              STRAIN-Sprague-Dawley; TISSUE-Brain;
Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matrix (By similarity).
INDUCTION: DOWN REGULATED IN ENDOTHELIAL CELLS DERIVED FROM CIRRHOTIC LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

ADAMTS-1.

CYSTEINE SWITCH (POTENTIAL).

CYSTEINE SWITCH (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley, TISSUE-Liver,
MEDLINE-20304099, PubMed-10847486,
Diamantis I., Luethi M., Hoesli M., Reichen J.;
Cloning of the rat ADAMTS-1 gene and its down regulation in
Endothelial cells in cirrhotic rats.";
                                                                                                                                                                   "Induction of a disintegrin and metalloprotease with the thrombospondin type I motif (ADAMTS)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001762; Disintegrin.
InterPro; IPR001870; Pep_M12B_propep.
InterPro; IPR001890; Rep_M12B_propep.
InterPro; IPR001891; TSP1.
InterPro; IPR001884; TSP1.
InterPro; IPR001804; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 6.
Pfam; PF01622; Pep_M12B_propep; 2.
SMART; SM00209; TSP1; 3.
PROSITE; PS00142; ZND_RTREASE; 1.
PROSITE; PS00142; ZND_RTREASE; 1.
PROSITE; PS00142; ZND_RTREASE; 1.
PROSITE; PS00142; DISINTEGRIN, 1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycopr
Repeat; Extracellular matrix; Heparin-binding.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF149118; AAD34012.1; -. EMBL; AF304446; AAG29823.1; -.
                                                                                                                                                                                                                                                  SEQUENCE OF 18-967 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252
967
205
401
402
405
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                                                                                              SEQUENCE FROM
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METAL
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181 ILLQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAF 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 YEEQKGPEVTSNAALTLRNFCSWQKQHNSPSDRDPEHYDTAILFTRQDLCGSHTCDTLGM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FVSIPRYVETLVVADDESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
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OST373; Q90N83.

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2002 (Rel. 41, Last annoration update)

15-JW1-2002 (Rel. 41, Last annoration update)

ADAM75-4 precursor (EC 3.4.24-) (A disintegrin and metalloprotein with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 GEESTHCPDAASTCSTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                  (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...)
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6
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 967;
                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTY N-A (IN REF. 2).

K-> F (IN REF. 2).

K-> F (IN REF. 2).

TMLV -> NILK (IN REF. 2).

TMLY -> NILK (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105705 MW; F93C864F6DCDB4CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.0%; Score 1327; DB 1;
62.7%; Pred. No. 1.3e-102;
                        DISINTEGRIN-LIKE.
TSP TYPE-1 1.
     (CATALYTIC)
                                                                                                                               TSP TYPE-1 2.
TSP TYPE-1 3.
                                                                             CYS-RICH.
                                                                                                                                                                                         POLY-ARG
                                                                                                           SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.7
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612 DCPDN-NGKTFREEQ 625
     4111
558
615
724
857
9907
9967
720
720
782
945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936
962
967 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUCECTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-1. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

-1. TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED AT VERY LOW LEVEL. IN PLACENTA AND SKELETAL MUSCLES.

-1. INDUCTION: BY INTERLEUKIN.1.

-1. DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

-1. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

-1. SIMILARITY: ENLONGS TO PEPPIDASE FAMILY M12B.

-1. SIMILARITY: CONTAINS 1 DISINTEGRIN.LIKE DOMAIN.

-1. SIMILARITY: CONTAINS 1 TYPE-1 DOMAIN.

-1. SIMILARITY: CONTAINS 1 TYPE-1 DOMAIN.

-1. CAUTION: HAS SOMETIMES BEEN REFERRED TO AS ADAMTS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tortorella M.D., Pratta M.J., Liu R.-O., Abbaszade I., Ross H.,
Burn T.C., Arner E.C.;
Burn T.C., Arner E.C.;
Burn T.C., Arner E.C.;
Burn T.C., Arner E.C.;
J. Burn T.C., Arner E.C.;
aggreean substrate recognition and cleavage.";
J. Biol. Chem. 275:25791-25797(2000).
J. Biol. Chem. 275:25791-25797(2000).
INVOLVED IN ITS TORNOVER.N. A CARTILAGE PROTEOGIYCAN, AND MAY BE DESTRUCTION: CLEAVAS AGGRECAN, A CARTILAGE PROTEOGIYCAN, AND MAY BE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. COULD ALSO BE A ONE CRITICAL FACTOR IN THE EXACERBATION OF NEUROBEGENERATION IN ALZHEIMER'S DISEASE.
                                                                                                                                                                                                                                                      MEDIINE-92286303; PubMed-10356395; Abbaszade I., Hollis J.M., Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M., Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R., Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R., Magase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K., Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L., Trzaskos J.M., Arner E.C.; Purification and cloning of aggrecanase-1: a member of the AbbANTS family of proteins."
                                                                                                                        "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new CDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-1-Ala-393
                                                                                      Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani.H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Saklatvala J:, Clark A.R.; Sawali T., Nagase H., Saklatvala J:, Clark A.R.; ADDATS-4 genomic locus."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE, AND CHARACTERIZATION.
MEDLINE=20400518; Pubmed=10827174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
                                                              MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB014588; BAA31663.1; -. EMBL; AF148213; AAD41494.1; -. EMBL; AY044847; AAL02262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         family of proteins.";
Science 284:1664-1666(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; M12.221; -.
Genew; HGNC:220; ADAMTS4.
                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
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61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM 120
                                                                                                                                                                                                                                                                                                                                                                                               121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKL-RANHMMS 179
                                                                                                                                                                                                                                                                                                                                                                                                          PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                      1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 FGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF000421; tsp_l; l.
Pfam; PF01421; Reprolysin; l.
SMART; SM00209; TSP1; l.
PROSITE; PS00142; ZINC_PROTEASE; l.
PROSITE; PS50015; ADAM_MEPRO; l.
PROSITE; PS50015; ADAM_MEPRO; l.
PROSITE; PS001427; DISINTEGRIN_l; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Extracellular matrix.
                                                                                                                                                                                                                       .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                    5,
                                                                                                                          CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                  57.9%; Score 1182.5; DB 1; Length 837;
                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                               5DF9C9AC137DF41F CRC64;
                                                                                                                                                      ZINC (CATALYTIC) (BY SZINC (CATALYTIC) (BY SDISINTEGRIN-LIKE.
TSP TYPE-1.
CYS.RICH.
                                                                                                                                                                                                                                                                                          ; Pred. No. 1.2e-90; 56; Mismatches 106;
                                                                                                                                                                                                                                  A -> T (IN REF. 1).
R -> Q (IN REF. 3).
G -> R (IN REF. 3).
                                                                                                                                                                                                               POLY-ALA.
N-LINKED (GLCNAC.
                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                 90224 MW;
                                                                                                                                                                                                                                                                                           55.5%;
                                                                                                                                                                                                                                                                                                     Matches 208; Conservative
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573 DCP-TGSALTFREEQ 586
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                                                                                                                                                                                                                                          626
682
637 AA;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                        52
213
1194
3361
3361
437
520
577
686
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METAL
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CONFLICT
CONFLICT
SEQUENCE
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CARBOHYD
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DOMAIN
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1 FVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
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                                                                                                                                                                                                                                                                                                                 matix (By similarity).

TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 1 DISINIEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                            BE
                                                                                                                              Satch K., Suzuki N., Yokota H.; "ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin
                                                                                                                                                                             astrocytes.";
Neurosci. Lett. 289:177-180(2000).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY
INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE
DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                              motifs) is transcriptionally induced in beta-amyloid treated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ALA.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%; Score 1153.5; DB 1; Length 630; 54.7%; Pred. No. 2.2e-88; ive 52; Mismatches 113; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Glycoprotein; Zymogen; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKED (GLCNAC. . .) (P. 63A428753167C7EF CRC64;
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SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB042272; BAB16474.1; --
EMBL; AB042271; BAB16473.1; --
EMBL; AB042273; BAB16473.1; --
InterPro; IPR00150; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01421; Reprolysin; 1.
PROSITE; PS50125; ADAM_MEPRO; 1.
PROSITE; PS50012; TSP1; 1.
                                                                                                    STRAIN-Wistar; TISSUE-Brain;
MEDLINE-20415831; PubMed-10961658;
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1158
1158
1164
303
478
630
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                                                     NCBI_TaxID=10116;
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METAL
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PROPEP
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4;

Gaps

Conservative

al Similarity 205; Conserv

Query Match

Best Local

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last amondation update)
ADAWES-8 precursor (EC 34.24..) (A disintegrin and metalloproteinase
with thrombospondin motifs 8) (ADAM-IS 8) (ADAM-TS 8) (METH-2).
                                                                                                                                                        PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELA 239
                                                                                                                                                                                                                                                                                        306 KDFNIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTKFVPRNGGKYCEGRRTPFRSCNTK 365
                                                      120
                                                                                                 121 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRANHMMS
                                                                                                                                                                          240 FGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNL
                                                                                                                                                                                                                                 299 NKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCINPIPANGGKYCEGVRVKYRSCNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i-SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         905
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF175282; AAF25805.1; -.
                                                                                                                                                                                                                                                                                                                                                       || | :|||||
366 NCP-HGSALTFREEQ 379
                                                                                                                                                                                                                                                                                                                                      357 PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                           TISSUE-Lung;
MEDLINE-99367466; PubMed-10438512;
Wazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
Lombardo M., Iruela-Arispe M.L.;
"METH-1, a human ortholog of ADAWTS-1, and METH-2 are members of a new
family of proteins with angio-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIDNEY.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                    MEDLINE-20079168; PubMed=10610729; Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.; Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.; Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.; AbAM-TS8, a novel metalloprotease of the ADAM-TS family located on mouse chromosome 9 and human chromosome 11."; Geomaics 62:312-315 (1999).

-I- FUNCTION: HAS ANIT-ANGIOGENIC PROPERTIES.
-I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-I- SUBSELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By Similarity).
-I- TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWER EXPRESSION IN BRAIN, PLACENTA, HEARF, STOMACH AND FETAL BRAIN AND
     15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2)
                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR0012890; Reprolysin.
InterPro; IPR001690; Reprolysin.
InterPro; IPR001690; Rapl.1; 2.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR00130; Zn_MTpeptdse.
InterPro; IPR00121; Reprolysin, 1.
IPR01121; Ps01421; TsP1; 2.
IPR051TE; Ps000142; ZINC_PR0TEASE; 1.
IPR051TE; Ps000142; ZINC_PR0TEASE; 1.
IPR051TE; Ps000427; DISINTEGRIN_1; FALSE_NEG.
IPR051TE; Ps004427; DISINTEGRIN_1; FALSE_NEG.
IPR051TE; Ps004427; DISINTEGRIN_1; Hepeatin-binding.
IPR051TE; Ps004427; DISINTEGRIN_1; Hepeatin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY. ADAMTS-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF175283; AAF25806.1; -.
                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M12.226; -. Genew; HGNC:224; ADAMTS8.
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890
364
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                                                                                                                                                              SEQUENCE FROM N.A.
                                                                  ADAMTS8 OR METH2
                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 605175; -
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PROPEP
CHAIN
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 VERHNLN--KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGAS--YTLSQQCE 237
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                                                                                                                                                                                                                                                                                                                                                                                                              SPACER.
TYPE-1 2.
N-LINKED (GLCNAC...) (POTENTIAL).
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PROSTE; PS00142; ZINC_PROTEASE; 1.

PROSTE; PS50015; ADAW_MEPRO; 1.

PROSITE; PS50092; TSPI; 1.

PROSITE; PS00427; DISINTERRIN_1; FALSE_NEG.

Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

Repeat; Extracellular_matrix; Heparin-binding.
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                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC SINCERIN LIKE.
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 905;
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                                                                                                                                                                                                                                                                      BY SIMILARITY. ADAMTS-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.2%; Score 1128; 53.8%; Pred. No. 4.
                                                                                                                                                                                                                                                       POTÈNTIAL
          MEROPS, M.2.226...
MGD; MGI:132468, Adamts8.
InterPro; IPR001762; Disintegrin.
InterPro; IPR0010590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
Ffam, PF00090; LSP_1; 2...MTpeptdse.
Pfam, PF00421; Reprolysin; 1.
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905 AA;
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METAL
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AC Q9UP79;
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DT 16-OCT-
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Biol. Chem. 274:25555-25563(1999)

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16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-DECURSON (Rel. 41, 42, 424.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS 5) (AGAGECANASE-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           350
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Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, novel members of a new family of
                                                                                                                                                                                                                                                                                                  EDEKWGPEVSDNGGLILRNFCNWQRRFNQPSDRHPEHYDTAILLTRQNFCGQEGLCDTLG
                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                 (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                            .) (POTENTIAL)
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           SIMILARITY)
SIMILARITY)
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YLTELLDGGHGDCLLDAPGAALPLPTGL ->
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                                                                                                                                                                                                    55.2%; Score 1126.5; DB 1; Length
53.3%; Pred. No. 5.6e-86;
ive 64; Mismatches 101; Indels
                                                                                                                 (GLCNAC. . .)
BY SIMILARITY.
ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
                                                                                                           (GLCNAC. . .)
                                                                                             N-LINKED (GLCNAC.
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                                                                          TSP TYPE-1 2.
POLY-PRO.
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                                                                                                          N-LINKED
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                                                                 SPACER
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QSCHTEECP--PDGKSFREQQ 592
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                 96671 MW;
                                                                                                                                                                                                                            Conservative
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  musculus (Mouse).
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                                                                                                                                                                                   890 AA;
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                                                                                                                                                                                                                  Similarity
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Best Local Simi
Matches 203;
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Q9R001;
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CARBOHYD
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CARBOHYD
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                                 DOMAIN
DOMAIN
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                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
      FUNCTION: CLEAVES AGGRECAN, A CÁRTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE BESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLYL DURING THE PERI-IMPLANTATION PERIOD CATAVITY: Cleaves, aggrecan at the 392-Glu-1-Ala-393
                                                                                                             SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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R MGD) MGI.1346321; Adamts5.

R InterPro; IPR001762; Disintegrin.

R InterPro; IPR0012870; Pep_M12B_propep.

R InterPro; IPR001890; Reprolysin.

R InterPro; IPR000180; Zn_MTpeptdse.

R InterPro; IPR000180; Zn_MTpeptdse.

R Pfam; PF01421; Reprolysin; 1.

R Pfam; PF01422; Pep_M12B_propep; 1.

R RART; SM00209; TSP1, 2.

R PROSITE; PS50012; ADAM_MBRRRO; 1.

R PROSITE; PS00142; INC_PR0TEASE; 1.

R PROSITE; PS00142; INC_PR0TEASE; 1.

R PROSITE; PS00142; INTERRIN.1; FALSE_NEG.
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POLY-ARG
POLY-ARG
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-TINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                            matrix (By similarity).
DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-
IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.6%; Score 1114; DB 1; Length 930; 53.6%; Pred. No. 6.4e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84DE84B26170D4DC CRC64;
                                                                                                                                                                                                                                  SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINIFGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
                                                                                                  COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSTEINE SWITCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP TYPE-1 2.
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                                                                                                                                                                          UNDECTABLE LEVEL THEREAFTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF140673; AAD56356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix.
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930
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410
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874
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930 AA;
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METAL
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Best Local 9
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        Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

A Park H.-S., Toydda A., Ishli K., Totoki Y., Choi D.-K., Soeda E.,

A Ohki M., Takagi T., Sakaki Y., Tatoki Y., Blechschmidt K., Polley A.,

Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

Reichwald K., Rumpf K., Lehmann R., Patterson D.,

Rosenthal A., Kudoh J., Shibuya K., Rawasaki K., Asakawa S.,

Shintani A., Sasaki T., Naqamine K., Mitsuyama S.,

Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

The DNA sequence of human chromosome 21.";

Lehrach H., Reinhardt R., Yaspo M.-L.;

The DNA sequence of human chromosome 21.";
                                                                                                                                                                        242 VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER----H 296
                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS 5) (AGGrecanase-2)
DVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPT 181
                                                                                           LIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFG 241
                                                                                                                                        503 PEYSVCPGMDVCARLWCAVVRQGQMVCLTKKLPAVEGTPCGKGRVCLQGKCVDKTKKKYY 562
                                                                                                                                                                                                                     NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                    STSSH---GNWGSWGPWGQCSRSCGGGVQFAXRHCNNPAPRNSGRYCTGKRAIYRSCSVT 619
                                   DRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99367476; PubMed-10438522;
Abbaszade I., Liu R.-Q., Yang F., Rosenfeld S.A., Ross O.H.,
Liu J. Liu R.-Q., Yang F., Rosenfeld S.A., Ross O.H.,
Lin J.R., Ellis D.M., Toxtorella M.D., Pratta M.A., Hollis J.M.,
Wynn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K.,
Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H.,
Arner E.C., Burn T.C.,
Arner E.C., Burn T.C.,
"Cloning and characterization of ADAMTSIl, an aggrecanase from the
ADAMTS family.",
D. Biol. Chem. 274:23443-23450(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    930 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-20289799; PubMed-10830953;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAMTS5 OR ADMP2 OR ADAMTS11.
                                                                                                                                                                                                                                                                                 ||| :||||| ||
PCP--PNGKSFRHEQ 632
                                                                                                                                                                                                                                                                     PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (ADAM-TS 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                               Q9UNA0; Q9UKP2;
                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                (ADMP-2)
                                                                                                                                                                                                                                                                                                                             RESULT 9
ATS5_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Burpaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                 zinc metalloproteases.";
J. Biol. Chem. 274:2555-25563(1999).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOCLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI IMPLANTATION PERIOD.
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-ala-393
                                                                                                                                                                                                                                                                                                                                                                                                              matrix (By similarity).
TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA
BUT ALSO IN OTHER TISSUES, SUCH AS HEART AND BRAIN, AND ALSO
CERVIX, UTERICS, BLADDER, ESOPHAGUS, RIB CARTILAGE,
CHONDROBLASTOMA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                         TISSUE=Fetal brain;
MEDLINE-99395124; PubMed=10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, novel members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC. (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
SPACER.
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PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FÀLSE_NEG.
PROSITE; PS00192; TSP1: 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAMTS-5.
CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM, 605007; ...
InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001890; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; Z, MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF142099; AAD49577.1; -. EMBL; AP001698; BAA95504.1; -. EMBL; AP001697; BAA95503.1; -. EMBL; AF141293; AAF02493.1; -. HSSP; Q9PW35; 1BUD.
SEQUENCE OF 413-930 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:221; ADAMTS5.
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ACT_SITE
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3;
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                                                                                                                                                                                                                                                                                                                                                     SISSH---GNWGSWGSWGSCSGGVOFAYRHCNNPAPRNNGRYCTGKRAIYRSCSLM 619
                                                                                                                                                                                                                                                                                   263 ISRARQVELLLVADASMARLYGRGLQHYLLTLASIANRLYSHASIENHIRLAVVKVVVLG 322
                                                                                                                                                                                                                                                                                                                                                                                                   DVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER----H 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLE 356
                                                                                                                                                                                                                                                                                                                                  DRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMA 121
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
                                                                                                                                                                                                 54.4%; Score 1110; DB 1; Length 930;
53.6%; Pred. No. 1.4e-84;
ive 56; Mismatches 108; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maki R.A.;
"ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20181126; Pubmed-10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
                                                                                                                                                                  101715 MW; B64281502F28193B CRC64;
                                               N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
A -> G (IN REF. 2).
P -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1629 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20396138; PubMed-10936055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 67:343-350(2000).
                                                                                                                                                                                                                                    201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 PCPSSASGKSFREEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 PCP--PNGKSFRHEQ 632
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                                                                                                                                                                                                                      Similarity
                                                                                                                                                                   930 AA;
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                                                                                 CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                    CARBOHYD
CARBOHYD
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     DOMAIN
                                    DOMAIN
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                                                                                                                                                                                                                                                                                              DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
             "Prediction of the coding sequences of unidentified human genes. XVI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 4.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 11.
POLY-SER.
CYSPEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.

SIGNAL 1 8 POTENTIAL.
PROPER 19 287 BY SIMILARITY.
CHAIN 288 1629 ADAMTS-9.
DOMAIN 509 587 DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                          PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY). SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS50092; TSP1; 9.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Ffam; PF010421; Reprolysin; 1.
Ffam; PF01421; Reprolysin; 1.
Ffam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:13202; ADAMTS9.
MIM; 605421;
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1108
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752
880
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-I. COGRACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-I. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNL 355
                                                                                                                                                                                                                                                                                                                  61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA-TTCDTLG 119
                                                                                                                                                                                                                                                                                                                                                                       120 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMS 179
                                                                                                                                                                                                                                                                                                                                                                                      metalloproteinase
                                                                                                                                                                                                                                                                             348 HNEQDGPSISFNAQTTLKNFCQWQHSKNSPGGIH---HDTAVLLTRQDICRAHDKCDTLG 404
                                                                                                                                                                                                     . Score 1046.5; DB 1; Length 1629;
Pred. No. 4.9e-79;
57; Mismatches 109; Indels 15; Gaps
                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                             PTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-SKPISLPEDLPGASYTLSQQCEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
CLUTCGKGH - > VEWEGCYEP (IN SHORT ISOFORM).
                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matrix (By similarity).
-i- TISSUE SPECIFICITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG,
                                                                                                                                                                              C1C4CEFF58B8941F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 3.4.24.-) (A disintegrin and me with thrombospondin motifs 7) (ADAM-TS 7) (ADAM-TS7).
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51.9%;
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                                                                                                                                                                                                                                  Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                             112
135
271
749
840
1213
1267
                                                                                                                                                     1629
                                                                                                                                                                   367
                                                                                                                                                                            1629 AA;
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                              1213
1267
1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATS7_HUMAN
Q9UKP4;
    METAL
METAL
CARBOHYD
                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                  CONFLICT
                                            CARBOHYD
                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATT--CDTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 GMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD-NVKVCEEVFGKLRANHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP-ISLPEDLPGASYTLSQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50092; TSP1: 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSP TYPE-1 1.
CYS-RICH.
SPACER.
TYPE TYPE-1 2.
N-LINKED (GLCNAC. . . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ADAMYS-7.
CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYIC) (BY SIMILARITY)
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SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 819; DB 1; Length 99; Pred. No. 2.2e-60; 43; Mismatches 140; Indels
                                                                                 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ZINC (CATALYTIC) (BY
ZINC (CATALYTIC) (BY
                                                                 -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-1- SIMILARITY: CONTAINS 1 DISINTEGRIA-LIKE DOMA.
-1- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISINTEGRIN-LIKE
                                                                                                                                                                                                                                                                                                                 Pep_M12B_propep
                                                                                                                                                                                                                                                                                              InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_proper
InterPro; IPR001590; Reprolysin.
InterPro; IPR000084; TRP1.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; Pf00090; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00209; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
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Pfam; PF01562; Pep_M12B_propep; 1.
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X
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778
997 AA;
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                                                       SIMILARITY).
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233
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Matches 177;
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SITE
METAL
ACT_SITE
METAL
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

FIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

PTM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND IS-1 DOMAINS AND
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR IS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matrix (By similarity).
-1- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                   DOMÁIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                 355
415 MSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDPPAKDIIDFPSVPPGVLYDVSHQC 474
                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMYS-12 precursor (RC 3.4.24, ) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-
                                                                               237 ELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER
                                           RLQYGAYSAFCEDMDNVCHTLWCSVGT - - - TCHSKLDAAVDGTRCGENKWCLSGECVP -
                                                                 296 HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNL
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMITARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                             PRT;
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                                                                                                              371
                                                                                                                                   590 QACP -- AGRPSFRHVQ 603
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                     ADAMTS-12 precursor (EC
                                                                                                              356 EPCPSSASGKSFREEQ
                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                          AT12_HUMAN
P58397;
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AT12_HUMAN
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RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA--TTCDTL 118
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242 ISKERWVETLYVADTKMIEYHGSENVESYILTIMNMYTGLFHNPSIGNAIHIVVVRLILL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSIPRYVETLVVADESMYKFHGAD-LEHYLLTLLTLATAARLYRHPSILNPINIVVVKVLLL 60
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                                                                                                                                                                                                                         PASE; 1.
Zinc; Signal; Glycoprotein; Zymogen;
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(BY
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2.1e-57;
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DISINTEGRIN-LIKE.
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF001562; Pep_M12B_propep; 1.
SMART; SW00209; FSP1; 8.
PROSITE; PS500215; ADAM_MEPRO; 1.
PROSITE; PS50092; FSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Repeat; Extracellular matrix.
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TSP TYPE-1 3.
TSP TYPE-1 4.
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TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 8.
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N-LINKED (N-LINKED (N-LIN
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Matches 163; Conservative
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CARBOHYD
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Best Local
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36.8%;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-10 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase
with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matrix (By similarity).
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE I DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombospondin type I repeats.";
Submitted (UN-1999) to the BMEL/GenBank/DDBJ databases.
-!- COFACTOR: BINDS I ZIMC ION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
: | : | | : | | : | | : | | 533 -TVGKKPESIPGEGERKRYRLC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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R InterPro; IRR00186; Dep_M12B_propep.
R InterPro; IRR00180; Reprolysin.
R InterPro; IRR00180; Reprolysin.
R InterPro; IRR00180; TSP1.
R InterPro; IRR000180; Zn_MTpeptdse.
R Pfan; PF00190; Esp_1; 5.
R Pfan; PF01562; Pep_M12B_propep; 1.
R Pfan; PF01562; Pep_M12B_propep; 1.
R RSMAT; SM00209; TSP1; 5.
R PROSITE; PSS0015; ADAM MEPRO; 1.
R PROSITE; PSS0015; ADAM MEPRO; 1.
R PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
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ZINC (CATALYTIC) (BY S
BY SIMILARITY.
ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
CYS-RCCH.
                                                                                                                                                                                                                                                                                                                                       PRT; 1077 AA.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:13201; ADAMTS10
                                                                                                  354 NLEPCPSSASGKSFREEQ 371
                                                                                                                                      |: || | | : || 592 NVHPCRSEA--PIFRQMQ 607
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                    AT10_HUMAN
Q9H324;
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METAL
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AT10_HUMAN

AT10_H

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AT10_H

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DT 15-JUM

DE ADAMTS

DE ADAMTS

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16-OCT-2001 (Rel. 40, Last sequence update)
115-UNE 2002 (Rel. 41, Last annotation update)
115-UNE 2002 (Rel. 41, Last annotation update)
ADAMNS-2 precursor (EC 3.4 24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I
Procollagen I/II amino-propeptide processing enzyme)
ADAMNS2 OR PCINP OR PCPNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RDRDSGPKVTGNAALTLRNFCAWQKKL-----NKVSDKHPEYWDTAILFTRQDLC--G 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 ---KLRANHMMSPTLIQIDRANP--WSACSAAIITDFLDSGHGDCLLDQPSK-PISLPED 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VSIPRYVETLVVADESMVKFHG-ADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99347935; PubMed=10417273; Colige A., Sieron A.L., Li S.-W., Schwarze U., Petty E., Wertelecki W., Wilcox W., Krakow D., Cohn D.H., Reardon W., Byers P.H., Laplere C.M., Prockop D.J., Nusgens B.V.; "Human Ehlers-Danlos syndrome type VII C and bovine dermatosparaxis are caused by mutations in the procollagen I N-proteinase gene.";
225 LPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 KL----CLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 DPAKLMAAHITMKT-----NPFVWSSCNRDYITSFLDSGLGLCLNNRPPRQDFVYPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ATTCDTLGMADYGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE
                                                                                                                                                                                                                                                                                                                                                                                       55; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 KYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 371
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SEQUENCE
                                                                                                                                                                                                                                         Query Match
                                                                 CARBOHYD
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            DOMAIN
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                                                                                                                                                             MALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI;
ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-
PROCOLLAGEN PEPTIDASE ACTIVITY.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON
AND AORTA AND AT LOW LEVELS IN THYMUS AND BRAIN.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MAIRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                             - JSERASE: Defects in ADAMTS2 are the cause of Ehlers-Danlos syndrome type VIC (EDS-VICC), a recessively inherited connective-tissue disorder characterized clinically by severe skin fragility and joint hypermobility and blochemically by the presence in skin of procollagen incompletely processed at the N-terminus.
-: SIMILARITY: ENLONGS TO PEPTIDASE FAMILY MI2B.
-: SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOWAIN.
-: SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOWAIN.
-: SIMILARITY: SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                       COFACTOR: BINDS 1 2INC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS5002; TSF1, 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS00142; DISINTEGRIL.]; FALSE_NEG.
HYDROJASE; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Collagen degradation; Extracellular matrix; Heparin-binding;
              and II collagen prior
                                                                CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains
    J. Hum. Genet. 65:308-317(1999). Proceedings of type I and II collagen price FUNCTION: Cleaves the propeptides of type III collagen. May also to fibril assembly. Does not act on type III collagen. May also play a role in development that is independant of its role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN'LIKE.
TYPE-1 1.
CYS-RICH.
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehlers-Danlos syndrome POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY. ADAMTS-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001762; Disintegrin.
Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00090; tsp_1; 4.
Pfam: PF01421; Reprolysin: 1.
SWART; SW00209; TSPI, 4.
PROSITE: PS50315; ADAM_MEPRO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR000130; Zn_MTpeptdse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ003125; CAA05880.1; -.
                                                         collagen biosynthesis.
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Genew; HGNC:218; ADAMTS2.
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253
1211
408
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560
617
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693
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                                                                                                Ala-1-Glu.
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408
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015072, Q9BXZ8;
16-CCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-202 (Rel. 41, Last annotation update)
15-JUN-202 (Rel. 43, Last annotation update)
15-JUN-202 (Rel. 43, Last annotation update)
15-JUN-202 (Rel. 43, Last annotation update)
15-JUN-202 (Rel. 41, Last annotation update)
16-JUN-202 (Rel. 41, Last annotation update)
17-JUN-202 (Rel. 41, Last annotation update)
18-JUN-202 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 PKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 IEVLLGVDDSVVQFHGKEHVQKYLLTLMNIVNEIYHDESLGAHINVVLVRIILLSYGKSM 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESCUENCE OF 1-227 FROM N.A.
MEDLINE-21402912; PubMed-11408482;
MEDLINE-21402912; PubMed-11408482;
Estrandes R.J., Hirohata S., Engle J.M., Colige A., Cohn D.H.,
Eyre D.R., Apte S.S.;
"Procollagen II amino propeptide processing by ADAMTS-3. Insights of the procollagen and the processing processing by ADAMTS-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 SLIEIGNPSQSLENVCRWAYLQQKPDTGHDEYHDHAIFLTRQDF-GPSGMQ--GYAPVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 MCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 IDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 LGYMMCTAFRTEDPCKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHCFKGHCIWLTPD
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Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                               N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLGGGGRWIA (IN ISOFORM SPNPI).
MISSING (IN ISOFORM SPNPI).
MY. BECEEF25C23CAD2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Mismatches 142;
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Pred. No. 7.2e-45;
   4 m 7
                                       TYPE-1
TYPE-1
TSP TYPE-1
TSP TYPE-1
TSP TYPE-1
POLY-ALA.
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38.4%;
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Matches 146; Conservative
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                                                                                                                                                                                                                    matrix (By similarity).
--- TISSUE SPECIFICITY: Found in cartilage and skin.
--- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLUIAR MATRIX.
--- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                 Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Mivajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new CDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                               TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 4.

POLY-ARG.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOWAIN.
-!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-!- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Metalloprotease; Zinc; Signal; Glyc
Repeat; Extracellular matrix; Heparin-binding.
SIGNAL 1 20 POTENTIAL.
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TSP TYPE-1 1.
CYS-RICH.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001809; Reprolysin.
InterPro; IPR001809; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
Ffam; PF00402; FSP_1; 4.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMART; SM00209; TSP1; 4.
PROSITE; PS00042; TSP1; 2.
PROSITE; PS00042; ISP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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dermatosparaxis.";
J. Biol. Chem. 276:31502-31509(2001).
                                                                                                                                          code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
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                                                       TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
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                                        SEQUENCE OF 5-1205 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   430 QAAFHRYHWSRCSGGELKRYIHS--YDCLLDDPFDHDWP-KLPE-LPGINYSWDEQCRFD 485
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75 N-LINKED (GLCNAC. . .) (POTENTIAL).
14 N-LINKED (GLCNAC. . .) (POTENTIAL).
42 N-LINKED (GLCNAC. . .) (POTENTIAL).
135570 MW; EB07B286FC85FB87 CRC64;
                                                                                                                                                    27;
                                                                                                                Score 631.5; DB 1; Length 1205; Pred. No. 1.1e-44;
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38.4%;
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Matches 144; Conservative
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Nagase

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Result No.

4,224,02

Human metalloprote Human metalloprote Human aggrecanase

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OM protein

Run on:

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Metalloprotease with aggrecanase activity for treating joint diseases
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AAU29199
AAB66178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG62299 standard; protein; 950
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16-MAY-2000; 2000JP-0144020.
 (first entry)
WPI; 2001-343602/36.
N-PSDB; AAH41003.
WO200134785-A1.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                             This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors, and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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                                                                                                                        Query Match 100.0%; Score 3744; DB 22; Length 950; Best Local Similarity 100.0%; Pred. No. 4.4e-285; Matches 687; Conservative 0; Mismatches 0; Indels 0;
                 Claim 1; Page 56-60; 85pp; Japanese.
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biological disorder; obesity;
tissue disorder; infertility;
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Pred. No. 1.9e-284;
0; Mismatches 1;
                                                                                      protease;
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                                                                                                            pressure; arthritis;
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                                                                                      Human; novel human protein;
                                                                                                                                                                                                                                                                                                                      27-SEP-2001; 2001WO-US30350.
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entry)
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                                                                                                                                  gene therapy; enzyme
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N-PSDB; AAD35569.
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                                                                                                                                                                                                                           WO200226949-A2.
                                             Human protease
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Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic, antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroprotective; anabolic; anorectic; antimiflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoletic; breast; colon; limn; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
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                                                                                                   540
                                                                                                                           900
HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG 420
                                    RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLA
                                                                                                                                    DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVC
                                                                        QTRHFPWADGISCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLAR
                                                                                                                                                                       VAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCD
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The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a

Claim 28; Figure 2G; 232pp; English

disorders

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disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, hypotension, psychotic disorders, neurological disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72810 represent human protease amino acid sequences of the invention.
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0; Mismatches 1;
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                                                                                                                                                                     tch 99.5%;
al Similarity 99.7%;
686; Conservative 0
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N-PSDB; AAA95827.
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                                                                                                cardiovascular; atherosclerosis; autoimmune disorder; dermatitis; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; cell profilerative disorder; developmental disorder; epilepsy; buchenne muscular dystrophy; epithelial disorder; neurological disorder; reproductive disorder; endometriosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM; Delegeane AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA; Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT; Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
                                                                                    protease; PRTS; gastrointestinal; Crohn's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3725.5; DB 23; Length 952;
Pred. No. 1.2e-283;
); Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Twenty one human proteases (referred to as PRTS-1 to PRTS-21), in the diagnosis, treatment and prevention of gastrointestinal gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders
                                                   Human protease PRTS-11 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 144-146; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.5%;
Best Local Similarity 99.7%;
Matches 686; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2000; 2000US-213955P.
29-JUN-2000; 2000US-215396P.
07-JUL-2000; 2000US-216821P.
14-JUL-2000; 2000US-218946P.
                                                                                                                                                                                                                                                                                                                                                                       L6-JUN-2000; 2000US-212336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                   13-JUN-2001; 2001WO-US19178
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-090437/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      952 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-090437/
N-PSDB; ABK12894.
                                                                                                                                                                                                                                                          WO200198468-A2.
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kallick DA;
                                                                                                                                                                                                                                                                                              27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
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540 540

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thrombospondin domain;

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and metalloproteinase domain;
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N-PSDB; AAA95831.
                                                                                                                            Misc-difference 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA;
                                                                                                                                                  Misc-difference
                                                                                                      Misc-difference
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                          WO200053774-A2
  disintegrin
                                                                    Homo sapiens
                                                                                                                                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                  14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358;
                                                                                                                                                                                                                                                                                                                             Kelner GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                The present sequence is rat metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAMT family and Metalloproteinase Domain, family, wembers of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
Polynucleotide encoding novel members of a disintegrin, metalloprotelnase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                             329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                                                   RAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
                                                                                                                                                                                                                                                                                                                                                                                               89 QGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                     13 QRLTGSSLDLRRCFYSGYVNAEPDSFAAVSLCGGLRGAFGYQGAEYVISPLPNTSAPEAO
                                                                                                                                                                                                                                                                                                                                                   149 RNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSG
                                                                                                                                                                                                                                                                                                                                                                                                                               269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 ELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARR--QCTNPTPANGGKYCEGVRVKYRSCN
                                                                                                                                                                                                                                          Score 2497.5; DB 21; Length 505;
Pred. No. 1.4e-187;
8; Mismatches 21; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ADAMTS-5; metalloproteinase; ADAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human metalloproteinase ADAMTS-5,
                                           Claim 12; Fig 14; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB21261 standard; Protein; 381
                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                      Best Local Similarity 93.5
Matches 462; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 LEPCPSSASGKSFR 505
                                                                                                                                                                                                                    505 AA;
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                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                           Query Match
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The present sequence is human metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addittion to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or angiogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
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vaccine; nootropic; neuroprotective; antiparkinsonian;
erebroprotective; cytostatitc; antiarthrituit.; immunosuppressive;
Alzheimer's disease; parkinson's disease; stroke; cancer; arthritis;
autoimmune disease; brain tumour; brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 381;
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Pred. No. 5.3e-146;
3; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                         /note= "Xaa= any amino
308
                                                                                                                                                                                                                                                           /note= "Xaa= any amino
                                                                                                                                                                                                                                                                                                                          any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Xaa= any amino
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 23; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US06237
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8; Conservative
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AAY49511 represent sequences given in the exemplification of the present

invention.

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MAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                            539
                       141 CQTRHFPWADGTSCGEGKFCLKGACVEXHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autofinaune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatod arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; hememagioma; detection; anticormation; immune deficiency.
COTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM;
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                                                                                                                                                                                                                                                                                                                                                                   AAY49501 standard; Protein; 950 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Fig 1; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GA,
                                                                                                                                                                                                LAVAWVPKYSGVSPRDKCKLI 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US01313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0072298
98US-0098539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HASTINGS G A.
RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human METH1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-590684/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ32000.
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28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49501;
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(RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
                                                                                                                                                                                                                                                       166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS 207
                                                                                                                                                                                                                                                                                                                                                                                                     DILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
                                                                                  Gaps
                                                                                                          1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS------PQDPALQGVGQP-TGTGS
                                                                                                                                                                                                                                                                                                                                                      KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
                                                                                                                                                                                                                                                                                                                                                                   LILLAAALLAVSDALGRPSEEDEELVVP-ELE-----RAP---GHGTTRLHAF
                                                                                                                                                                                                          AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG
                                                                                                                                                                                                                                                                                                        GRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
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                                                                                 67;
                                                        52.4%; Score 1960.5; DB 20; Length
53.6%; Pred. No. 4.7e-145;
.ive 91; Mismatches 178; Indels
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                                                           Query Match
Best Local Similarity
Matches 388; Conserv
                                   950 AA;
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Human; METH1; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular anglogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb anglogenesis; obter Webber syndrome; plaque neovascularisation; telanglectasia; hamophiliac joint; anglofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control.
                                                                                                                                                      SCHLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN
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                                                                                           RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
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SMITHKLINE BECCHAM CORP.
BETH ISRAEL DRACONESS MEDICAL CENT.
IRUELA-ARISPE L.
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990S-0144882.
990S-0147823.
990S-0373658.
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Fornwald JA, Terrett JA;
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JONAK Z L.
TRULLI S H.
FORNWALD J A
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N-PSDB; AAC90057.
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13-AUG-1999;
22-DEC-1999;
22-FEB-2000;
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709 KISG 712
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20-JUL-1999;
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                                                                                                                                                                                                                                                                  A new metal protease and its preparation for use as an anti-cancer and anti-arthritic therapeutic \dot{\cdot}
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53.6%; Pred. No. 4.7e-145;
Linatches 178; Indels
A Disintegrin And Metalloprotease; cancer; arthritis.
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                                                                                                                                                                                       (YAMA ) YAMANOUCHI PHARM CO LTD
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N-PSDB; AAH20224.
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                                   thrombospondin). METHI can be used for inhibiting angiogenesis in an individual, and for treating cancer, bendype tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque heovascularisation, telanglectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METHI can also be used in birth control. METHI can also be used in diagnostic methods for the prognosis of cancer.
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53.6%; Pred. No. 4.7e-145;
.ive 91; Mismatches 178; Indels
rheumatoid arthritis and psoriasis
                   Fig 1; 768pp; English.
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Best Local Similarity 53.6
Matches 388; Conservative
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                                                                                                                                                                                                                       ITGL-TSP; integrin ligand; anglogenic disease; cancer; atherosclerosis; chronic inflammatory disorder; rheumatoid arthritis; tissue remodeling; macular degeneration; diabetic retinopathy; Alzhelmer's disease; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terrett JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%; Score 1960.5; DB 19
53.6%; Pred. No. 4.8e-145;
ive 91; Mismatches 178;
                                                                                                                                                                  Human integrin ligand polypeptide ITGL-TSP.
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(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
AAW80285 standard; Protein; 967
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Best Local Similarity 53.6
Matches 388; Conservative
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Human; METH1; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; obler-Webber syndrome; plaque neovascularisation; telangiectasia; heamophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
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metalloprocease and TH for thrombospondin; see AAB50002 and AAB50003).
METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer. The present sequence is a protein isolated in the present invention.
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                                                                                                                                                                                            SH;
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                                                                                                                                                                                                                                                                                                                                                                        present invention relates to human METH1 and METH2 (ME
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                            SMITHKLINE BEECHAM CORP.
BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                        Claim 15; Pages 759-763; 768pp; English.
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               HUMAN GENOME SCI INC
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                                                            IRUELA-ARISPE L.
HASTINGS G A.
                                                                                          RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
TERRETT J A.
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                              506
                                                548
                                                                                                                     563
                                                                              623
                                                                                                                                                 GTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New TANGO polypeptides and nucleic acids encoding them - useful as diagnostic agents and for treating disorders caused by aberrant expression of TANGO
                                                                                                                                                                                                                                                                                                                                          Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
                             CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE
                                                                                                           SCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                             AAY04142 standard; Protein; 967 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US16502
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97US-0054966
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention and protection.
                                                                                                                                                                                                                                                                                                                     Human Tango-71 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-167426/14.
N-PSDB; AAX19955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodearl ADJ,
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727 KISG 730
                                                                                                                                                                                        KVTG 687
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06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                   detection.
                                                                                                                                                                                                                                                                                 AAY04142;
                                                                                                                                                                                                                                                                                                                                            Human;
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SCNLEDCPDN-NGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAK 665
                                                                                                                                                                  : | | ||: |||| ||: ||:|| DQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 136
                                                                                                                                                                                                                  115 AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG 165
                                                                                                        81
                                                                      1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; ADAMIS-1; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis;
                                                                                                                                                                                                                                     61 QEDFYLHLTPDAQFLAPAFSTEHLG------VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
                                                                                                                                                                                                                                                                                                                     197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPOWS-----PQDPALQGVGQP-TGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 RHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN
                                                                                                          LLILLAAALLAVSDALRRPSEEDEELVVP-ELE-----RAP---GHGTTRLRLHAF
                                                                                                                                                                                                                                                                                       PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
                                     67;
                                   178; Indels
Score 1959.5; DB 2
Pred. No. 5.8e-145;
1; Mismatches 178;
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                                   91;
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52.3%;
ilarity 53.6%;
Conservative 9
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                    Similarity
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KISG 729
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 Query Match
Best Local Simi
Matches 388;
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13-JUN-1997;
13-JUN-1997;
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13-JUN-1997;
13-JUN-1997;
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                                                                                                                                                                                                                                                                                        The present sequence is mouse metalloproteinase ADAMTS-1. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family, Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or angiogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                  Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's, disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLVVVKILVIYEEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTAILFTRQDLC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 TAFQEDFYLHLIPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATICDILGMADVGIMCDPKRSCSVIEDDGLPSAFTIAHELGHVFNMPHDNVKVCEEVFG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLLLGILTLAFAGRTAGG -- FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LILLASITMILCARGAHGRPTEEDEELVLP-SLE------RAPGHDSTTTRL--RL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPGSAAALSLCEGVRGAFYLQGEEFFIQPAPGVATERLAPAVPEEESSARPQFHILRRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 896;
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52.3%; Pred. No. 4.6e-144;
.ive 95; Mismatches 176; Indels
autoimmune disease; brain tumour; brain injury.
                                                                                                                                             (NEUR-) NEUROCRINE BIOSCIENCES INC.
                                                                                                                                                                                                                                                                  Disclosure; Fig 17; 129pp; English.
                                                                                                                                                                      Clark M, Maki RA;
                                                                                              08-MAR-2000; 2000WO-US06237.
                                                                                                                      99US-0264585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 52.3
nes 381; Conservative
                                                                                                                                                                                           WPI; 2000-594326/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 AA;
                                               WO200053774-A2.
                         Mus musculus
                                                                                                                     08-MAR-1999;
                                                                       14-SEP-2000.
                                                                                                                                                                    Kelner GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thynus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                  618
407 VIGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLY 466
                                                                                                                                                                                                                                                                                                                                 645 TCEAKGIGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGN 704
                                                                                         GACVERHNINKH --- RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                          TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
                                                                                                                                                                                                                                                                                               RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL
                                                                                                                                                                                                                                                                                                                                                                                                                  ICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein encoded by gene 64 clone HOUCQ17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW78189 standard; Protein; 967 AA.
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97US-0049548.
97US-0049549.
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970S-0049606
970S-0049607.
970S-0049608.
970S-0049609.
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WPI; 2000-072633/06.
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KISG 729
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The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04440; amino acid sequences: AAX043125) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).
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Y, Young P;
                                                                                                                                                                                                                                                                                                                                         New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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ben SM, Shi
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en HS, Rosen CA, Ruben SM,
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GON-1; metalloproteinase; cell migration; modulator; ADAMTS-1; metalloproteinase domain; thrombospondin domain; abnormal cell migration; organ shaping; sterility; cancer metastasis.
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                                                                                      DILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN
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                                                           KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC
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The present sequence represents a murine ADAMTS-1 protein. ADAMTS-1 is a metalloprotease, a C. elegans GON-1 protein, that lacks a transmembrane domain and possesses a predicted metalloprotease domain between residues to metalloprotease domain between residues comain and possesses a predicted metalloprotease domain between residues to produce elongated tubes, whereas in males, GON-1 is required for migration of a single linker cell to produce a single clongated tube. The protein is used in the method of the invention. The specification describes a method for identifying a modulator of a protein that contains a method for identifying a modulator of a protein that contains a method for identifying a modulator of a protein that contains a method for identifying a modulator of a compound, and determining any change in migration or shape of the cell compound, and determining any change in migration or shape of the cell attributable to the test compound. The compounds identified are contential therapeutic modulators of abnormal cell migration and organ shaping, e.g. for rendering animals (specifically nematodes) sterile and for inhibiting cancer metastases. 

950 AA; Sequence

17; TCEARGIGYFFVLOPRVVDGTPCSPDSTSVCVQGOCVKAGCDRIIDSKKKFDKCGVCGGN 703 :| | ||:||| |:|||| :||| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :| 383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY 442 406 VSGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLY 465 GACVERHNINKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 558 RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL 618 619 ICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGD 678 ----RRGSGGAKCGVMD-----DETLPTSDSRPESQNTRNQWPVRDPTPQDAGKP 226 323 GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG 382 443 TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK 501 58 TAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNA 109 EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161 Query Match 51.3%; Score 1921; DB 21; Length 950; Best Local Similarity 52.0%; Pred. No. 5.9e-142; Matches 379; Conservative 95; Mismatches 177; Indels 78; Gaps 20 LLLLASITMLLCARGAHGRPTEEDEELVLP-SLE-----RAPGHDSTTTRL--RL 66 1 MLLLGILTLAFAGRTAGG - FEPEREVVVPIRLDPDINGRRYYWRGP - EDSGDQGLIFQI 57 ----SGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI 162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRR---------Best Local Simitants, Matches 379; Conservative 526 110 263 502 559 585 181 207 qq 셤 δŏ 셤 δ g g q 8 δ g ò δ g g ò ò à à g δý ò

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
Sequence:
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Sequence 3 Sequence 1

US-09-411-329C-3 US-09-411-329C-17

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RESULT 1
US-09-130-491-2
i Sequence 2, Application US/09130491
i Patent No. 6416974
i Patent No. 6416974
i GENERAL INFORMATION:
APPLICANT: HOLTZMAN. DOUGJAS A.
APPLICANT: HOLTZMAN. DOUGJAS A.
TITLE OF INVENTION: TANGO-71, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/0410101
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER PLING DATE: 1997-09-05
EARLIER PLING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                     Sequence 4, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 13, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 64, Appli
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 Sequence 3, Al
Sequence 6, Al
Sequence 18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||| || || :| :|| || :| :|| || 36 ILLLAAALLAVSDALGRPSEEDEELVVP-ELE------RAP---GHGTTRLRHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.4%; Score 1960.5; DB 4; Length 967;
53.6%; Pred. No. 9.6e-156;
.ive 91; Mismatches 178; Indels 67;
US-08-836-442-3

US-09-026-001A-18

US-09-9026-001A-18

US-09-920-048-4

US-09-920-048-2

US-09-920-048-2

US-09-026-001A-10

US-08-477-407-4

US-08-477-407-4

US-08-477-407-4

US-08-484-355-4

US-08-477-407-3

US-08-123-542-3

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Matches 388; Conservative
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6211
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CORGANISM: Homo sapiens
US-09-130-491-2
  SEQ ID NO 2
LENGIH: 967
  Query Match
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655

539 595 595

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HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                                                                                                              420 YGHCLLDKPEAPLHLPVTFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGH 479
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                                        AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG
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46.7%; Pred. No. 3.4e-132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
APPLICANT: Mirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding
FILE REFERENCE: 26473/4007/10-30-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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US-09-369-364A-9
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                         CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                       SCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN 623
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                                                                                                                                         RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
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89 GETLLLELEQDSGVQVEGLTVQYLGQAPE-LLGGAEP--GTYLTGTINGDPESVASLHWD
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                                                                  HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BILSTOL Myers Squibb Company
TITLE OF INVENTION: AGERECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.1%; Score 1689.5; DB 4; Best Local Similarity 47.2%; Pred. No. 4e-133; Matches 328; Conservative 103; Mismatches 215;
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; ORGANISM: Homo sapiens
US-09-122-126B-2
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US-09-122-126B-2
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Length 905; Indels

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194 RRAGFGES---RSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 QRRG-----VPGGPS------GDPTSRCGVASGWNPAIL--RALDPYKP 193
SGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLR---RCFYS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 GDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPL---PNASAPAAQRNSQGA----HLL 157
                                                                                                                          SAIITEFLDDGHGNCLLDLPRKQILGPEELPGQTYDATQQCNLTFGPEYSVCPGMDVCAR
                                                                                                                                                                                      348 IEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACS
                                                               AAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTK
                                                                                                                                                                      LWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER-----HNLNKHRVDGSWAKW
                                                                                                                                                                                                                                   523 DPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREE
                                                                                                                                                                                                                                                                                               583 QCEAFINGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FITLE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SED ID NOS: 21
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09122126B
Patent No. 6451575
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-122-126B-15
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 SVNLVVVKVLIVEKERNGPEVSDNGGLILRNFCSNQRRFNKPSDRHPEHYDTAILFIRQN 336
                                                               VFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG 439
                                                                                                                          AS--YTLSQQCELAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTS 492
                                                                                                                                                                                                                                   CGEGKLCLKGACVERHNLN--KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPAN 550
                                                                                                                                                                                                                                                                                                 GGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGV 610
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                                              LCG-ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE 379
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 2647374007710-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILNG DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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43.0%; Score 1611; DB 4;
Best Local Similarity 47.3%; Pred. No. 1.7e-126;
Matches 305; Conservative 82; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09369364A; Patent No. 6391610; GENERAL INFORMATION:
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US-09-369-364A-2
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FACENTEAL INFORMATION:
APPLICANT: HOltzman, Douglas A.
APPLICANT: Goodearl. Andrew D.J.
TILE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT PELICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
SEALIER FILING DATE: 1997-09-06
NUMBER OF SEQ ID NOS: 16
SOOTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 QFTFGEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNK 243
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           HDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP
                                                      431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG
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llarity 63.6%; Pred. No. 1.9e-120;
Conservative 57; Mismatches 91;
                                                                                                                                                                                                                                                                                           RESULT 6
US-09-130-491-13
Sequence 13, Application US/09130491
; Patent No. 6416974
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es 269; Conserv
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362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKK
                                                                                                                                                                    TGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKK
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369, 364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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NAME/KEY: MOD_RES
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Similarity
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Matches 284;
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US-09-364A-7
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                                   GKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRT
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                                                                                                                                                                                                                                                 Sequence 15. Application US/09369364A
Patent No. 6321610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: HICHAIA, Satoshi
TITLE OF INVENTION: NuCleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 2647344007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Watch 37.2%; Score 1394.5; DB 4; Length 874; Best Local Similarity 44.6%; Pred. No. 2.2e-108; Matches 271; Conservative 86; Mismatches 202; Indels 49;
                                                                                                                                                                           652 GKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
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US-09-369-364A-15
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145 PAAQRNSQGAHLLQRRGVP----GGPSGDPTSRCGVASGWNPALLRALDPYKPRRAGFG 199
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                                                                                                                                                                         560 VKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLI
                                                                                          620 CRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDN
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38.4%; Pred. No. 1.1e-81;
tive 82; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TILE OF INVENTION: Nucleic Acids Encoding Zin;
FILE REFERENCE: 26473/400/7/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A;
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEC ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
SEC ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
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US-09-369-364A-7
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US-09-369-364A-22; Sequence 22, Application US/09369364A; Patent No. 6391610
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US-09-491-522-5
; Sequence 5, Application US/09491522
; Patent No. 6428998
; GENERAL INFORMATION:
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-5
                                                                                                                                                                                                                                                                                                                                                        26.8%;
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; OTHER INFORMATION: Xaa = M
US-09-369-364A-22
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NAME/KEY: MOD_RES
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STATE:
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Best Local 9
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Squence 16, Application US/09130491

Patent No. 6416974

GENERALI INFORMATION:

APPLICANT: HOLIZAMAN DOUGLAS A.

APPLICANT: GOOGGAI, Andrew D.J.

TITLE OF INVENTION: TANGO-71, TANGO-74, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT FILING DATE: 1996-08-07

EARLIER APPLICATION NUMBER: US 60/058,108

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-09-05

SARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                             572 YKGRYCVGERKRFRLCNLQACP--AGRPSFRHVQCSHFDAMLYKGQLHT----WVPVVND 625
   513 GTRCGENKWCLSGECVP-VGFRPEAVDGGWSGWSAWSICSRSCGMGVQSAERQCTQPTPK 571
                                                                                                                                                                                          LPGASYTLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKLCLKGACVERHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPA 549
                                                                                                          550 NGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSG 609
                                                                                                                                                                        610 VSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP--DSTSVCVQGKCIKAGCDGNLGSKK 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 CEEVFGKLRANHMASPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPED 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKC 672
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                                                                                                                                                                                                                                                                683 MEDRCGVCHGNGSTCHTVSG 702
                                                                                                                                                                                                                                    RFDKCGVCGGDNKSCKKVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.79
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Rattus rattus US-09-130-491-16
                                                                                                                                                                                                                                                                                                                             -09-130-491-16
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 IDOPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTR 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Colige, Alain
APPLICANT: Colige, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF OVERSESONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 ARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 LAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAG
GENERAL INFORMATION:

APPLICANT: Apte, Suneel
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SSQ ID NO 22
LENGTH: 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1004; DB 4; Length 51; Pred. No. 5.7e-76; 42; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 CDGIIGSKLQYDKCGVCGGDNSSCTKIVG 324
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 YSGDVN--AEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG-AHLLQR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 RGVPGGPSGDPTSRCGVASGWNPALLRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLI 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDK 615
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAF 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV---- 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 IAAAADPPGGPLGHGAERILAVPVRTDAQGRLVSHVVSAATSRAGVRARRAAPVRTPSFP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1211;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.1%; Score 976; DB 4; Length 12 Best Local Similarity 35.5%; Pred. No. 4e-73; Matches 260; Conservative 93; Mismatches 282; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --INGRR--
OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                            8389-0060-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LAFAGRIAG --- GFEPEREVVVPIRLDPD--
                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
TYPE: amino acid
                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: Single;
; TOPOLOGY: linear
US-09-491-522-5
                                                                FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0219-193A
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
ENGTH: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                     104 SGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG---AHLLQRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 LDPYKPRRAGFGESRSRRRSGRAKRFVSJPRYVETLVVADESMVKFHG-ADLEHYLLTLL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 STEPHAPGASEVLVTSRTWELAHQPLHSSDLRLGLPQKQHFCGRRKKYMPQPPKEDLFIL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 PDEYK---SCLRHKRSLLRSHRNEEL----NVETLVVVDKKMMQNHGHENITTYVLTIL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 ATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-NKVSDK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 NMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISHHADHTLSSFCQWQSGLMGKDGTR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 HPEYWDTAILFTRODLCG--ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 QGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSS------DLRRCFY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G----VPGGPSGDPTSR-----ILRA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLDQPSKPI---SLPEDLPGASYTLSQQCELAFGVGSKPCPY---MQYCTKLWC--TGKA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQC----EAFNG 589
516 CKLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 KGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.9%; Score 968.5; DB 4; Length 1224; 35.1%; Pred. No. 1.7e-72;
                                                                                                                                                                                                   Sequence 4, Application US/09930872
Patent No. 6448388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                              715 CGGDNSHCKVVKG 727
                                                                     675 CGGDNKSCKKVTG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sım
Matches 243;
                                                                                                                                                                               US-09-930-872-4
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                   82 EHLGVPLQGLTGGSSDLRRCFYSGDV-NAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLP 140
590 YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 VRTRRAAPAQIPGLSG-----GSEEDPGGRLFYNYTVFGRDLHLRLRFNARLVAPGATV 129
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                                                                                                                                                         Sequence 11, Application US/09491522

Patent No. 642898
GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Procokop, Darwin J.
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%; Score 944.5; DB 4; 33.5%; Pred. No. 1.7e-70; tive 96; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLLGILTLAFAGRTAG------GFEPEREVVVPIRLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FREEESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE:
                                                                              8389-0060-688
                                                            VQGKCIKAGCDGNLGSKKRPDKCGVCGGDNKSC
                                                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds, LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1205 amino acids
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Best Local Similarity 33.5
Matches 256; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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US-09-491-522-11
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                                                                                                                                              247 ATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKV-TGNAALTLRNFCAWOKKLNKVSDK 305
                                                                                                                                                                                                                                                                                                                                            DQP---SKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQY---CTKLWCTGKAKGQM 478
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                                                                                                                                                                                                                                                                                                                   366 VFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLL 424
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; Patent No. 6391610
; GENERAL INCPRARTION:
APPLICANT: Apte, Suneel
; APPLICANT: Hischarta, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding 2inc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 17
; SEQ ID NO 17
TCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHG-AD
                                                                                                                                                                                                                                  HPEYNDTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 VCQTRH-FPWADGTSCGEGKLCLKGAC-----VERHNLNKHRVDGSWAKWDPYGPCSR
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; Pred. No. 2.2e-69;
82; Mismatches 276;
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35.3%;
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US-09-369-364A-17
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Best Local Simi
Matches 232;
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us-10-009-332-1\_copy\_1\_687.rai

	LEHYLLTLATAARLYRHPSILNPINIVVVVVVVLLLRDRDSGPKVTGNAALTLRNFCAWQK 297	VEQYVLAIMNIVAKLEQDSSLGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQK 297	KLNKVSDKHPEYWDTALLFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVI 348	SIVNHSGHGNAIPENGVANHDTAVLITRYDICIYKNKPCGTLGLAR-WAECVSAREAAAS 356	EDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANP 402	RRTLAATSVHHCHEIGHTFGMNHDGVGNSCGARGQDPAKLMAAHITMKTNPFV 409	WSACSAAIIIDFLDSGHGDCLLDQPSK-PISLPEDLPGASYILSQQCELAFGVGSKPCPY 461	WSSCNRDYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHGVKSRQCKY 469	MQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDG 517	GEVCSELWCLSKSNRCITNSIPAAEGTLCQTHTIDKGWCYKRVCVP-FGSRPEGVDG 525	SWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGK 577	AMGPWTPWGDCSRTCGGGVSSSRHCDSPRPTIGGRYCLGERRRHRSCNTDDCPPGSQ 583	SFREEQCEAFINGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYV 630	DFREVQCAEFDSIPFRGKFYKWKTYRGGGVKACSLTSLAEGFNFYTE 630	LAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKRRFDKCGVCGGDNKSCKKVTG 687	RAAAVVDGTPCRPDTVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEG 687
181	238	238	298	298	349	357	403	410	462	470	518	526	578	584	631	631
qq	Οy	DP	Qy	qq	ΟŶ	qq	οy	qq	δλ	QΩ	ογ	qq	οy	qa	Qy	QQ

Search completed: April 29, 2003, 17:11:55 Job time : 15.1439 secs

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US-10-178-708-352
US-10-174-572-352
US-10-174-588-352
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US-10-175-740-352
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Matches 686; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homo sapiens
  RESULT 1
US-09-965-631-4
  10688 5 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 1 5 10688 
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Sequence 4, Appli
Sequence 7, Appli
Sequence 6, Appli
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Sequence 12, Appli
Sequence 12, Appli
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                                                                                                                                                  (without alignments)
3604.758 Million cell updates/sec
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                                                                                                                                                                                                    US-10-009-332-1_COPY_1_687
3744
1 MLLGILTLAFAGRTAGGFE......RFDKCGVCGGDNKSCKKVTG 687
                                                                                                                       April 29, 2003, 17:12:21 ; Search time 15.2713 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_USECOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-91-987B-4
US-10-163-316-7
0 US-09-965-631-6
US-10-097-597-1
US-10-097-580-1
0 US-09-445-023A-1
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US-10-163-316-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 4, Application US/09965631
Patent No. US2020115842a1
GENERAL INFORMATION:
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
CURRENT APPLICANTON NO. US20020115842a1e1 Human Proteases and Polynucleotides Enco CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT PILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOGTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.8e-276;
0; Mismatches 1;
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US-10-176-758-352 US-10-176-758-352

US-10-097-597-12 US-10-097-580-12

Sequence

US-10-173-706-352 US-10-175-738-352 US-10-175-752-352 US-10-176-482-352

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                         241 YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWGKKLN
                                                                                                                                       DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVC
                                                                                                      QTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLAR
                                                                                                                                                                 RQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSINRLILA
                                                            HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                    APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and
TITLE OF INVENTION: Therefor
FITLE REFERENCE: MP101-02591RNM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/297,863
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 823;
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Pred. No. 2.3e-274;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                             GNLGSKKRFDKCGVCGGDNKSCKKVTG
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Best Local Similarity 96.5
Matches 685; Conservative
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LENGTH: 823
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Sequence 2, Application US/10105929

Sequence 2, Application US/10105929

Patent NO. US20020137142A1

GENERAL INFORMATION:

APPLICANT: HOLIZMAN. Douglas A.

APPLICANT: HOLIZMAN. Douglas A.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

FILE REPERENCE: 09404/041001,

CURRENT APPLICATION NUMBER: GARLIER APPLICATION NUMBER: 09/130,491

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-07

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-09-05
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FastSEQ for Windows Version 3.0
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Best Local Similarity 53.6%
Matches 388; Conservative
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ORGANISM: Homo sapiens
US-10-105-929-2
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US-10-105-929-2
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                                                                                                                                   197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS-----PQDPALQGVGQP-TGTGS 247
                                                        HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ 447
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                                                                                                                                                                                                                                                                         507 RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
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                                            GRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09321987B
Fatent No. US20020102210A1
GENERAL INFORMATION:
APPLICANT: Kimble, Judith E
APPLICANT: Kimble, Judith E
TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386
CURRENT APPLICATION NUMBER: US/09/321,987B
CURRENT FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
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Best Local Similarity 52.3%
Matches 381; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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US-09-321-987B-4
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KISG 729
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US-09-321-987B-4
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LENGTH: 950
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                                                                              110 EPDSFAAVSLCGGLRCAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG
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Publication No. US2002019770341

GENERAL INFORMATION:
APPLICAMT: Rapeller-Libermann, Rosana
TITLE OF INVENTION: 6552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MPIOL-025PINM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                      ----SGRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI
                                                                                                                                                                                                                                                         227 SGPGSIRKKRFVSSPRYVETMLVADQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 KLRANHAMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
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                                                                                                                                                          162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRR------
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Matches 381; Conservative
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ORGANISM: Mus musculus
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TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,
TITLE OF INVENTION: Pharmaceutical
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADA
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,597
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-160422
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64.0%; Pred. No. 2.4e-125;
tive 68; Mismatches 100;
                                   Score 1913; DB 10;
Pred. No. 4.7e-138;
0; Mismatches 1;
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Publication No. US20030022352A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hirose, Kunitaka
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
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                                     Query Match 51.1%;
Best Local Similarity 99.7%;
Matches 363; Conservative
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Matches 309; Conservative
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US-09-965-631-6
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APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Grant G
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|----RRGSGGAKCGVMD------DETLPTSDSRPESQNTRNQWPVRDPTPQDAGKP
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                        1 MLLLGILTLAFAGRTAGG--FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQI
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Patent No. US20020115842A1
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ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                             565 CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANG
                                                                                                        MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
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64.0%; Pred. No. 2.4e-125;
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APPLICANT: Harose, Kunitaka
APPLICANT: Inoguchi, Eiji
APPLICANT: Ishacasi, Michinori
APPLICANT: Ishiosa, Keiko
APPLICANT: Ishiosa, Keiko
APPLICANT: Matsushima, Kouji
APPLICANT: More Scolia
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: Composition and method of
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
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Patent No. US20020119167A1
GENERAL INFORMATION:
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Matches 309; Conservative
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ISG 489
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                                                                                                                                                                              ELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER 507
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Best Local Similarity 64.0%; Pred. No. 2.4e-125;
Matches 309; Conservative 68; Mismatches 100;
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APPLICANT: Inoguchi, Eiji
APPLICANT: Hakozaki, Michinori
APPLICANT: Hakozaki, Michinori
APPLICANT: Ishicka, Keiko
APPLICANT: Ishicka, Keiko
APPLICANT: Misushima, Kouji
APPLICANT: Muno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: Composition and method of
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT FILING DATE: 2002-03-15
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 14
SOFTHARE: PATENTIN VERSION 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10097580 Publication No. US20030032168A1 GENERAL INFORMATION:
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ISG 489
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US-10-097-580-1
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Sequence 12, Application US/10097580

Sequence 12, Application WS/10097580

Sequence 12, Application WS/1009032168A1

Sequence 12, Application WS. US20030032168A1

SET INCORMATION:

APPLICANT: HIGOSA, Kunitaka

APPLICANT: Insugeni, Editor, Yuakao

APPLICANT: Ishioka, Keiko

APPLICANT: Ishioka, Keiko

APPLICANT: Runo, Kouji

APPLICANT: Watushina, Wouji

APPLICANT: Watushina, Wouji

TITLE OF INVENTION: composition and method of immunologically analyzing human ADA

FILE REFERENCE: O57092

CURRENT FILING DATE: 2002-03-15

PRIOR APPLICATION NUMBER: US/10/097,580

CURRENT FILING DATE: 1999-12-03

PRIOR PPLICATION NUMBER: JP 9-160422

PRIOR PPLICATION NUMBER: JP 9-160422

PRIOR FILING DATE: 1997-06-03
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                                     ELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER
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SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 727
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ses 306; Conserv
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APPLICANT: Histore, Kunitaka
APPLICANT: Inoquchi, Eiji
APPLICANT: Inoquchi, Eiji
APPLICANT: Ishioka, Ketko
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Watsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS
TITLE OF INVENTION NUMBER: 09702-03-15
PRIOR APPLICATION NUMBER: 097445,023
PRIOR PILING DATE: 1999-12-03
PRIOR FILING DATE: 1997-06-03
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                                                                                                  249 QFTFGEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNK 308
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       MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 448
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63.4%; Pred. No. 2.3e-124;
ive 68; Mismatches 103; Indels
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SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENCTH: 727
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Best Local Similarity 63.4<sup>1</sup>
Matches 306; Conservative
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; ORGANISM: Mus sp.
US-10-097-597-12
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ISG 489
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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith Victoria
APPLICANT: Smith Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Schith Victoria
APPLICANT: Schith ACT Semin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
FILO APPLICATION FROM CONTROL SECOND FOR THE SAME
FILO APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
FILO APPLICATION FROM CONTROL SECOND FOR THE SAME
FILO APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
FILO APPLICANT: SECOND FOR THE SAME
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                                                                                                                                                            146 GGALLGVLQYRGAELHLQPLEGGTPNSA --GGPGAHILRRK----SPASGQGPMCNV--- 196
             TDM-KHFATPVHGSWGPWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRS 367
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                                                                                          **CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 352, Application US/10174590 ; Publication No. US20030008352A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-352
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US-10-174-590-352
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APPLICANT: Hakozaki, Michinori
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Muno, Kouji
TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT APPLICATION NUMBER: US 9-160422
PRIOR FILING DATE: 1997-106-03
NUMBER: OF SEO ID NOS: 14
249 QFTFGEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNK 308
                                                                                                                                                                       565 CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANG 624
                                                                                                                                                                                                       625 TGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKK 684
                                                                                                                                                                                                                                                                                                         209 RAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
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                                                                                                          MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
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; Pred. No. 2.3e-124;
68; Mismatches 103;
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Best Local Similarity 63.4%
Matches 306; Conservative
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MSG 489
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austria L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: And Zamin I.
APPLICANT: APPLICANT: ALONG Zemin I.
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APPLICANT: ALONG Zemin I.
APPLICANT: CANTENTION: SCREED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430RIGION
CURRENT APPLICANTON NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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536 VQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTN
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NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                           653 KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
                                                                                                                                                                                                                                                                                                                                                                           Sequence 352, Application US/10176758 publication No. US20030008353Al GENERAL INFORMATION:
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US-10-176-758-352
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US-10-176-758-352
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                  240 RYLLIVWAAAARAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGL
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                                                                        NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT
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45.1%; Score 1688.5; DB 9;
Best Local Similarity 47.2%; Pred. No. 1.6e-120;
Matches 328; Conservative 103; Mismatches 215;
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Publication No. US20030013153A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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US-10-175-737-352
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Title: US-10-009-332-1\_COPY\_1\_687
Perfect score: 3744
Sequence: 1 MLLGILTLAFAGRIAGGFE.....RFDKCGVCGGDNKSCKKVTG 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	+Oxa L.SHWEGE GOOD	hot ica	. –	. –	, 2	٠,		~	hypothetical prote			Catrocollastatin n	meltrin alnha . mo	٥	metalloproteinase	moreartoprocessings	hunothotical prote	nypormerical proce	fibroles redurated	motollase (EC 3.4.	meralloproteinase	trigramin program	fibring precurso	fibring which metal	atrolysin 7 (EC 3	vascular apoptosis	orthographic of the contract o	trimmein preemsor	disintegrin-like m	
SUMMARIES	ID		T00355	T21371	T47158	T18517	T18856	T16892	C89114	T34395	T15976	S24789	S55270	560257	S48160	548169	A60385	T00250	528259	HYSNEA	266260	A55796	A30065	104880	JC4342	S41609	JC7530	HYRSAC	843125	G02390	
	DB	7	~	7	7	~	~	~	N	7	~	N	7	7	7	~	~	2	2	-	۰,	1 (1	Н	~	2	7	7	-	~	N	
	Length	951	837	2165	550	1205	1444	860	1558	2167	957	571	609	903	617	549	826	951	789	411	407	616	480	478	481	414	610	414	481	Н	
æ	Query Match	52.0	45.1	32.7	29.0	26.2	12.8	11.4					0.6			8.4						8.0									
	Score	1947.5	1687.5	1223	1084	980.5	479	426.5	406.5	406.5	362	344.5	337	329	323.5	313	313	309.5	307.5	307	304	300.5	297	292	290.5	289	286.5	284	280	277.5	
	Result No.	1	71	e	4	ιń	9	7	ω .	o ;	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	

## ALIGNMENTS

RESULT TOOOLY General C. Spec A C. Spec B C. Spec B C. Spec B C. Spec B Spec A Spe	RESULT 1 T00017 C; Species: Mus musculus C; Date: 22-Jan-1999 #se C; Accession: 100017 R; Kuno, K; Lizasa, H; Genomics 46, 466-471 1 A; Title: The exon/intro A; Title: The exon/intro A; Accession: T00017 A; Accession: T0017 A; Ccsoretics: EMB A; Experimental source: CGenetics: Accession: Abants. C; Genetics: Accession: Acc	RESULT 1 T00017 T00017 T00018 C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000 R; Kuuo, K.; Lizasa, H.; Ohno, S.; Matsushima, K. Genomics 46, 466-471, 1997 A; Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gh; Reference number: 214055; MUID:98110583; PMID:9441751 A; Reference number: 214055; MUID:98110583; PMID:9441751 A; Residues: 1-951 «KUN> A; Residues: 1-9
	1 MLL 20 LLLL 20 LLLLL 58 TAFO 67 DAFG 110 EPDS: 122 DPGS: 162 VPGGI 181: 207:	MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYMRGP-EDSGDQGLIFQ1 57   1   1   1   1   1   1   1   1   1
oy Oy	263 NIVVV ::   287 SLVVV 323 GATTC	

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A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F25H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accassion: T21371; T24896
R;Gajadsty, S.
submitted to the EMBL Data Library, February 1996
A;Rcession: T21371
A;Rcession: T21371
A;Rcession: T21371
A;Rolecule type: DRIL
A;Residues: 1-2165 <MIL>
A;Cross-references: EMBL: Z69360; PIDN:CAA93287.1; GSPDB:GN00022; CESP:F25H8.3
A;Rcession: T24896
A;Rcession: T24896
A;Rcession: T24896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-2165 <MIL>
A;Rocession: T24896
A;Rcession: T24896
A;Residues: 1-2165 <MIL>
A;Rolecule type: DNA
A;Residues: 1-2165 <MIL>
A;Residues: 1-2165 <MIL
A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLLQRRGVPGGPSGDPTSRCGV-----ASGWNPAILRALDPYKPRRAGFGESRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLVRKFDPMHFKSFDHLNSTSVNETETTVATWQDQWEDVIER--------KARSR
                                                                                                                                                                           419 HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ
                                                                                                                                                                                                   420 YGHCLLDKPEAPLHLPVTFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG
                                                                                                                                                                                                                                                                                                   VQLARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSIN
                                                                                                                                                                                                                                                                                                                                                                                                        RLTL---AVAWYPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQG
                                                                           AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.7%; Score 1223; DB 2; Length 2165; Best Local Similarity 40.5%; Pred. No. 1.7e-78; Matches 257; Conservative 87; Mismatches 214; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: F25H8.3
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Or-Peb-1999 #sequence_revision Ol-Feb-1999 #text_change 21-Jul-2000
C; Accession: T00355
R; Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A; Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A; Reference number: 214142; MUID: 98403880; PMID: 9734811
A; Accession: T00355
A; Status: prediction of the coding sequences of unidentified human genes. X. The complete
A; Reference number: 214142; MUID: 98403880; PMID: 9734811
A; Molecule type: mRNA
A; Residues: 1-837 < ISB>
A; Residues: 1-837 < ISB>
A; Cross references: EMBL: AB014588; NID: 93327189; PIDN: BAA31663.1; PID: 93327190
A; Experimental source: brain
C; Genetics:
A; Genetics:
A; Csuperfamily: thrombospondin type 1 repeat homology
F; 519-575/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                    618
                                                                                                                                                                                                                                                                                                                                                                                                                   644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 GSHTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNG
                                                                                                                                                                                        RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL
                                                                                                                                                                                                                                                                                                                                                                                           GACVERHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                                                                                                                              443 TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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45.1%; Score 1687.5; DB 2;
Best Local Similarity 47.2%; Pred. No. 5.5e-112;
Matches 328; Conservative 103; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKSCKKVTG 687
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GSTCKKMSG 713
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Hypothetical protein DKFzp762C1110.1 - human (fragment)
C;Speciaes: Homo sapiens (man)
C;Speciaes: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47158
R;Blum, H; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224379
A;Accession: T47158
A;Status: preliminary
A;Accession: T47158
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-550 <AAA>
A;Cross-references: EMBL:Al162080
A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762C1110
C;Genetics:
A;Note: DKFZp762C1110.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                     |||||:::|: ::||::|| || ||::|| ||: || ||:|| ||:|:|| ||:|:|:|:|
VVVKLIVLATENAGPRITQNAQQILQDFCRWQQYINDPDDSSVQHHDVAILLTRKDICRS 386
                                                                                                                                                                                                                                                                          482 TRHFPWADGTSCGEGK--LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA 539
                                                                                                                                                                                                                                                                                                QPSKPISLPE----DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQ 481
                                                                                                                                                                                                                                                                                                                                                                                                                                       |----THWVPKYANVAPNERCKLYCRLSGSAAFYLLRDKVVDGTPCDRNGDDICVAGA 739
VVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 NHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQ 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       506 ERHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGDNKSC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 LRDCDSPRPRNGGYCVGQRERYRSCNTQECPWDT--QPYREVQCSENNKDIGIQGVAS
                                                                                                                                                          447 NKVCKFQSTKFDKTQFQNNFHIMAPTLEYNTHPWSWSPCSAGMLERFLENNRGQTQCLFD
                                                                                                                                                                                                                                 TNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGK
                                                                     T-TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEV---
                                                                                                                                        ------FGKLRAN----HMMSPTLIQIDRANPWSACSAAIITDFLDSGHG--DCLLD
                                                                                                                                                                                                                                                                                                                                                 RRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYN-----HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 1084; DB 2; 61.3%; Pred. No. 2.6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
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A; Description: catalyzes cleavage of the propeptides of type I and II collagens prior C; Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                 NyAlternate names: Procolagen N-Endopeptidase (EC 3.4.24.14) I - bovine
NyAlternate names: procolagen N-proteinase
C; Species: Bos primiqenius taurus (cattle)
C; Species: Bos primiqenius taurus (cattle)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R; Collige, A.; Nusgens, B.V.; Lapiere, C.M.
submitted to the EMBL Data Library, February 1996
A; Description: Cloning of the CDNA of the bovine procollagen I N-proteinase.
A; Reference number: 218941
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1205 < CCDL>
A; Cross-references: EMBL: X96389; NID:e990769; PID:e228215; PIDN:CAA65253.1
C; Genetics:
A; Gene: PC I-NP
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::| | ::| ::| ::| 36 VRTRRAAPAQIPGLSG-----GSEEDPGGRLFYNVTVFGRDLHLRLRPNARLVAPGATV 129
248 KGIGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EHLGVPLQGLTGGSSDLRRCFYSGDV-NAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 EWGE--SGATRVEPLLGTCLYVGDVAGLAESSSVALSNCDGLAGLIRMEEEEFFIEPLE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311. DTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 NASAPAAQRNSQG-AHLLQRRGVP-----GGPSGDPTSRCGVASGWNPAILRALDPYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 RRAGFGESRSRRRSGRAKRFVSIPRY-VETLVVADESMVKFHGAD-LEHYLLTLLATAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 LYRHPSILNPINIVVVKVLLLRDRDSGPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 HDWP-ALPQ-LPGLHYSMNEQCRFDFGLGYMMCTAFRTFDPCKQLWCS-HPDNPYFCKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFPWADGTSCGEGKLCLKGACV-----ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%; Score 980.5; DB 2;
.larity 33.9%; Pred. No. 1.4e-61;
Conservative 97; Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLLGILTLAFAGRTAG------GFEPEREVVVPIRLD--
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257; Conserv
                                                                                       KKISG 312
                                              KKVTG 687
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A; Cross-references: EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CESP:T1
C; Genetics:
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A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T19D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 TVAGYAPVKGMCSGVRSCTINEGLDFGSVFVVTHEMGHSLGMYHDGDNECD-----LRC- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMMSPTLIQIDRANPWSACSAAIITDFLDSGH-GD-----CLLD---QPSKPISLPE-D 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFR 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1: 1 | 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILGMADVGIMCDPKRSCSVIEDDGLPSAFITAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
--- TWSDCSVREFNAFLLQLDE 423
                                                                                                                                                              EEQ-----CEAF-----NGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 VETLVVADESM----VKFHGADLEHYLLTLLATAAR----LYRHPSILNPINIVVVKVLL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEGTYCGFGMICRQGQCVGSSQLMRVTV-GGWSTWNDRPAPTCGGRCSQCEIRGQIRIMR
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                                                                                        SGHGDCLIDQPSKPISLPE----DLPGASYTLSQQCELAFGVGSK-PCP----YMQYCTK
                                                                                                                                                                                                                                                                                    LWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE-RHNLNKHRVDGSWAKWD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 KGCPIQQCAVSGSITVQGQHRDCVNPAPNNGGKTCEGANIRGIVCG----ATSSNCLGFT
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11.4%; Score 426.5; DB 2; Length 860;
Best Local Similarity 26.3%; Pred. No. 2.2e-22;
Matches 150; Conservative 70; Mismatches 223; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T16892
R;Bentley, D.
Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-860 <BEN>
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    EMGHNMGNVHDGVQNQCNKGCCLMSAVNGAGKT - - -
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A; Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3;
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anglogenesis inhibitor homolog - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C; Accession: T18856; T24653
R; McMuray, A.
submitted to the EMBL Data Library, July 1995
A; Reference number: 219031
A; Accession: T18856
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1444 < WIL>
A; Cross-references: EMBL:250004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
A; Experimental source: clone C02B4
R; McMuray, A.
submitted to the EMBL Data Library, July 1995
A; Reference number: 219917
A; Accession: T24653
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1444 < WIL>
A; Residues: 1-1444 < WIL>
A; Residues: 1-1444 < WIL>
A; Experimental source: clone T07C5
C; Ganetine
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576 KFRTRQCDNPHPANGGRTCSGLAYDFQLCNSQDCPDALA--DFREEQCRQWDLYFEHGDA
                                                                                                                                                                                                                                                      -NHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCS-PDSTSV
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; Pred. No. 7.5e-26;
89; Mismatches 284; Indels 154;
                                                                537 QLARROCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGY-
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25.1%;
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Matches 177; Conservative
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A; Gene: CESP:C37C3.6b; CESP:C37C3.6a
A; Map position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 15
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A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TDFRAEQCSKFNDEALDGNYHK------WTP-YKG---KNKCELVCKPESGNFYYKW 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 QSDLIVELAVEVDENLWRHFSSKHGGMADRKLQDYTLTLLNNIQIMYYQPTASPPLTFRV 275
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                                                                                                                                                                                                                                                                                                                                                                  77 GNWGPWYPENECSRSCGGGYQLEKRQCSGD-----CTGASVRYISCNLNAC---ESG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                  577 KSFREEQCEAFN-----GYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVL 631
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                        517 GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASG
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                                                                                                                                                                                 Length 2167;
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                                                                                                                                                                             Query Match 10.9%; Score 406.5; DB 2; Best Local Similarity 43.8%; Pred. No. 1.7e-20; Matches 77; Conservative 18; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.7%; Score 362; DB 2; L
23.3%; Pred. No. 9.6e-18;
tive 90; Mismatches 293;
A; Experimental source: strain Bristol N2; clone C37C3
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                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 23.3'
Matches 190; Conservative
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:chr_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023; CESP:C37C3. C;Genetics: A;Gene: C37C3.6a
A;Gene: C37C3.6a
A;Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
C;Accession: T34395; T34394
R;Gelsel, C:; Bradshaw, H.
R;Gelsel, C:; Bradshaw, H.
B;Description: The EMBL Data Library, July 1996
A;Bescription: The sequence of C. elegans cosmid C37C3.
A;Reference number: 221518
A;Recession: T34395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roccule type: DNA
A;Recession: T24395
A;Recession: T34395
A;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1555, SKF' <GE2>
A;Cross-references: EMBL:UG4857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein C37C3.6a [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C691H #sequence_revision 10-May-2001 #text_change 10-May-2001
S;anonymous, The C. elegans Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEADCPLS'1Q'TTTPPMPHYHSVDQFAGKTNPYKEHKKTPFLNEWSGWSVWSECVTYDC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 KSFREEQCEAFN----GYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVL 631
                                --KLICRANGTGY 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                632 APKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
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                            574 ASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKC-
                                                                                                                                                                                                                                                                           DGNLGSKKRFDKC--GVCGG---DNKSCKK 684
                                                                                                                                                                                                                                                                                                                 H-TQGVKVRVRCLAGVCAGALRERQPCTR
                                                                                                                                                    FYVLAPKVVDGTLCSPDSTSV----
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Best Local Similarity 43.88
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A; Residues: 1-1558 <STO>
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A; Status: preliminary
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Catrocollastatin precursor - western diamondback rattlesnake
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Accession: S55270
R;Zhou, Q.; Smith, J.B.; Grossman, M.H.
Biochem. J. 307, 411-417, 1995
A;Title: Molecular cloning and expression of catrocollastatin, a snake-venom protein A;Reference number: S55264; MUID:95251603; PMID:7733877
A;Accession: S55270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------YIEFFVVVDQGTVTKNN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 NFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIED 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYR 130
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                                                                                                                                                                                                                                                                                                                                                             AGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAFQEDF-YLHLTP 70
                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATRPKGAVQPKYEDA--MQYEFKVNGEPVVLHLEKNKG------LFSKDYSEIHYSP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RETYFIEPLKLPDSEAHA------VFKYENVE--KEDEAPKMCGVTQNWKSYEPIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 YSPINLVVAVIMAHEMGHNLGIHHDT-----GSCSCGDYPCIMGPT-ISNEPSKFFFS
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                                                                                                                                                                                                                                                                                                          201;
A; Note: 361-Val was also found
C; Comment: Inhibits collagen- and ADP-induced platelet aggregation.
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Keywords: hydrolase; metalloproteinase; venom; zinc
F; 360-571/Product: jararhagin C #status experimental <AMT>
F; 252-299, 305/Binding site: zinc (His) #status predicted
F; 296/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                    Query Match 9.2%; Score 344.5; DB 2; Best Local Similarity 22.7%; Pred. No. 9.3e-17; Matches 160; Conservative 88; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ASQLAFTAEQQRYDPYK-----
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NiAlternate names: single chairac (fragment)
NiAlternate names: single chairac (fragment)
NiAlternate names: single chairaca (fragment)
NiAlternate names: single chairaca (jararaca)
C; Species: Bothrops jazaraca (jararaca)
C; Species: Bothrops jazaraca (jararaca)
C; Species: Debt. 1902
C; Species: Debt. 1902
C; Accession: S24789
NiAlternate number: V: Mittara, S: Shima, H: Yoshida, E.; Yoshioka, A.; Hirano, K.; Bidonhu. 201, 331-339, 1994
NiTtle: A 28 Kap protein
NiMolecule type: mRNA
NiMolecule type: mRNA
NiMolecule type: mRNA
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                                                                                                              439 ATICSOCTCNGILGSVGLAIARRTCSAPYPANGGSDCVGSTSRAVLCSROCGRASKSVDE 498
                                                                                                                                                                       ---FGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPW----A 488
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        ---KSDTLFTGTFCGPSKWCQLGRCVPWTGTNEIQPTVQHVAPVVTTLPSRIDGSWSGWG 438
                                                                                                                                                                                                                                                                                                             499 YISDKCMEQKRLKNDRELTGKGSQLNRFPQRACKVFCDVQ---QHYGSQRNYRFFGDNLP
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                                                              ---YTLSQQCELA-
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                                                                 --PSKPISLPEDLPGAS---
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Length 903;

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metalloproteinase (EC 3.4.24.-) H-I precursor - carpet viper N; Contains: disintegrin C; Species: Echis pyramidum leakeyi C; Species: Echis pyramidum leakeyi C; Date: 19-War-1997 *text_change 21-Jul-2000 C; Accession: S48160 *sequence_revision 19-Mar-1997 *text_change 21-Jul-2000 C; Accession: S48160 *sequence_revision Theakston, R.D.G.; Crampton, J.M. Eur. J. Biochem. 224, 483-488, 1994 A; Title: Cloning of metalloprotease genes in the carpet viper (Echis pyramidum leake A; Reference number: S48160; MUID: 95010025; PMID: 7925363
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A; Molecule type: mRNA
A; Residues: 1-617 < PAI>
A; Cross-references: GB: X78970; NID: 9763092; PIDN: CAA55565.1; PID: 9763093
                                                                                                                                                                                                                                                                                                         15 LLLALAGALLAPRAARGMSLWDQRGAYEVARASL--LSKDPGIPGQSI----PAKDHPDV
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501 PANVYLHDGHPCQGVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGNC
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                                                    Query Match 8.8%; Score 329; DB 2; Length 90. Best Local Similarity 21.5%; Pred. No. 2e-15; Matches 159; Conservative 74; Mismatches 245; Indels
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S60257
meltrin alpha - mouse
C.Species: Mus musculus (house mouse)
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C.Accession: S60257
R; Yagami-Hiromasa, T.; Sato, T.; Kurisaki, T.; Kamijo, K.; Nabeshima, Y.I.; Fujisawa-Seh Nature 377, 652-656, 1995
A; Title: A metalloprotease-disintegrin participating in myoblast fusion.
A; Recession: S60257; MUD: 96026308; PMID: 7566181
A; Recession: S60257; MUD: 96026308; PMID: 7566181
A; Accession: S60257
A; Multiple: Residues: 1-903 < AGS
A; Cross-references: EMBL: D50411; NID: 91054586; PIDN: BAA08912.1; PID: 91054587
C; Superfamily: mouse meltrin alpha; disintegrin homology
F; 421-503/Domain: disintegrin homology < PIS>
F; 349/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                              50 DQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 DADSTASISACNGLKGHFKLQGEMYLIEPLKLPDSEAHAVYKYENVE-----KE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 EDAMQYELKVNGEPVVLHLGKNKGLFSKDYSETHYSPDGREITTYPLVEDHCYYHGRIEN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 EPDSFAAVSLCGGLRGAFGYRGAEYVISP--LPNASAPAAQRNSQGAHLLQRRGVPGGPS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEALKMCGVTQNW------ESYEPIK-------KASQLVVTAEHQKYNPFRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 VETLVVADESMVKFHGADLEHY---LLTLLATAARLYRHPSILNPINIVVVKVLLLRDRD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGPKVT -- GNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMAD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KITVKPEAGYTLNAFGEWRKTDLLTRKH----DNAQLLTAIDL-----DRVIGLAY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGTMCDPKRSCSVIED----DGLPSAFTTAHELGHVFNMPHDN-VKVCEEVFGKLRANHMM 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 SPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP----SKPISLPEDLPGASYTL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 EPSTF-----FSNCSYFECWDFINNHNPECILNEPLGTDIISPPVCGNELL----EV 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEECD-----CGTPENCONECCDA----ATCKLK-----SGSQCGHGD-----C 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSCNLEPCP------SSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYS 608
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                              A;Molecule type: mRNĀ
A;Residues: 1-609 <2HO>
A;Cross-references: GB:U21003; NID:g710353; PIDN:AAC59672.1; PID:g710354
C;Superfamily: mouse meltrin alpha; disintegrin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIP-----RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGAC
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                                                                                                                                                                                                                                                ; Score 337; DB 2; Length 609;
; Pred. No. 3.4e-16;
90; Mismatches 259; Indels 160;
                                                                                                                                                                                                                                                9.0%;
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Best Local Similarity 22.8 Matches 150; Conservative
preliminary
A;Status:
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427

560

---GOMVCQTRHFPW 487

464

536

667

----CAMOCHGRGV

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F;1-138/Domain: propeptide (fragment) #status predicted <PRC F;139-549/Product: metalloproteinase H·II #status predicted F;350-432/Domain: disintegrin homology <pre>CDIS>
F;284/Active site: Glu #status predicted
                                                                                                                      Query Match
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C; Species: Echis pyramidum leakeyi
C; Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jun-2000
C; Accession: S48169
R; Paine, M.J.I.; Moura-Da-Silva, A.M.; Theakston, R.D.G.; Crampton, J.M.
Eur. J. Blochem. 224, 483-488, 1994
A; Title: Cloning of metalloprotease genes in the carpet viper (Echis pyramidum leakeyi).
A; Reference number: S48160; MUID:95010025; PMID:7925363
                                                                                                                                                                                               27;
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                                                                                                                                                                                                                                                                                                                                                   161
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Residues: 1-549 cPAI.
Cross-references: EMBL:X78971; NID:9763094; PIDN:CAA55566.1; PID:9763095
Superfamily: mouse meltrin alpha; disintegrin homology
                                                                                                                                                                                                                                                                        PEQKYEDIMRYEFKVNGEPVVLHLEKNKGLFSEDYSETHYSPDGREITTNPPVEDHCYYH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 DVGTMCDPKRSCSVIED---DGLPSAFTTAHELGHVFNMPHDNVKV-CEEVFGKLRANHM 389
                                                                                                                                                                                                                                     PEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYS 104
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metalloproteinase (EC 3.4.24.–) H-II precursor – carpet viper (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGPSGDPTSRCGVA-SGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVV-------VKVLLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 FVVVADYIMYRKYNND-----STAVRRIYEIVNILNMVYIVFNIHVALTHIEIWSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 MSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYT-LSQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 PEPVF-----SFSNCSRNDYRSFRNSDQSKCIDNKPLKTDIVSPSVCGNYFVEVGEEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 ARTECRRKIDDCDVPEYCTGQSGECPLDVFQRNGQPYQSNNGYCYNGNCPILKNQCIHLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GKYCEGVRVKYRSCNLEPCPSSASGKSF
                                                                                                                                                                                                                                                                                                                GDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPL--PNASAPAAQRNSQGAHLLQRRGV
                                                                                                                                                                                                                                                                                                                                                   110 GRIQNDADSTASMSACNGLKGYFMLRGETYLIEPLKIPDSEAHAVYKYENVE-----
                                                                                                                                                            617;
                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---NCQAFFS---SRN------PDYGMVDIGTKCADGKVCNSN 607
                         C;Keywords: hydrolase; metalloproteinase; venom
F;1-18/nomain: signal sequence #status predicted <SIG>
F;19-192/Domain: propeptide #status predicted <PRO>
F;193-617/Product: metalloproteinase H-I #status predicted
         Superfamily: mouse meltrin alpha; disintegrin homology
                                                                                                                                                          8.6%; Score 323.5; DB 2;
llarity 23.2%; Pred. No. 3.1e-15;
Conservative 74; Mismatches 267;
                                                                                                  F;403-485/Domain: disintegrin homology <DIS>F;337/Active site: Glu #status predicted
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                                                                                                                                                                         Best Local Similarity
Matches 150; Conserva
                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486
                                                                                                                                                                                                                                                                                                                                                                                                                    461 YMQYCTXLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWA 520
                                                                                                                                                                                            GLEGAFGYRGAEYVISPL--PNASAPAA-----QRNSQGAHLLQRRGVPGGPSGDPTSR 173
                                                                                               62 EDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCG 121
                                                                                                                                RKENDVPIPCAQEDVKCGRLFCETEPNMCRYPYGDEGMVDPGTKC--EDKKVCINGKCI 543
                                                                                                                                                                                                                                                                                                                       521 KWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AECLRMFSTRWKIMPKLSLLLOWTCPINQYQCYAHFGQNAVVGQDACFEINKEGKGDFYC
                                                                                                                                                                                                                                                                                                                                                                                           233 FHGAD--LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 SVIEDDGLPS----AFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 PWSACSAAIITDFLDSGHGDCLLDQPSK-PISLPEDLPGASYTLSQQCELAFGVGSKPCP
                                                                                                                                                                                                                          CGVA-SGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFCAWQKKLNKVSD-----KHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KLICRA--NGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCI
Length 549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEQCEAFNGYNHSTNRLTLAVAW---VPKY-----SGVSPRDKC-
                                                  77; Mismatches 234;
  8.4%; Score 313; DB 2; 23.7%; Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 29, 2003, 17:13:30 Job time: 20.8904 secs
                              Best Local Similarity 23.78
Matches 156; Conservative
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GenCore version 5.1.4_p5_4578
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using sw model protein search, protein MO

April 29, 2003, 17:10:24; Search time 8.4611 Seconds (without alignments) 3367.676 Million.cell updates/sec Run on:

1 MLLLGILTLAFAGRTAGGFE......RFDKCGVCGGDNKSCKKVTG 687 .US-10-009-332-1\_COPY\_1\_687 3744 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homo	uns u	Q9wuq1 rattus norv	Q9up79 homo sapien	homo	gnw		homod	homo	rattn	homo	рошо	homo	h ada	b ada	homod	^	bos t		P78325 homo sapien		homo sapi	bothr	เสนาย	homo	3 homo	u snw ț	mus	mus m	Q9p0k1 homo sapien	omod 1	u snw	Q63180 rattus norv
SUMMARIES		ATS1_HUMAN	ATS1_MOUSE	ATS1_RAT	ATS8_HUMAN	ATS4_HUMAN	ATS8_MOUSE	ATS5_MOUSE	ATS5_HUMAN	ATS9_HUMAN	ATS4_RAT	ATS7_HUMAN	AT10_HUMAN	AT12_HUMAN	ATS2_HUMAN	ATS2_BOVIN	ATS3_HUMAN	ATS6_HUMAN	ATS4_BOVIN	ATS5_BOVIN	AD08_HUMAN	AD28_MACFA	AD33_HUMAN	DISJ_BOTJA	AD28_MOUSE	AD28_HUMAN	AD19_HUMAN	AD12_MOUSE	AD19_MOUSE	AD22_MOUSE	AD22_HUMAN	AD12_HUMAN	AD08_MOUSE	AD07_RAT
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macaca fasc	028475	AD07_MACFA	-	116	6.9	257	45
~	042596	AD22_XENLA	<del>, -i</del>	932	7.0	260.5	44
homo sapien	09h2u9	ADO7_HUMAN	Н	754	7.0	260.5	43
mus musculu	Q923w9	AD33_MOUSE	Н	797	7.2	268	42
mus musculu	Q9r1v4	AD11_MOUSE	Н	773	7.2	270.5	41
crotalus at	P34182	HRTE_CROAT	Н	478	7.3	273.5	40
homo sapien	Q13444	AD15_HUMAN	П	814	7.4	277.5	39
homo sapien	075078	AD11_HUMAN	Н	769	7.5	279.5	38
crotalus at	P15167	HRTD_CROAT	Н	414	7.6	284	37
mus musculu	035227	AD07_MOUSE	Н	788	7.7	288	36
agkistrodon	Q9pw35	ACLA_AGKAC	Н	413	7.9	296	35
trimeresuru	P15503	DISA_TRIGA	7	480	7.9	297	34

## ALIGNMENTS

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Varquez F., Hastings G., Ortega M.-A., Lane T.F., Olkemus S., Lombardo M., Iruela-Arispe M.L.;
"METH-1, a human ortholog of ANDAMS-1, and METH-2 are members of a new femily of proteins with anglo-linhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-20289799; PubMed=10830953; Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Hattori M., Fujiyama A., Ishii K., Totoki Y., Chol D. K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schlilhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
ATSI_HUMAN STANDARD; PRT; 967 AA.

QUPHER; Q9UP80; Q9HR3; Q9Px0; Q9NSJ8;
30-MAY-2000 (Rel. 39, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondim motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).

ADAMTS1 OR METH1 OR KIAA1346.
                                                                                                                                                                                                                                                                                                      21 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000)
                                                                                                                                                   Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-Endothelial cells;
MEDLINE-20247184; PubMed-10785405;
Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,
Rosenthal A., Thierauch K.H.;
"Differential gene expression by endothelial cells in distinct
anglogenic states.";
Bur. J. Blochem. 267:2820-2830(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Heart;
MEDLINE-99367466; PubMed-10438512;
                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
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Blum H., Bauerasachs S., Mewes H.-W., Weil B., Wiemann S.;
Blum H., Bauerasachs S., Mewes H.-W., Weil B., Wiemann S.;
Blum H., Bauerasachs S., Mewes H.-W., Weil B., Wiemann S.;
Blum H., Bauerasachs S., Mewes H.-W., Weil B., Wiemann S.;
INVOLVED IN INTERNOVER GRECAN, A CATTLAGE PROTEGORIC INHIBITOR ACTIVITY. ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH ACTIVITY. PROCESSES A WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE.
CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE.
CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE.
CACHEXIA. MAY PLAY A CRITICAL ROLE SAGRECAN AT THE 1938-GLU-1-LEU-1939
SITE, WITHIN THE CHONNENIT SUIGNARY SIMILARITY).
C-1- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
C-1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TICHT INTERACTION WITH THE EXTRACELULAR MATRIX.
C-1- POWALITY THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Back A., Riages S., Henig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00000; tsp_1; 6.
Pfam; PF001000; tsp_1; 6.
Pfam; PF01010; Tsprolysin; 2.
Pfam; PF010109; Tsp1; 3.
PR051TE; PS001215; DAPA_MERRO; 1.
PR051TE; PS001215; DAPA_MERRO; 1.
PR051TE; PS00102; TSP1; 2.
PR051TE; PS001014; ZINC_PR0TEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ADAMTS-1.
CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i-SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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EMBL; AF060152; AAD48080.1; ALT_INIT.
EMBL; AR207664; AAF23772.1; -.
EMBL; AB037767; BAA92584.1; ALT_INIT.
EMBL; AP001697; BAA95502.1; -.
EMBL; AL162080; CAB82413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ninerpro: IPR001762; Disintegrin.
InterPro: IPR001807; Pep_M12B_propep.
InterPro: IPR001509; Reprolysin.
InterPro: IPR0001804; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                            SEQUENCE OF 418-967 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; M12.222; -. Genew; HGNC:217; ADAMTS1.
                                                                                                                                                    Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                   TISSUE-Melanoma;
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METAL
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SIGNAL
PROPEP
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 DOQLDLEIRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 KTD-RKHFDTPFHGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYR
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720 N-LINKED (GLCNAC. . .) (POTENTIAL).
744 N-LINKED (GLCNAC. . . .) (POTENTIAL).
727 P -> A (IN REF. 4 AND 5).
746 Q -> H (IN REF. 1).
756 S -> H (IN REF. 1).
757 S -> N (IN REF. 1).
758 Mw; C189389324741ED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                         Length 967;
                                                                                                                                                                                                                                                                                                                    ; Score 1960.5; DB 1; Length
; Pred. No. 2.9e-138;
91; Mismatches 178; Indels
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                                                                                                                                                                                                                                                                                                                         52.4%; Score 1960.5;
                                                 TSP TYPE-1 2.
TSP TYPE-1 3.
                                                                                                                                                                                                                                                                                                                                                        53.6%;
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Matches 388; Conservative
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KISG 729
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ID ATS1_N
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PTM: THE PRECURSOR IS CLEADED BY A FURIN ENDOPERTIDASE.

SIMILARIT: BELONGS TO PEPTIDASE FAMILY MI2B.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION?
          30-MAY-2000 (Rel. 39, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWIS-1 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).
                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of a gene encoding a new type of metalloproteinase-
disintegrin family protein with thrombospondin motifs as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cathepsin L proteases.";

Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).

-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEGGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIGGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ÁTTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-1-LEU-1692 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: SECRETED, ASSOCIATED WITH THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Progesterone-regulated genes in the ovulation process: ADAMTS-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-1, OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA CELLS OF PREOVULATORY FOLLICLES.
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND INDUCTION.
MEDLINE-20243757; PubMed-10781075;
Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.;
                                                                                                                                                                                                                 Kuno K., Lizasa H., Ohno S., Matsushima K.;
"The exon/Intron organization and chromosomal mapping of the mo
ADAMTS-1 gene encoding an ADAM family protein with TSP motifs."
Genomics 46:466-471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99303657; PubMed=10373500;
Kuno K., Terashima Y., Matsushima K.;
"ADAMTS-1 is an active metalloproteinase associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M., Ohno H., Matsushima K.; Matsushima K.; "ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan."; FEBS Lett. 478:241-245(2000).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97150761; Pubmed-8995297;
Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION, AND MUTAGENESIS OF GLU-403,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 274:18821-18826(1999),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20389568; PubMed=10930576;
                                                                                                                                                                                                   MEDLINE=98110583; PubMed=9441751;
                                                                                                                                                                                                                                                                                                                                                                           Inflammation associated gene.";
J. Biol. Chem. 272:556-562(1997).
                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular matrix.
                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                 Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION.
                                                                                    ADAMTS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161
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SNART; SN00209; TSP1; 3.
PROSITE; PSS0215; ADAM MEPRO; 1.
PROSITE; PSS0427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PSS00427; TSP1; 3.
PROSITE; PSS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Indicate the strategillar matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRR--------
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CYSTEINE SWITCH (POTENTIAL)
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
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T -> S (IN REF. 2)
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TSP TYPE-1 2.
TSP TYPE-1 3.
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CYS-RICH.
                                                                                                                                                   EMBL; AB001735; BAA24501.1; ALT_INIT. EMBL; D67076; BAA11088.1; ALT_FRAME. MEROPS; M12.222; ... MIS. M22.22; ... M22.22; ... M22.23; ... M22.24; ... M22.24; ... InterPro; IPR001762; Disintegrin. InterPro; IPR001870; Pep_M12B_Propep. InterPro; IPR001870; Reprolysin. InterPro; IPR00184; TSP1. InterPro; IPR00184; TSP1. InterPro; IPR00180; Zn_MTpeptdse. Pfam; PF019090; LSP_1; 3. Pfam; PF01421; Reprolysin; 1. Pfam; PF01562; Pep_M12B_Propep; 1.
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403
335
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968 AA;
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ATS1_RAT STANDARD; PRT; 967 AA.
O9WU01; OBER11;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS1).
ADAMTS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIVET 20:165-172(2000).

-!- FUNCTION: CLEAPUS AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN 1TS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CAGHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE-Brain;
Liu X., Tu Y., Xin T., Johnstone E.M., Stephenson D.T., Clemens J.A.
Little S.P.,
"Induction of a disintegrin and metalloprotease with the
thrombospondin type I motif (ADAWTS).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                     323 GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG
                                                                                                                                         484 DANRQCQFTFGEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVS
                                                                                                                                                                                                                               ----SGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI
            443 TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
                                                                                                                                                                                                                  502 GACVERHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                                                                                                                                                                                                                            RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL
                                                                                                                                                                                                                                                                        619 ICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGD
                                          263 NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC
                                                                                                                              383 KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-20304099; PubMed-10847486;
Diamantis I., Luethi M., Hoesli M., Reichen J.;
"Cloning of the rat ADAMTS-1 gene and its down regulation in endothelial cells in cirrhotic rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 18-967 FROM N.A.
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722 GSTCKKMSG 730
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                                                                                                                               DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1683-GLU-1-LEU-1684 SITE, WITHIN THE CHONDROITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLURAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity). INDUCTION: DOMN-REGULATED IN ENDOTHELIAL CELLS DERIVED FROM CIRRHOTIC LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R MEROPS; M12.222;
R InterPro; IPR001762; Disintegrin.
R InterPro; IPR001762; Disintegrin.
R InterPro; IPR001500; Reprolysin.
R InterPro; IPR001590; Reprolysin.
R InterPro; IPR00184; TSP1.
R InterPro; IPR000184; TSP1.
R Pfam; PF01421; Reprolysin; 2.
R Pfam; PF01421; Reprolysin; 2.
R Pfam; PF01421; Reprolysin; 2.
R Pfam; PF01421; ADAM_MERO; 1.
R PROSITE; PS00142; ADAM_MERO; 1.
R PROSITE; PS00142; TSP1; 3.
R PROSITE; PS00142; TSP1; 3.
R PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; M Repeat; Extracellular matrix; Heparin-binding.
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R -> P (IN REF. 2).
L -> TR (IN REF. 2).
L -> TR (IN REF. 2).
R -> G (IN REF. 2).
TMLV -> NLLK (IN REF. 2).
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ZINC (CATALYTIC) (BY S.
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TSP TYPE-1 1.
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L -> V (IN REF. 2)
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TSP TYPE-1 3.
POLY-ARG.
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Q9UP79; Q9NzS0;
16-0C7-2001 (Rel. 40, Created)
16-0C7-2001 (Rel. 40, Last sequence update)
15-0TN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS 8) (METH-2)
                                                                                                                                                                                                                                                                           454
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                                                                                                                                                                                                                                      335 VGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTL 394
                                                                                                                                                                                                                                                514 ---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPC 570
                                                                                                                                                                                                                                                                                                                                                                           PSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYV 630
                                                                  AFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNAE 110
                                                                                                  PDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLL--QRR 160
                                                                                                                                    214
                                                                                                                                                                            255 SSPRYVETWLVADQSMADFHGSGLKHYLLTLESVAARFYKHPSIRNSISLVVVKILVIYE 314
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                                1 MLLLGILTLAFAGRTAGG -- FEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQIT 58
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                                                                                                              161 GVPGGPSGD-----PTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFV
                                                                                                                                                   199 GSGGAKCGVMDEETLPTSNSGRESONTPDOWPLRNP-TPQGAG----KPTGPGSIRKKRFV
                                                                                                                                                                     SIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRD
                                                                                                                                                                                                                                                                       395 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
Length 967;
                 Indels
Score 1934; DB 1;
Pred. No. 2.8e-136;
                98; Mismatches 187;
51.7%; Score 1934; 52.7%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung;
MEDLINE=99367466; PubMed=10438512;
                Conservative
        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAMTS8 OR METH2
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                378;
Query Match
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        Best Local
Matches 37
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                                                                                                                                                                                                                                                                                                                                                                      matrix (By similarity).
TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWER
                                                   a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MAIRIX.
                                                                                                                                                                                                                                                                   Genomics 62:312-315(1999).
--- FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES.
--- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
--- COFACTOR: BINDS 1 ZINC SECRETEG. Associated with the extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                             family located
                                              members of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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BY SIMILARITY.
BY CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
Lombardo M., Iruela-Arispe M.L.; "METH-1, a human ortholog of ADAMTS-1, and METH-2 are family of proteins with anxio-indivite.
                                                                      family of proteins with anglo-inhibitory activity."; J. Biol. Chem. 274:23349-23357(1999).
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(GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                 MEDILINE-20079168; PubMed-10610729;
Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.
"ADAM-TS8, a novel metalloprotease of the ADAM-TS fa
mouse chromosome 9 and human chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Metalloprotease; Zinc; Signal; Glyco
Repeat; Extracellular_matrix; Heparin-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000130; Zn_Mrpeptdse.
Pfam; PF00090; tsp_1; 2.
Pfam; PF01421; Reprolygin; 1.
Pfam; PF01562; Pep_M12E_propep; 1.
SMART; SM00209; TSP1; 2.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP TYPE-1 2.
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 605175; -...
InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_pro
InterPro; IPR001500; Reprolysin.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF175283; AAF25806.1; -.
                                                                                                                                            SEQUENCE OF 195-440 FROM N.A.
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19;
             -> FSGCHLQGW
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075173; Q9UN83;
16-077-2001 (Rel. 40, Last sequence update)
16-077-2002 (Rel. 41, Last annotation update)
ADAMTS-4 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499
                                                                                                                                                                                267
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                                                                                                                                                                                                                                            117 VSLCRGLSGSFLLDGEEFTIQP-QGAGGSLAQ-----PHRLQR------------ 153
                                                                                                                                                                                                                                                                    -----RRS 207
                                                                                                                                                                                                                                                                                                                                                                       KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-T 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG--ASYTL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500 LKGACVERHNLNKHR--VDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG 557
                                                                                        Gaps
                                                                                                                 MLLLGILTLAFA----GRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQ 56
                                                                                                                              558 VRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCK
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                                                                                                                                                                 ITAFQEDFYLHLIPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAA
                                                                                                                                                                                                                                                                                                                     GRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOOCROIFGPDFRHCPNTSAQDVCAQLWCHTDG-AEPLCHTKNGSLPWADGTPCGPGHLC
                                                                                        91;
                                                              Length 890;
                         IHFKYLCKCVSELKCDLMP (IN REF. 2)
57D70EE03D5739D3 CRC64;
E -> R (IN REF. 2).
YLTELLDGGHGDCLLDAPGAALPLPTGL
                                                                                      Indels
                                                              DB 1;
                                                                            7.2e-119;
nes 198;
                                                                                                                                                                                                                                                                    177 ASGWNPAILRALDPYKPR---RAGFGESRSR-------
                                                            Query Match
45.4%; Score 1699.5;
Best Local Similarity 46.7%; Pred. No. 7.2e
Matches 341; Conservative 100; Mismatches
                                     96671 MW;
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                                    890 AA;
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195
             CONFLICT
                                     SEQUENCE
 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASES. COULD ALSO BE A ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                 MEDLINE-99286303; PubMed=10356395;

Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M., Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R., Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R., Nagase H., Itch Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K., Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L., Trzaskos J.M., Arner E.C., "Purification and cloning of aggrecanase-1: a member of the ADAMTS
                                                                                                                                       Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The thrombospondin motif of aggrecanase-1 (ADAWTS-4) is critical aggrecan substrate recognition and cleavage.";
J. Biol. Chem. 275:25791-25797(2000).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY INVOLVED IN ITS TUNNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. COULD ALSO BE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRITICAL FACTOR IN THE EXACERBATION OF NEURODEGENERATION IN ALZHEIMER'S DISEASE.
CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ross H.,
                  Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sawaji Y., Nagase H., Saklatvala J., Clark A.R.;
"ADAMTS-4 genomic locus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I.,
Burn T.C., Arner E.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND CHARACTERIZATION.
MEDLINE-20400518; Pubmed-10827174;
                                                                                                                          MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB014538; BAA31663.1; -.
EMBL; AF148213; AAD41494.1; -.
EMBL; AY04484.7; AAL02262.1; -.
MENCPS; M12.221; -.
Genew; HGNC:220; ADAMTS4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 284:1664-1666(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : ::| ::| | ::| 89 GETLLLELEQDSGVQVEGITVQYLGQAPE--LGGAEP--GTYLTGTINGDPESVASLHWD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------KAPLGSPSPRPR--RAKREASLSRFVETLVVADDKMAAFHGAGLK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 HYLLTILLATAARLYRHPSILNPINIVVVKYLLLRDRDSGPKVTGNAALTLRNFCAWQKKL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 RYLITYMAAAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00209; TSPI; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS500215; ADAM_MEPRO; 1.
PROSITE; PS50042; TSPI; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                       .) (POTENTIAL)
                                                                                                                                                                                                                                                ZINC (CATALYTIC) (BY SIMILARITY).

SINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.

TSP TYPE-1.
                                                                                                                                                                                                             CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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R -> Q (IN REF. 3).

G -> R (IN REF. 3).

5DF9C9AC137DF41F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             tch 45.1%; Score 1689.5; sal Similarity 47.2%; Pred. No. 3.7e-328; Conservative 103; Mismatches
                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                          POLY-ALA.
N-LINKED (
                                                                                                                                                                                                                                                                                                 CYS-RICH.
SPACER.
      InterPro; IPR001762; Disintegrin. InterPro; IPR001590; Reprolysin. InterPro; IPR000884; TSP1. InterPro; IPR000804; TSP1. Pfam; PP00090; CSP_1; I. Pfam; PP01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                     90224 MW;
                                                                                                                                                              Extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                    837 AA;
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METAL
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TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN ADULT LUNG AND HEART
AND LOW EXPRESSION DURING MOUSE DEVELOPMENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT.

FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS) (METH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSIN 595
                               RLTL---AVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQG
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS500142; ZINC_PROTEASE; 1.
PROSITE; PS50012; TSP1; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAI SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                   :|| |||| :|| :|||:||| ||| || || :|| RCIHAGCDRIIGSKKKFDKCMYCGGDGSGCSKQSG 690
                                                                                                                                                                                                                                                                KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
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InterPro: IPR001762; Disintegrin.
InterPro: IPR001509; Reprolysin.
InterPro: IPR0001808; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_l; 2.
Pfam: PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 2.
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                                                                                                                                                                                                                                                                                                                                                             208
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                                                                                                                                                                                                                                                                           54 IFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDS 113
                                                                                                                                                                                                                                                                                       114 FAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGA-----HLLQRRGVPGGP 166
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              2 LLLGILTL------AFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGL 53
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                                                 SIMILARITY)
SIMILARITY)
                             SIMILARITY)
                                                                                                                                                                                        Length 905;
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                                                                                                                                                          LINKED (GLCNAC. . .) (PC 124D4132B33A0CAE CRC64;
                                                                                                                TSP TYPE-1 2.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                             (BY
                                                 (BY
(BY
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44.8%; Score 1679; DB 1;
Best Local Similarity 46.7%; Pred. No. 2.4e-117;
Matches 344; Conservative 101; Mismatches 202;
                            (CATALYTIC)
                                                 ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                       DISINTEGRIN-LIKE
TSP TYPE-1 1.
      BY SIMILARITY. ADAMTS-8.
                                         SIMILARITY
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SPACER.
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                             ZINC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wor by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNDECTABLE LEVEL THEREAFTER.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-9935124; PubMed=10464288;
MEDLINE-9935124; PubMed=10464288;
MEDLINE-9935124; PubMed=10464288;
MEDLINE-9935124; PubMed=10464288;
ADAM-TS5, ADAM-TS6, and ADAM-TS7, novel members of a new family of zinc metalloproteases.";
J. Biol. Chem. 274.25555-2553(1999).
I. Biol. Chem. 274.25555-2553(1999).
INVOLVED IN ITS TURNOVER, MAY PLAY AN IMPORTANY ROLE IN THE DESTRUCTION: CLEAVES AGGRECAN. A RAPHITIC DISEASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANYATION PROPEDIATIC CATALYTIC CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-i- DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PERI-
IMPLANTATION PERIOD IN EMBRYO AND TROPHOBLAST AND AT LOW OR
                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS 5) (ABAM-TS 5)
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DR Pfam; PF00090; tsp_1; 2.

DR Pfam; PF01421; Reprolysin; 1.

DR Pfam; PF01422; Reprolysin; 1.

DR Pfam; PF01422; ADAM_12B_propep; 1.

SMART; SM00209; TSP1; 2.

DR ROSITE; PS50021; TSP1; 1.

PROSITE; PS00142; ZIRC_PROTEASE; 1.

R PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

W Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

W Repeat; Extracellular matrix.

T PROPEP 22 261 POTENTIAL.
                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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                     930
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InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001890; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF140673; AAD56356.1; -.
                                                                               (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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261
930
                                                                                                                                                                                                                                     (ADMP-2) (Implantin).
                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                  16-0CT-2001
                        ATS5_MOUSE
Q9R001;
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ATS5_MOUSE
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15-JUN-2002 (Rel. 41, Last annotation update)
ADAMYS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TSS) (Aggrecanase-2) (ADAM-TS 11).
ADAMTS5 OR ADAMP2 OR ADAMTS11.

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                                                                                                                                                                                                                           ESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAAL 287
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                                                                                                                                                                                                                                                                                               ------RAKRFVSIPRYVETLVVAD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 IYGDGSSRILHVYNREGFSFEALPPRASCETPASPSG---------
                                                                                                   POLY-ARG.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-TINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                107 N-LINKED (GLCNAC. . .) (POTENTIAL)
101780 MW; 84DE84B26170D4DC CRC64;
                                                                                                                                                                                                16;
             (BY SIMILARITY)
                             SIMILARITY)
SIMILARITY)
                                                                                                                                                                             Length 930;
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 CYSTEINE SWITCH (POTENTIAL)
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                            (BY
(BY
                                                                                                                                                                            Score 1613; DB 1;
Pred. No. 2.1e-112;
                                                                                                                                                                                               Mismatches 182;
        ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
TOSTRICH (
TYPE-1 1.
                                                                                     TSP TYPE-1 2.
                                                                                                POLY-ALA.
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                                                                             SPACER
                                                                                                                                                                                              81;
                                                                                                                                                                                    47.48;
                                                                                                                                                                                            Matches 306; Conservative
                                                                                                                                                         930 AA;
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                 ACT_SITE
METAL
                                                                                                        DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
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                                      METAL
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ATS5\_HUMAN STANDARD; PKT; 930 AA. Q9UNAO; Q9UKP2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)

ATS5\_HUMAN ID ATS5\_HI AC Q9UNAO DT 16-OCT

RESULT 8

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MEDLINE=20289799; PubMed=10830953;
MEDLINE=20289799; PubMed=10830953;
MEDLINE=20289799; PubMed=10830953;
MEDLINE=20289799; PubMed=10830953;
METOTIM, Fullylama A., Taylor T.D., Watanabe H., Yada T.,
A. Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kump K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A. Schartal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A. Scharfe M., Schoen O., Desario A., Reichelt J., Rause G., Bloecker H.,
Ramser J., Beck A., Klages S., Hennig S., Rlesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARTHRITIC PATIENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HISOME-99395124; PubMed-10464288; Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.; Seldin M.F., And Marker S., Biol. Chem. 274:25555-25563(1999).

1- FUNCTION: CLENVES AGGREGAN, A CARTILAGE PROTEGGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGREGAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTECTION OF AGGREGAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTECTION OF AGGREGAN AN ARTHRITIC DISEASES. MAY PLAY A ROLE IN CARALITIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matrix (By similarity).
TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA
BUT ALSO IN OTHER TISSUES, SUCH AS HEART AND BRAIN, AND ALSO
CERVIX, UTERUS, BLADDER, ESOPHAGUS, RIB CARFILAGE,
CHONDROBLASTOMA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                       Abbaszade I., Liu R. Q., Yang F., Rosenfeld S.A., Ross O.H., Link J.R., Ellis D.M., Tortorella M.D., Pratta M.A., Hollis J.M., Wynn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K., Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H., Ito Y., Newton R.C., Magolda R.L., Trzaskos J.M., Hollis G.F., Arner E.C., Burn T.C.,
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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                                                                                                            (Human)
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ATS9_HUMAN
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commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGGKVGYLVYAGGRRFLLDLERDGSVGIAGF-----VPAGG--GTSAPWRHRSHCFYR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPL---PNASAPAAQRNSQGA----HLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRRG-----VPGGPS------GDPTSRCGVASGWNPAIL--RALDPYKP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRAGFGES---RSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAA 250
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(POTENTIAL).
(POTENTIAL).
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Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01422; Pep_M12B_propep; 1.
SMART; SM00209; TSP; 2.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00144; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%; Score 1587.5; DB 1; Length 930;
47.2%; Pred. No. 1.6e-110;
tive 82; Mismatches 209; Indels 69;
                                                                                                                                                                                                                                                                                    CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                SIMILARITY)
SIMILARITY)
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-> H (IN REF. 3).
-> L (IN REF. 2).
B64281502F28193B CRC64;
                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN LIKE.
TSP TYPE-1 1.
CYS-RICH.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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TSP TYPE-1 2.
POLY-ALA.
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entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                               InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
                                                                                                                                 Interpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSP1.
Interpro; IPR000130; Zn_MTpeptdse.
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                                 EMBL; AF142099; AAD49577.1; --
EMBL; AP001698; BAA95504.1; --
EMBL; AF001697; BAA95503.1; --
EMBL; AF141293; AAF02493.1; --
HSSP; Q9PW35; IBUD.
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                                                                                              HGNC:221; ADAMTS5.
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498
728
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930 AA;
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Matches 322;
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CARBOHYD
CARBOHYD
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CONFLICT
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TISSUE=Brain;
MEDINE=20181126; Pubmed=10718198;
MEDINE=20181126; Pubmed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000).
-i. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metalloproteinase
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RLYSHASIENHIRLAVVKVVVLGDKDKSLEVSKNAATTLKNFCKWQHQHNQLGDDHEEHY
                                                 DTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP
                                                                                                                                                                                                                                                                  491 TSCGEGKICLKGACVER----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTN
                                                                       HDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP
                                                                                                                                                                                                                                     ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark M.E., Kelner G.S., Turbeville L.A., boyer A., Arden K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maki R.A.;
"ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPPING, ONR 29; Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and multh thromospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
ADAMTS9 OR KIAA1312.
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MEDLINE=20396138; PubMed=10936055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKRFDKCGVCGGDNKSCKKVTG 687
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                          Přám. PP00090; tsp.1, 11.
Přám. PP010562; Pep.M12B_propep; 1.
SMART; SM00209; Tspl., 12.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS50042; Tspl., 9.
PROSITE; PS50042; Zspl., 9.
PROSITE; PS60042; Zinc, PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix; Alternative splicing.
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                        SIMILARITY).
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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C1C4CEFF58B8941F CRC64;
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MISSING (IN SHORT ISOFORM)
                                                            --- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINVEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
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ADAMTS-9.
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
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BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
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TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 6.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 9.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 11.
POLY SER.
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Interpro; IPR002870; Pep_M12B_propep.
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InterPro: IPR001590; Reprolysin.
InterPro: IPR000884; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
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                                                SIMILARITY).
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MIM; 605421; -
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13;
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OBESPR; O9ESPB;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-4 precursor (EC 3.4.24..) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
                                                                                                                           EYEIVSPIRVNALGEPFPTNVHFKRTRRSINSATDPWPAFASSSSSSTSSQAHYRLSAFG 106
                                                                                                                                                                                                                                                                       RAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDFYLHLTPDAQFLAPAFSTEHLGVP----LQGLTGGSSDLRRCFYSGDVNAEPDSFAAV 117
                                                                                                                                                              118 SLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVA 177
                                                                                                                                                                                                                                                                                                                           VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA-TTC 327
                                                                                                                                                                                                                                                                                                                                                                               DTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRAN 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxDD=10116;
                               71; Gaps
                                                        --DINGRRYYW----RGPEDSGDQGLIFQITAFQ 61
                                                                                                                                                                                   SLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEEEQNKPHIIYRRSAPQREPSTGRHACDIS
                                                                                                                                                                                                                     -----SRSRRRSG
                                                                                                                                                                                                                                                                                                                                            LIVIHNEQDGPSISFNAQTTLKNFCQWQHSKNSPGGIH---HDTAVLLTRQDICRAHDKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHKN - - - RHSKDKKKTRARKWGERINLAGDVAALNSGLATEAFSAYGNKTDNTREKRTHR
                                                                                                                                                                                                                                                                                                                                                                                                                                     HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-SKPISLPEDLPGASYTLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCELAFGVGSKPCPYMQYCTKLWC - - TGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGA
     DB 1; Length 1629;
                             246; Indels
 Score 1543.5; D
Pred. No. 6e-107
); Mismatches 2
                          , 66
                                                                                                                                                                                                                  SGWNPAILRALDPYKPRRAGFGE---
41.2%;
                          Matches 308; Conservative
                                                       EREVVVPIRLDP---
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687
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 Query Match
Best Local S
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269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD 328

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                    -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLUIAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).
-1- TISSUE SPECIFICITY: ONLY EXPRESSED IN BRAIN.
-1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
-1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI2B.
-1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.6%; Score 1518.5; DB 1; Length 630;
55.8%; Pred. No. 1.4e-105;
iive 67; Mismatches 137; Indels 11; Gaps
                                                                                                                                   BE
                                        Satoh K., Suzuki N., Yokota H.;
"ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin motifs) is transcriptionally induced in beta-amyloid treated rat astrocytes.";
                                                                                                                rosci. Lett. 289:177-180(2000).
FUNCTION: CLEAPES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY FUNCTION: CLEAPES TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISBASES.
                                                                                                                                                                             CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ALA.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Metalloprotease; Zinc; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (PC 63A428753167C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ZINC (CATALYTIC) (BY S
ZINC (CATALYTIC) (BY S
DISINTEGRIN-LIKE.
TSP TYPE-1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF000421; LSP1. 2.
Pfam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50015; ADAM_MEPRO; 1.
PROSITE; PS000427; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPACER.
(1)
EQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Brain;
MEDLINE-20415831; PubMed-10961658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB042272; BAB16474.1; -.
EMBL; AB042271; BAB16473.1; -.
BABL; AB042273; BAB16475.1; -.
INTERPRO; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68384 MW;
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630
1154
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1164
303
367
478
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NON_TER 1
PROPEP <1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            datches 271;
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METAL
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RAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268

209

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MEDLINE-99395124; PubMed=10464288;
MEDLINE-99395124; PubMed=1046428;
MEDLINE-99395124; PubMed=10464288;
MEDLINE-99395124; PubMed=1046428;
MEDLINE-99395124; PubMed=1046428;
MEDLINE-99395124; PubMed=1046428;
MEDLINE-99395124; PubMed=1046428;
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MEDLINE-99395124; PubMed=10464288;
MEDLINE-99395124; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993951244; PubMed=1046428;
MEDLINE-993961244; PubMed=1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15-UTU-2002 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 34.24-.) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAM-TS 7) (ADAM-TS 7).
                                                                                                                                                                                                                       447
                                                                                                                                                                                                                                                             ARALGYYYVLEPRVADGTPCSPDSSSVCVQCRCIHAGCDRIIGSKKKFDKCMVCGGNGSS 477
329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRAN 387
                                                                                                                           CELAFGYGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                                                                                                                                                                     507 RHNLNKHRVD--GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRS 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTL---AVAWVPKYSGVSPRDKCKLICR 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKS
                                                                                                                                                                                                                       HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butheleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 687
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478 CSKQSG 483
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Q9UKP4;
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                           62
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                                                                                                                                                                                                                                                                                                                                                          448
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InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_WIPeptdse.
Pfam; PF00090; tsp_1; 5.
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF163762; AAG35563.1; -.
MEROPS; M12.235; -.
                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                           |:|||| |: :| |:|
683 MEDRCGVCHGNGSTCHTVSG 702
                                                                                                                                                                                                                                              RFDKCGVCGGDNKSCKKVTG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:13201; ADAMTS10.
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         RESULT 12
AT10_HUMAN
ID AT10_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                         ADAMTS10
                                                                                                                                                                                                                                                                                                                                                Q9H324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 APAFYELQYRGRE-----LRFNLTANQ-----HL------LAPGFVSETRRG----GL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGSSDLR----RCFYSGDVNAEPD---SFAAVSLCGGLRGAFGYRGAEYVISPLPNASA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GRAHIRAHTPACHLLGEVQ-DPELEGGLAAISACDGLKGVFQLSNEDYFIEPLD--SA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESRSRRRSGRAKRF----VSIPRYVETLVVADESMVKFHG-ADLEHYLLTLLATAARLYR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 -NVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP- 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAAQRNSQGAHLLQRRGVP----GGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLLLGILTLAFAGRTAGGFEPER---EVVVPIRLDP---------DINGRR- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LLLLCALAPGAPGPAPGRATEGRAALDIVHPVRVDAGGSFLSYELWPRALRKRDVSVRRD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---YY---WRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAF--STEHLGVPLQGL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFTRQDLCGATT--CDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD
                                                                                                                                                                                  SMART; SMO0209; TEP1: 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS500215; ADAM_MEPRO; 1.
PROSITE; PS50042; TEP1: 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                 114 SFACER.

190 TSP TYPE-1 2.

94 N-LINKED (GLCNAC. .) (POTENTIAL).

109694 MW; 6587044ED02FC104 CRC64;
                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 997;
                                                                                                                                                                                                                                                                                                                  CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1087; DB 1;
; Pred. No. 3.2e-73;
82; Mismatches 264;
                                                                                                                                                                                                                                                                                         BY SIMILARITY. ADAMTS-7.
send an email to license@isb-sib.ch).
                                                                                  InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000184; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfan; PF01421; Reprolysin; 1.
Pfan; PF01421; Reprolysin; 1.
Pfan; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                             POTENTIAL
                       EMBL; AF140675; AAD56358.1; -.
                                                                                                                                                                                                                                                              Repeat; Extracellular matrix. SIGNAL 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.0%;
38.6%;
                                                              HGNC:223; ADAMTS7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 38.00
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   914
990
94
693
                                     1ATL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997 AA;
                                               MEROPS; M12.231;
                                                                         MIM; 605009,
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METAL
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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DOMAIN
                                                                Genew;
                                                                                                                                                                                                                                                                                         PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix (By similarity).
-1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                                                                                                                      550 NGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSG 609
431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWAD 489
                                                                                         610 VSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP--DSTSVCVQGKCIKAGCDGNLGSKK 667
                                                                                                                                                                                                                                   Apte S.S.; "ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-10 precursor (EC 3.4.24.-) (A disintegrin and metalloproteins with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
                                                                                                                                                            IDFPSVPPGVLYDVSHQCRLQYGAYSAFCEDMDNVCHTLWCSVGT----TCHSKLDAAVD
                                                                   490 GTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTECRIN-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                          1077 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01421; Reprolysin; 1.
PF01562; Pep_M12B_propep; 1.
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528
                                                                                                                                                                                                                                                                                                                                                                                                                LAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAE-PDSFAAVSLCGGLRGAFGYRGAE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 YVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGV--ASGW--NPAILRALD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-----NK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHELGHVFNMPHDNVKVCEEVFG----KLRANHMMSPTLIQIDRANP--WSACSAAIITD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLDSGHGDCLLDQPSK-PISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFN 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                  EVVVPIRLDPDINGR-----RYYWRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQF 74
                                                                                                                                                                                                                                                                                                                                                                                                                           302 VSDKHPEYWDTAILFTRQDLC--GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT
                                                                                                                                                                                                                                                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSNR---CITNSIPAAEGTLCQTHTIDKGWCYKRVCVP-FGSRPEGVDGAWGPWTPWGDC
                                                                                                                                                                                                                                                                                                                              Length 1077;
                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                             SIMILARITY).
                                                                                                                                 SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                 Indels
SMART; SM00209; TSP1; 5.
PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS50092; TSP1, 2.
PROSITE: PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00427; DISINTEGRIN_1: FALSE_NEG.
Hydrolase: Metalloprotease; Zinc; Glycoprotein; Zymogen;
                                                                                                                                                                                             TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 3.
TSP TYPE-1 5.
ISB TYPE-1 6.
N-LINKED (GLCNAC. . . ) (1)
                                                                                                             (BY :
                                                                                                                                 (BY
                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                        3914DE18DCBBF587
                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.2e-72;
89; Mismatches 280;
                                                                                     10.

10.

10.

ENG (CATALTIC) (E.

BY SIMILARITY.

ZINC (CATATTY.

ZINC (CATATTY.

DIT.
                                                                                                                                 ZINC (CATALYTIC)
ZINC (CATALYTIC)
DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                           Score 1072.5;
Pred. No. 4.2e
                                                                                                                                                               CYS-RICH.
SPACER.
TSP TYPE-
                                                                                                                                                                                                                                                                                                                              28.68;
                                                                                                                                                                                                                                                                                                        118072
                                                                                                                                                                                                                                                                                                                                      36.8%;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 36.8
Matches 260; Conservative
                                                                                                                                                                                                                              1031
64
196
297
714
769
866
                                                              Repeat; Extracellular
NON_TER 1 1 1 PROPEP <1 207
CHAIN 208 1077
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                                                                                                                    ACT_SITE
METAL
                                                                                                                                                                                                                              DOMAIN
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                               DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.

PURT THE PRECUREOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.

PTH : IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND

TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Is widely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fetal lung;
MEDLINE-21264577; Pubmed-11279086;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Ottin C.;
Cal S., Argueelles J.M., Fernandez P.L., Lopez-Ottin C.;
Tidentification, characterization, and intracellular processing of ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats.";
J. Biol. Chem. 276:17932-17940(2001).
-! COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-! SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
641
                                                                                                                                                                                                                                                                                                                          (ADAM-
G-----YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLC
                                  SIPFRGKFYKWKTYR-------GGGVK---ACSLTSLAEGFNFYTERAAAVVDGTPC
                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                 P58397;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWTS-12 precursor (EC 3.4.24.-) (A disintegrin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     origin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in fetal lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in gastric carcinomas and in cancer cells of
                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
                                                                          SPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matrix (By similarity).
TISSUE SPECIFICITY: Expressed exclusively
                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                           1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001762; Disintegrin.
Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001509; Reprolysin.
Interpro; IPR0001804; TSP1.
Interpro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1; 6.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF01562; Pep_MI2B_propep; 1.
SWART; SW00209; TSP1; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ250725; CAC20419.1; -.
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MIM; 606184; -.
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                       AT12_HUMAN
P58397;
                                                                                                                                                                                                                                                                                                                                              TS12).
ADAMTS12.
                                    592
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589
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoutation update)
15-JUN-2002 (Rel. 41, Last amoutation update)
ADAMTS-2 precursor (EC 3-4.44) (A disintegrin and metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2) (Procollagen III amino-propeptide processing enzyme) (Procollagen I N-proteinase) (PC 1-NP) (Procollagen N-endopeptidase) (PNPI) (Procollagen I/II amino-propeptide processing enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNT: MAY BELDONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON AND ACRTA AND AT LOW LEVELS IN THYMUS AND BRAIN.

DOMAIN: THE SPACER DOMAIN ATHE TEP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: Defects in ADAWTS2 are the cause of Ehlers-Danlos syndrome type VIIC (EDS-VIIC), a recessively inherited connective-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colige A., Sieron A.L., II S. W., Schwarze U., Petty E., Wertelecki W., Wilcox W., Krakow D., Cohn D.H., Reardon W., Byers P.H., Lapiere C.M., Prockop D.J., Nusgens B.V.;
Byers P.H., Lapiere C.M., Prockop D.J., Nusgens B.V.;
Human Ehlers-Danlos syndrome type VII c and bovine dermatosparaxis are caused by mutations in the procollagen I N-proteinase gene.";
Am. J. Hum. Genet. 65:308-317(1999).

1- FUNCTION: Cleaves the propeptides of type I and II collagen prior to fibril assembly. Does not act on type III collagen. May also play a role in development that is independant of its role in
                                                                                                                                                                                                                                                                                                                  ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-PROCOLLAGEN PEPTIDASE ACTIVITY.
                                                                                                                                                 395 GHSFGIQHDGKENDCEPVG---RHPYIMSRQLQYDPTPLTWSKCSEEYITRFLDRGWGFC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen biosynthesis.
CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains at Ala-|-Gln.
                                                                                                                                                                                                                                    LLDQPSKP-ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQ-YCTKLWCTGKAKGQMVC
                                                                                                                           QTRHFPWADGTSCGEGKLCLKGACVERHNLNK -- HRVDGSWAKWDPYGPCSRTCGGGVQL
                                                                                                                                                                                                            539 ARROCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSINRLI
                                                                                                                                                                                                                                                                                            LAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLC--SPDSTSVCVQGKCIK
                                                                                452 LDDIPKKKGLKSKVIAPGVIYDVHHQCQLQYGPNATFCQEVENVCQTLWCSVKG----FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matrix (By similarity).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE
                                                                                                                                                                                                                                                                                                                                                                             657 AGCDGNLGSKKRFDKCGVCGGDNKSCKKV 685
                                                                                                                                                                                                                                                                                                                                                                                                                      VGCDYEIDSNATEDRCGVCLGDGSSCQTV 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR PCINP OR PCPNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 ELWREKWERHNL-PSRSLSR-----RSISKERWVETLVVADTKMIEYHGSENVESYILTI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPEYWDTAILFTRQDLCGA--TTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHVFNMPHDNVK-VCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 PEYHVVGPVRVDASGHFLSYGLHYPITSSRR----KRDLDGSEDWVYYRISHEEKDLFFNL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPD--SFAAVSLCGGLRGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVNQGFLSNSYIMEKRYGNLSHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEREVVVPIRLD------PDINGRRYYWRGPEDSGDQGLIFQITAFQEDFYLHL 68
                                       PROSITE; PS50092; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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106; Mismatches
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ZINC (CATALYTIC
ZINC (CATALYTIC
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TSP TYPE-1 3.
TSP TYPE-1 4.
SPACER 2.
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ADAM_MEPRO; 1.
DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                          TYPE-1 1.
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tissue disorder characterized clinically by severe skin fragility and joint hypermobility and biochemically by the presence in skin of procollagen incompletely processed at the N-terminus. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. MILLARITY: CONTAINS I DISTREGRIN'LIKE DOMAIN. SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS. CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCFKGHCIWLTPDILKRDGSWGA -> FRPGAVAHACYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50192; TSP1, 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS001427; DISINTEGRIN_1; FALSE_NEG.
Hydroclase, Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Hydroclase, Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Alternative splicing; Entracellular matrix; Heparin-binding;
Alternative splicing; Entracellular matrix; Heparin-binding;
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BY SIMILARITY.
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SIMILARITY)
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MISSING (IN ISOFORM SPNPI).
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N-LINKED (GLCNAC.

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TSP TYPE-1 1.
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TSP TYPE-1 3
TSP TYPE-1 4
                                                                                                                                                                                                                                                                                                   InterPro: IPR001762; Disintegrin.
InterPro: IPR001870; Pep_M12B_propep.
InterPro: IPR001870; Reprolysin.
InterPro: IPR000184; TSP1.
InterPro: IPR000130; Zn_MTpeptdse.
Pfam: PF00402; tsp_1; 4.
Pfam: PF01421; Reprolysin; 1.
Pfam: PF01562; Pep_M12B_propep; 1.
SMART; SM00209; TSP1; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134722
                                                                                                                                                                                                                                                            Genew; HGNC:218; ADAMTS2.
MIM; 604539; -.
MIM; 225410; -.
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1211 AA;
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CARBOHYD
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SEQUENCE
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VARSPLIC
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and metalloproteinsee with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2)
metalloproteinsee with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2)
                 452
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                                                                 103 YSGDVN--AEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG-AHLLQR 159
                                                                                                                                                                                                                                                                      278 GPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVG 336
                                                                                                                                                                                                                                                                                                                                       337 IMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLI 395
                                                                                  GLGY.MMCTAFRTFDPCKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHCFKGHCIWLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCF
                                                                                                                                                       220 -VETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDS
                                                                                                                                                                                                                                                                                                                                                                       384 GMCHPVRSCTLNHEDGFSSAFVVAHETGHVLGMEHDGOGNRCGD---EVRLGSIMAPLVQ
                                                                                                                                                                                                                                                                                                                                                                                                          396 QIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 ---ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 RSCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLCSRQDCPDSLA--DFREEQCROWDLYFEHGDAOHH-------WLP-HEHRDAKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616 CKLICRANGTGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGV
                                                                                                                                    RGVPGGPSGDPTSRCGVASGWNPA1LRALDPYKPRRAGFGESRSRRRSGRAKRFVS1PRY
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MEDLINE=97225960; Pubmed=9122202;
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Gaps

; Pred. No. 3.4e-66; 94; Mismatches 280; Indels

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LAFAGRTAG ---GFEPEREVVVPIRLDPD-----

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Matches 261; Conservative

Similarity

Local

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO
COLLAGEN TYPE XIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matrix (By similarity).

TISSUE SPECIFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVEL
IN ALL TYPE I COLLAGEN-RICH TISSUES SUCH AS SKIN, BONES, TENDONS
AND AORTA AND AT LOW LEVEL IN BRAIN AND THYMUS. THE MRNA LEVELS
WERE DISPROPORTIONATELY HIGH IN HEART, LIVER, RETINA AND MUSCLE.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERRACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN ADAMIS2 ARE THE CAUSE OF DERMATOSPARAXIS, A RECESSIVELY INHERITED DISORDER CHARACTERIZED BY SEVERE SKIN FRACILITY AND BIOCHEMICALLY BY THE PRESENCE IN SKIN OF PROCLLAGEN
                                                                                                                                                                                                Colige A., Beschin A., Samyn B., Goebels Y., Van Beeumen J.,
Nusgens B.V., Lapiere C.M.;
Nusgens B.V., Lapiere C.M.;
Characterization and partial amino acid sequencing of a 107-kDa
procollagen I N-proteinase purified by affinity chromatography on
immobilized type XIV collagen.",
J. Biol. Chem. 270:16724-16730(1995).
I- FUNCTION: CLEAVES THE PROPEPTIDES OF TYPE I AND II COLLAGEN PRIOR
TO FIBRIL ASSEMBLY. DOES NOT ACT ON TYPE III COLLAGEN PRIOR
PLAY A ROLE IN DEVELOPMENT THAT IS INDEPENDANT OF ITS ROLE IN
COLLAGEN BIOSYNTHESIS.
                                new member of the superfamily of zinc-metalloproteinases a sites for cells and other matrix components.";

Proc. Natl. Acad. Sci. U.S.A. 94:2374-2379(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-(-Gln and of alpha-1(II) and alpha-2(I) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS5015; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZNN__PROFEASE; FALSE_NEG.
PROSITE; PS00477; DISINTERIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Collagen degradation; Extracellular matrix; Heparin-binding.
                                                                                                                               3
                        "cDNA cloning and expression of bovine procollagen I N-proteinase: new member of the superfamily of zinc-metalloproteinases with bind:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: THE N-TERMINUS IS BLOCKED.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCOMPLETELY PROCESSED AT THE AMINO TERMINUS.
--- SIMILARITY: BELONGS TO PEPTIDAEE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
--- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY. ADAMTS-2.
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InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000884; TSP1.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 4.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SWART; SM00209; TSP1, 4.
                                                                                                                                                                             MEDLINE=95348096; PubMed=7622483;
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                                                                                                                                                     PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at Ala-1-Gln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; M12.301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
Lapiere C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 NASAPAAQRNSQG-AHLLQRRGVP-----GGPSGDPTSRCGVASGWNPAILRALDPYKP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 KGL--AAKEAEOGRVHVVYHRPTTSRPPPLGGPQALDT---GISADSLDSLSRAL---- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GVLEERVNSSRRRMRRHAADDDYNIEVLLGVDDSVVQFHGTEHVQKYLLTLMNIYNE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 LYRHPSILNPINIVVVKVLLLRDRDSGPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
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Search completed: April 29, 2003, 17:14:08 Job time : 12.4611 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model	April 29, 2003, 17:10:24 ; Search time 41.8928 Seconds (without alignments) 3378.970 Million cell updates/sec	US-10-009-332-1_COPY_1_687 3744 1 MLIGILTIAFAGRTAGGEE DEDWCCYCCONWCCYWWG 607	BLOSUM62
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Listing first 45 summaries

Database: SPTREMBL\_21:\*
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SUMMARIES

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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA
                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                             Length 2165;
                                                                                                                                                                                                                                                                                                                           32.7%; Score 1223; DB 5; Length 21
40.5%; Pred. No. 1.4e-92;
Live 87; Mismatches 214; Indels
                                                                                                    InterPro; FIRE 1357 -.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000849; TSP1.
InterPro; IPR000804; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Fram; PF004020; Reprolysin; 1.
Fram; PF000009; TSP1; 14.
SMART; SM00209; TSP1; 18.
PROSITE; PS50012; TSP1; 18.
PROSITE; PS00142; ZTSP1; 18.
PROSITE; PS00142; ZTSP1; E.
PROSITE; PS00142; ZTSP1; E.
SEQUENCE 2165 AA; 244397 MW; FCC3DA8AAAAQC4888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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              CAA93288.1; JOINED. CAA93287.1; -. CAA93287.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.59
Matches 257; Conservative
                                                                             1DTH.
                                                                                                MEROPS; M12,135;
EMBL; Z69361; C
EMBL; Z69360; C
EMBL; Z69360; C
EMBL; Z69361; C
HSSP; P15167; 1
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RESULT 4
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                                                                                                                                                                                                                                                      24;
                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                    107 VNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAP-----AAQRNSQGAHLLQ 158
                                                                                                                                                                                                                                                                         FQITARQEDFYLHLTPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD 106
                                                                                                                                                                                                                                                                                       386 AN---HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLPG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASYTLSQQCELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCG-E 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGE----SRSRRRSGRAKRFV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  | :|| :|||||: | :||||||: | 355 VEDPPHSMVSVSLCGGMTGYIKTSFGALLIQPVNRTSSDEVLHRVFRKSQRNAR--HAVS.
                                                                                                                                                                                                                                                                                                                                                                                215 SIPRYV---ETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                        GKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDRDSGPKV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKLCLKGACVERHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                               Length 1688;
                                                                                                                                                                                                                           / Match 27.3%; Score 1022; DB 5; Length 1 Local Similarity 35.1%; Pred. No. 5.8e-76; les 237; Conservative 104; Mismatches 237; Indels
                                                                                                                                                                                        EMBL; AY094716; AAM11069.1; -. SEQUENCE 1688 AA; 189867 MW; 48FB8DD4DE0CA4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 KFEL------
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                                                                                         SEQUENCE FROM N.A.
                                                                                                    STRAIN-BERKELEY;
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SK--PISLPEDLPGASYTLSQQCELAFGVGSKPCP---YMQYCTKLWC--TGKAKGQMVC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLTPDAQFLAPAFSTEHLGVPLQGLTGGSS----DLRRCFYSGDVNAEPDSFAAVSLCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 DTAILFTRQDLCG--ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, expression analysis, and structural characterization seven novel human ADAWTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).

EMBL: AJ311903; CAC83612.1; -. SEQUENCE 1081 AA; 119655 MW; 0438BF645676461E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada
                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                           Last sequence update)
Last annotation update)
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    1081
                                                                                                Created)
    PRT;
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                             ..... (TrEMBLrel. 21
v.1-JUN-2002 (TrEMBLrel. 21,
ADAMTS18 protein.
ADAMTS18.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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Lopez-Otin C.;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., II P.W., Hoskins R.A., Galle R.F.,
RA Adams G.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C. Baldwin D.,
RA Abril J.R., Basu A., Baxendala J., Bayarktroglu L., Basaley E.M.,
RA Beson K.Y., Basu A., Baxendala J., Bayarktroglu L., Basaley E.M.,
RA Berkova D., Botchan M.R., Bulker H., Zaddeu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller G., Davenport L.B., Davies P.,
RA Burtis K.D., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis M.L., Doup L.E., Downes M., Dayan-Kocha S., Dunkov B.C., Dunn P.,
RA Burtis M.L., Bangelista C.C., Ferraz C., Ferriard S., Dunkov B.C., Dunn P.,
RA Boston K., Doup L.E., Downes M., Dayan-Kocha S., Dunkov B.C., Dunn P.,
RA Boston D., Harvey D., Helman T.J., Hernandez J.R., Harris M.,
R. Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Harris M.,
R. Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Harris M.,
Rabal B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liako P., Lei Y., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy D., Puri V., Reese M.G.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,
RA Shier R., Webserman D.A., Weinstock G.M., Weissenbach J.,
RA Shier R., Abong F.N., Walner F., Wang G., Zheng Y.,
RA Shier R., Walse B.C., Stapleton M., Strong R., Sheng L.,
RA Shier R., Abong F.N., Weissenbach J.,
RA Shier R., Zaveri J. Singeson M., Strong R., Shen H.,
Ra Perisas R., Weiges E., Spradling G.M., Venter J.C.;
RA Sheng X.H., Zhong F.N., Zhon W., Zhon W., Zhu S., Zhu X., Zhu K., Z
                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
03-096 protein.
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                               669 ------WKP-YTKVEEEDRCKLYCKAENFEFFFAMSGKVKDGTPCSPNKNDVCIDGVCE 720
  RLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCI 655
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                                                                                                                               721 LVGCDHELGSKAVSDACGVCKGDNSTCKFYKG 752
                                                                                                     656 KAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTG 687
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Interpro; IPR001590; Reprolysin.
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InterPro; IPR000130;
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                                                                                                                                                                                                                                               17 GGFEP-----GREVVVPIRLDPD------INGRRYYWR----GPED 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 P--AAQRNS-QGAHLLQRRG--VPGGPSGD--PTSRCGVASGWNPAILRALDPYKPRR--
                                                                                                                                                                  Query Match
Best Local Similarity 33.2%; Pred. No. 1.2e-75;
Matches 266; Conservative 93; Mismatches 269; Indels 174;
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DC1545555CB6212 CRC64;
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Pfam; PF01562; Pep_M12B_propep; 1. Pfam; PF01421; Reprolysin; 1. Pfam; PF00009; tsp_1; 2. PRSTRT; SM00209; TSP1; 2. PROSITE; PS50215; ADAM_MEPRO; 1. PROSITE; PS50092; TSP1; 1. PROSITE; PS01042; ZINC_PROTEASE; UN SEQUENCE 1054 AA; 118616 MW; DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 FYSGRVLGHPGSLVSLSACGAAGGLVGLIQLGQEQVLIQPLNNSQGPFSGRE----HLIR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 RR-GVPGGPSGD---PTSRCGVASGWNPAILRALDPYKPRRAGFGE-SRSRRRSGRAKRF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 TS-EHTVETLVVADADMVQYHGAEAAQRFILTVMNMYNMFQHQSLGIKINIQVTKLVLL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 C--GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 VFGKLRANHMMSPTLIQIDRANP----WSACSAAIITDFLDSGHGDCLL---DQPSKPIS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 HSSCAGRSHIMSGEWYK--GRNPSDLSWSSCSRDDLENFLKSKVSTCLLVTDPRSQHTVR 460
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                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                  MEDLINE=21856482; PubMed=11867212; Cal S., Obsya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.; "Cloning, expression analysis, and structural characterization seven novel human ADAMTSS, a family of metalloproteinases with disintegrin and thrombospondin-1 domains:";
                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1095;
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Last annotation update)
17, with thrombospondin domains.
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                                                                                                                                                                                                                                                                                                                                                      tch 26.7%; Score 998.5; DB 4; al Similarity 34.3%; Pred. No. 2.9e-74; 253; Conservative 106; Mismatches 285;
                                                                                                                                                                                                                                                                          Gene 283:49-62(2002).
EMBL; AJ315735; CAC86016.1; -.
                           01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                               01-JUN-2002 (TrEMBLrel. 21, Metalloprotease disintegrin
              01-JUN-2002 (TrEMBLrel.
                                                                                           Homo sapiens (Human)
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RA MEDLINE=Z1194006; Publous, 1011 R.A., Evans C.A., Gocayne J.D.,
RA Manatides P.G., Scherer S.E., Ii P.M., Hoskins R.A., Galle R.F.,
RA Ganger R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Worthan J.R., Zandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Worthan J.R., Zandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Baxter E.G., Helt G., Champen M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bouck J., Brokstein P., Brothafer P.,
RA BOTKOWA D., Botchan M.R., Bouck J., Brokstein P., Brothafer P.,
RA BOTKOWA D., Botchan M.R., Bouck J., Brokstein P., Brothafer P.,
RA BOTKOWA D., Botchan M.R., Bouck J., Brokstein P., Brothafer P.,
RA BOTKOWA D., Botchan M.R., Bouck J., Brokstein P., Brothafer P.,
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Faragelista C.C., Ferraz C., Ferriar S., Patischman W.,
RA Durbin K.J., Paragelista C.C., Ferraz C., Ferriar S., Morok J.,
RA Durbin K.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A.,
RA Lasko P., Lell Y., Levitsky A.B., Li J., Il J., Ilang Y., Lin X.,
Ilu X., Matteil B., Morntosh T.C., Mortis J., Woshrefi A.,
Mour S.M., Nelson K.A., Moroh K.A., Wosher B., Sun E.,
Spirakas R., Tector C., Turner R., Vanter E., Shen H.,
RA Shie B. C., Stabler W., Wolley K.D., Smith T.,
Shie B. C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O, R.
Shie B.C., Siden Kiamos I., Shangon M., Zhou K., Zhu X., Smith H.O.,
Steine 2019 S.C., Procence 2019 S.2000, R.,
Steine 2019 S.C., Stabler M., Zhang G., Zhao O, Zheng L.,
Steine 2019 S.C., Stapler M., Zhang G., Zhao G., Shang C., Shang C., Sheeler F., Spie
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
628 VDDKPCELYCSPLGKESPLLVADRVLDGTPCGPYETDLCVHGKCQKIGCDGIIGSAAKED 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                             PRT; 1229 AA.
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InterPro; IPR001590; Reprolysin.
InterPro; IPR0010804; TSP1.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF00090; tsp.1; 2.
SMART; SM00209; TSP1; 3.
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EMBL; AE003709; AAF55199.1;
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                                                                                                                                             688 RCGVCSGDGKTCHLVKG 704
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                                                                          671 KCGVCGGDNKSCKKVTG
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                               348 DVDNQVYTLEVLIAVDNSMKOFHGEDLQPYILIIMSIVSSIFADASIGNSIRILLVRLIS 407
                                                                                                 55 FQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD 106
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                                                                                                                                                                                                                                                                                                                                                   SGHWCQRGKCVS----NKHGYGRQVNGGWGPWTPFTPCSLTCGGGVQESRRECNQPVPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        326 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR
                                                                                                                                                                                                                                                                                                                                         AN---HMMSPTL-IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLP
                                                                                                                                                                                                                                                                                                                                                                              GASYTLSQQCELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGV
                                                                                                                                                                              159 RRGVPGGPSGDPTSRCGVASGWNPAİLRALDPYKPRRAGFGE----SRSRRRSGRAKRFV
                                                                                                                                                                                                                     215 SIPRYV---ETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type I motif.
ADAMTS16.
                                                            Length 1229;
                               Hydrolase; Metalloprotease; Zinc.
SEQUENCE 1229 AA; 138136 MW; C1293180AB19B700 CRC64;
                                                                 1.9e-73;
ches 227;
                                                         DB 5;
                                                                      Best Local Similarity 35.0%; Pred. No. 1.9e Matches 237; Conservative 102; Mismatches
                                                            Score 989.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1072
 PROSITE; PS50215; ADAM_MEPRO; 2. PROSITE; PS50092; TSP1; 2. PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                            26.4%;
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                                                                                                                                                                                                                                                                                                                                                                 SGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG---AHLLQRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                           G----VPGGPSGDPTSR----ILRA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                     51 QGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSS------DLRRCFY 103
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-NKVSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 HPEYWDTAILFTRQDLCG--ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  590 YNHSTNRLTLAVAWVPKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSPDSTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEPHAPGASEVLVISRIWELAHQPLHSSDLRLGLPQKQHFCGRRKKYMPQPPKEDLFIL
                                                        of
                                                                                                                                                                                                        25.8%; Score 967.5; DB 4; Length 1072;
llarity 35.1%; Pred. No. 1.1e-71;
Conservative 86; Mismatches 261; Indels 103;
              Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
EMBL; AJ315734; CAC86015.1; -.
                                                                                                                                                                        1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
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MEDLINE=21856482; PubMed=11867212;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                            Integrin; Protease.
                                                                                                                                                                                                                                   Local Similarity
nes 243; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDKHPEY---W------DTALLFTRQDLC--GATTCDTLGMADVGTMCDPKRSCSVIED 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 HLGVPLQGLTGGSSDLR-----RCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKW
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                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID-9606;
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization aseven novel human ADAWTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002)
EMBL; AJ311904; CAC84565.1; -.
SEQUENCE 1207 AA; 134061 MW; AF36F6BF5886FDE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.1%; Score 941.5; DB 4; Length 1207; Best Local Similarity 32.2%; Pred. No. 1.9e-69; Matches 247; Conservative 100; Mismatches 278; Indels 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 LQRRGVP----GGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYRREAVQQEWAEPDGDLHNE-AFGLGDLPNLLGLVGDQ-----LGDTERKRHAKPGS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVSIPRYVETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLL 271
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
A disintegrin-like and metalloprotease with thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21638061; Pubmed=11779638;
A Bolz H., Ramirez A., von Brederlow B., Kubisch C.;
T. "Characterization of ADAMTS14, a novel member of the ADAMTS
T. "Characterization of ADAMTS14, a novel member of the ADAMTS
T. Biochim. Biophys. Acta 1522:221-225(2001).
Biochim. Biophys. Acta 1522:221-225(2001).
R EMBL; AF58866; AA440229-1;
R InterPro; IPR001870; Pep_M12B_propep.
R InterPro; IPR001870; Reprolysin.
R Pfam; PF0152; Pep_M12B_propep; 1.
R Pfam; PF0162; Pep_M12B_propep; 1.
R Pfam; PF016090; tsp_1; 4.
R RAMAT; SM00209; Tsp_1; 4.
R RAMAT; SM00209; Tsp_1; 4.
R ROSITE; PS50015; ADAM_MPRO; 1.
R RIGHT: PS50015; Tsp1; 1.
R Signal; Integrin; Protease; Metalloprotease.
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 1223 AA; 133871 MW; 36394AC4D92F170F CRC64;
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1223 AA.
PRT;
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Matches 222; Conservative
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                                                                                                                                                                                           ADAMTS14.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eulheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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[Lopez-Otin C.;
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Gene 283:49-62(2002).
EMBL; AJ345089; CAC87943.1;
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TSSUB-FFETAL LUNG:
MEDLINE-21856482; Pubwed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
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33.1%; Pred. No. 2.5e-68;
tive 95; Mismatches 276; Indels
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Collige A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,

Collige A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,

Li S.W., Prockop D.J., Laptere C.M., Nusgens B.V.;

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High HomoLogy with ADAMTS-2 and ADAMTS-3.";

J. Biol. Chem. 277:5756-5766(2002).

SEMBL, AF366351; AAL/99841.;

SEQUENCE 1159 AA; 127336 MW; A5B130149BF7FF34 CRC64;
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-VMAPLVQAAFHRFHWSRCSKLELSRYLPS--YDCLLDDPFDPAWPQPPELPGINYSMDE 480
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                                                                      LQRRGVP----GGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRSGRAKR
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                                                                                                                                  CVERHILLINKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR
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                                          QCELAFGVGSKPC---PYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBL_TaxID-9606;
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Last annotation update)
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ADAMTS14.
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Q8TEY8
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214 VSIPRYVETLVVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLR 273
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                                                                                                                 ----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
                                                                                                                                            333 ADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 392
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                        449 ELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER- 507
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75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE.
1427 AA; 153632 MW; EBIBC3AABC1A4442 CRC64;
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BENBL, AVG55376; AAL17622.1; -...
MEROPS; MI2.241; -...
InterPro; IPR001099; Reprolysin.
InterPro; IPR000130; Zn_MTpéptdse.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,
Fujikawa K.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
von Willebrand factor-cleaving protease precursor.
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Pfam; PF00090; tsp_1; 4.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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nes 179; Conserv
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Goad D.L., Goad M.E.;
"Molecular cloning of lapine aggrecanase-2 (ADAMTS-11) from articular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 448
304 GYAPVTGMCHPLRSCALNHEDGFSSAFVIAHETGHVLGMEHDGQGNGCADETSLGS---- 359
                                             HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI-SLPEDLPGASYTLSQ 446
                                                                      447 QCELAFGVGSKPC---PYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGA 503
                                                                                                                                                                                  OCRFDFGSGYQTCLAFRTFEPCKQLWCS-HPDNPYFCKTKKGPPLDGTECAPGKWCFKGH 475
                                                                                                                                                                                                                              504 CVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
                                                                                                                                                                                                                                                                                                                       564 SCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDKCK 617
                                                                                                                                                                                                                                                                                                                                                                                                                LICRANGIGYFYVLAPKVVDGTLCS-PDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCG 676
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                                                                                                                                                                                                                                                                                                                                                    ADÁMTS-11.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chondrocytes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317415; AAG33062.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aggrecanase-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 1.
PMOSTT; SM0209; TSP1; 1.
PROSTTE; PS500215; ADAM_MEPRO; 1.
PROSTTE; PS50092; TSP1; 1.
PROSTTE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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MEROPS; M12.225; -.
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----DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHPPDAQPGLYYS 306
                                                                                                                                           559 RVKYRSCNLEPCPSSASGKSFREEQCEAFNG------YNHSTNRLTLAVAW---V 604
                                                                                                                                                                                                  605 PKYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP----DST-SVCVQGKCIKAG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 332 MADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRANHMM 390
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                                                                                                                                                                                                                    444 LSQQCELAFGVGSKPCPY - - - - MQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLC
                                                                                    500 LKGACVERHNLNK-HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                                                                                                                                                                                                                                                                                                                                                                                            Aggrecanase-1 (Fragment).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; Score 55%; DB 6; Length 192; 51.0%; Pred. No. 1.4e-38; Live 26; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flannery C.R., Little C.B.;
Expression and activity of equine aggrecanases.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF366321; AAK53425.1;
InterPro; IPR001190; Reprolysin.
InterPro; IPR001190; Reprolysin.
InterPro; IPR00130; Zn_WTpeptdse.
PROSITE; PS50215; ADAM_MEPRO; 1.
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20670 MW; 9013B0E19FCE8C56 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                        Search completed: April 29, 2003, 17:17:53 Job time: 45.8928 secs
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LQEFNIPQAGGW 192
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SEQUENCE 192 AA;
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/NCT\_NEW\_PUB.pep:\*
3: /cgn2\_6/ptodata/2/pubpaa/NCS06\_NEW\_PUB.pep:\*
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
6: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
7: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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14: /cgn2\_6/ptodata/2/pubpaa/US00\_NEW\_PUB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/US00\_NEW\_PUB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/US00\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	i face A occopioso	Segmence 4, Appli	Segmence & Appli	Segmence 2, Applia					Segmence 12 Appl	Segmence 12, April	Sequence 1 April	Segmence 1 Appli		٠,		Sections 350 App	25.0	250,	
	ID	US-09-965-631-4	US-10-163-316-2	US-09-965-631-6	US-09-965-631-2	US-09-321-987B-4	US-10-163-316-7	US-10-105-929-2	US-10-097-597-12	US-10-097-580-12	US-09-445-023A-12	US-10-097-597-1	US-10-097-580-1	US-09-445-023A-1	US-10-174-590-352	US-10-176-758-352	US-10-175-737-352	US-10-173-706-352	US-10-175-738-352	US-10-175-752-352
	gth DB	950 10	823 9	367 10	321 10	950 · 10	6 896	967 12	727 9	727 9	727 10	727 9	727 9	727 10	σ	σ	σ	837 9	837 9	837 9
ф	Query Match Length DB	99.7	98.8	60.5	52.8	49.4	49.4	49.3	42.8	42.8	42.8	42.7	42.7	42.7	42.3	42.3	42.3	42.3	42.3	42.3
	Score	3155	3126.5	1913	1669	1562.5	1562.5	1560.5	1353	1353	1353	1351	1351	1351	1337.5	1337.5	1337.5	1337.5	1337.5	1337.5
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-94	-941	-941	180-	180-	173-	174-	174-	174-	174-	175-	17		176-	-941	176-	176-	176-	176-	176-	-91	1	184-	173-	173-	173-
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20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	42

## ALIGNMENTS

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Sequence 4, Application US/09965631
Patent No. US20020115842A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. US20020115842A1e1 Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0241-USA
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR PRICIATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
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Pred. No. 9.9e-251;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 582; Conservative
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; ORGANISM: homo sapiens
US-09-965-631-4
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LENGTH: 950
US-09-965-631-4
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Best Local S
Matches 363
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TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: THERE
TILE REPRENCE: MPT01-025PIRM
CURRENT FILLING DATE: 2002-06-05
PRIOR PILLING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 823
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                                                                    HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
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                                                                                                                                                                                                                                                           Sequence 2, Application US/10163316 Publication No. US20020197703A1 GENERAL INFORMATION:
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US-10-163-316-2
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US-10-163-316-2
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HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
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Pred. No. 3e-149;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TILE OF INVENTION: NO. US20020115842Alel Hum
FILE REFERENCE: LEX-0241-USA
CURRENT APPLICATION NUMBER: US/09/965,631
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/236,689
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09965631 Patent No. US20020115842A1
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al Similarity 99.7%;
363; Conservative (
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ORGANISM: homo sapiens
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58 TAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNA 109
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                                                                                                                                                                                                                                          EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161
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TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and Uses
TITLE OF INVENTION: 7 Therefor
FILE REPERENCE: MPIO1-025PIRMM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-66-05
PRIOR PPLICATION UNMER: 60/297,863
PRIOR FILING DATE: 2001-06-13
                                                                                                  1 MLLLGILTLAFAGRTAGG--FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQI
                                                                                                                        ::||: || || || || || 467 DANRQCQFTFGEESKHCPDAASTCTTLMCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVS
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                                      DB 10; Length 950;
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                                                                       Indels
                                                                                                                                                                                                                                                                                                            162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRR---
                                  ; Score 1562.5; DB 10; Pred. No. 6.3e-120; 79; Mismatches 154;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                    49.4%;
                               Query Match
Best Local Similarity 50.44
Matches 315; Conservative
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US-09-321-987B-4
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US-10-163-316-7
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SEQ ID NO 7
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ORGANISM:
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                                                                                                    APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTOR: No. US20020115842Alel Human Proteases and Polynucleotides Encodin
FILE REFERENCE: LEX-0241-05A
CURRENT APPLICATION NUMBER: US 60/236, 631
FRIOR PRING APPLICATION NUMBER: US 60/236, 689
FROR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeQ for Windows Version 4.0
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APPLICANT: Kimble, Judith E
APPLICANT: Blelloch, Robert H
TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296, 95386
CURRENT APPLICATION NUMBER: US/09/321, 987B
CURRENT APPLICATION NUMBER: US/09/321, 987B
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/103, 170
PRIOR APPLICATION NUMBER: 60/103, 023
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 950
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Pred. No. 2.8e-129;
1; Mismatches 1;
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                                                        ; Sequence 2, Application US/09965631; Patent No. US20020115842A1; GENERAL INFORMATION:
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Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: Murine
                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 321
                                        09-965-631-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-321-987B-4
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APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83;
FILE REPERENCE: 09404/041001.

CURRENT APPLICATION NUMBER: US/10/105,929

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491

PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-07

PRIOR FILING DATE: BARLIER FILING DATE: 1997-09-05

PRIOR PILING DATE: EARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 2

LENGTH: 967

LENGTH: 967
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                                                                                                                                            161
                                                                                                                                                             58 TAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS------SDLRRCFYSGDVNA 109
             Gaps
                                                    1 MLLLGILTLAFAGRTAGG--FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQI 57
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                                                                                                                                            EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APPAAQRNSQGA----HLLQRRG
                                                                                                                                                                                                                        ----RRGSGGAKCGVMD-----DETLPTSDSRPESONTRNOWPVRDPTPQDAGKP
                                                                                                                                                                                                                                                  ----SGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI
                                                                                                                                                                                                                                                                                                     NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC
             77;
             Indels
                                                                                                                                                                                                VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRR----
 Pred. No. 6.4e-120;
); Mismatches 154;
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illarity 50.4%; Pr
Conservative 79;
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 Best Local Similarity
Matches 315; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLGMADYGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
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APPLICANT: Hirose, Kunitaka
APPLICANT: Harose, Kunitaka
APPLICANT: Harose, Kunitaka
APPLICANT: Harose, Kunitaka
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Keiko
APPLICANT: Ishida, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: composition and method of immunologically analyzin:
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,597
CURRENT PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
                                                                                                                                                                                                                                                                                                         207
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                                        Gaps
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                                                                                                         61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
                                                                                                                                                                                                                                                        166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRAGFGESRSRRRS
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Length 967;
                                        Indels
  49.3%; Score 1560.5; DB 12;
51.6%; Pred. No. 9.4e-120;
iive 73; Mismatches 160; I
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PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 12, Application US/10097597; Publication No. US20030022352A1; GENERAL INFORMATION:
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| SCNLEDCPDN-NGKTFREEQ 625
                                          Conservative
                          Similarity
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                          Best Local Sim
Matches 320;
        Query Match
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                                                                                                                                                                                                                                                                                                                                                                          HNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRS 564
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63.3%; Pred. No. 7.2e-103;
ilve 52; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hirose, Kunitaka
APPLICANT: Harose, Kunitaka
APPLICANT: Harose, Kunitaka
APPLICANT: Harozaki, Michinori
APPLICANT: Harozaki, Michinori
APPLICANT: Harozaki, Keiko
APPLICANT: Masushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Composition and method of
TITLE OF INVENTION: Composition and method of
FILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09445023A Patent No. US20020119167A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 CNLEPCPSSASGKSFREEQ 583
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Matches 240; Conservative
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; ORGANISM: MUS
US-09-445-023A-12
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SEQ ID NO 12
LENGTH: 727
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APPLICANT: Hisose, Kunitaka
APPLICANT: Hacose, Kunitaka
APPLICANT: Hacose, Heiko
APPLICANT: Hakozeki, Michinori
APPLICANT: Hakozeki, Michinori
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS
TILE REFERENCE: 057092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT TILNG DATE: 1090-10-10
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR APPLICATION NUMBER: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SEGFWARE: PatentIn version 3.0
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ilarity 63.3%; Pred. No. 7.2e-103;
Conservative 52; Mismatches 81;
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63.3%; Pred. No. 7.2e-103;
clve 52; Mismatches 81;
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; Publication No. US2003003216BA1
; GENERAL INFORMATION:
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368 CNIEDCPDN-NGKTFREEQ 385
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Matches 240; Conservative
                                                                                                                                  Similarity
                                                       ; ORGANISM: Mus sp. US-10-097-597-12
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SEQ ID NO 12
LENGTH: 727
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LENGTH: 727
                                       TYPE: PRT
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63.6%; Pred. No. 1e-102;
Live 50; Mismatches 82; Indels
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GENERAL INFORMATION:
APPLICANT: Incguchi, Eiji
APPLICANT: Hakozaki, Michhori
APPLICANT: Hakozaki, Michhori
APPLICANT: Ishida, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Osmojalion and method of
TITLE OF INVENTION: Human ADAMTS-1 protein, gen
TITLE OF INVENTION: Gomposition and method of
TITLE OF INVENTION: UNBER: US/10/097,580
CURRENT APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 14
SOFTHARE: Patentin Version 3:0
SEQ ID NO 1
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                                                                                                                                   ; Sequence 1, Application US/10097580; Publication No. US20030032168A1; GENERAL INFORMATION:
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368 CNLEDCPDN-NGKTFREEQ 385
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CNLEDCPDN-NGKTFREEQ 385
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CNLEPCPSSASGKSFREED
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiji
APPLICANT: Ishida, Kukako
SPLICANT: Ishida, Yukako
APPLICANT: Ishida, Yukako
APPLICANT: Matsubina, Kouji
APPLICANT: Watsubina, Kouji
APPLICANT: Watsubina, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Kouji
APPLICANT: Kuno, Rouji
APPLICANT: Kuno, Rouji
APPLICANT: Kuno, Rouji
APPLICANT: Now TO Composition and method of immunologically analyzing human ADAMTE
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTE
TITLE OF INVENTION NUMBER: US/10/097,597
CURRENT PELLOR DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-160-03
PRIOR PILING DATE: 1999-7-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 727
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Publication No. US20030022352A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                        - See File Wrapper or Palm
                                                                                                                                                                              42.3%; Score 1337.5; DB 9; ilarity 45.1%; Pred. No. 1.6e-101; Conservative 88; Mismatches 192;
       CURRENT APPLICATION NUMBER: US/10/174,590 CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                          Prior application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 352
LENGTH: 837
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                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-352
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Matches 265;
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                        APPLICANT: Ishioka, Keiko
APPLICANT: Ishioka, Kukako
APPLICANT: Ishioka, Yukako
APPLICANT: Ishioka, Yukako
APPLICANT: Matsushima, Kouji
ITILE OF INVENTION: Wouji
TITLE OF INVENTION: Composition and method of immunologically analyzing human ADAMTS
FILE REPRENCE: 057092
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
FRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENOTH: 727
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                                                                                                                                                                                                                                                                                                                                                                                                                               209 RAKREVSIPRYVETLYVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 QFTFGEDSKHCPDAASTCSTLWCTGTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNK 308
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
Inoguchi, Eiji
Hakozaki, Michinori
Ishioka, Keiko
Ishida, Yukako
Matsushima, Kouji
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CNLEDCPDN-NGKTFREEQ 385
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                               241; Conservative
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US-09-445-023A-1
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Best Local Similarity
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US-10-174-590-352
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MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG 535
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                                                                                                                                                                                                                                                                                   61 QEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                                                                                                                                                                                              Gaps
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                                                                                                                                                                                              43;
                                                                                                                                                                  DB 9; Length 837;
                                                                                                                                                                 Query Match 42.3%; Score 1337.5; DB 9; Length 8 Best Local Similarity 45.1%; Pred. No. 1.6e-101; Matches 265; Conservative 88; Mismatches 192; Indels
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FILE REFERENCE: P3430R1C104
CURRENT APPLICATION WUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 352
LENGTH: 837
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                                                                                                       TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-758-352
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2003, 17:10:24; Search time 13.4848 Seconds (without alignments) 4156.253 Million cell updates/sec Run on:

US-10-009-332-1\_COPY\_1\_583 3163 1 MLLIGILTLAFAGRTAGGFE.....SCNLEPCPSSASGKSFREEQ 583 Perfect score: Sequence:

BLOSUM62. Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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A:Gene: CESP:F25H8.3
A:Map position: 4
A:Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
                                                                                                                                                                                                                                                                                                                                               C. Accession: 1413/1; 144030

R. Gajadsty, S.
R. Stajadsty, C. the EMBL Data Library, February 1996

A. Reference number: 219413

A. Accession: 121371

A. Accession: 121371

A. Molecule type: DNA

A. Molecule type: DNA

A. Mosidues: 1-2165 < WILL>
A. Experimental source: clone F25H8

A. Experimental source: clone F25H8

A. Experimental source: clone F25H8

A. Scajadsty, S.
Submitted to the EMBL Data Library, February 1996

A. Reference number: 219949

A. Accession: T24896

A. Accession: T24896

A. Residues: 1-2165 < WILL>
A. Molecule type: DNA

A. Residues: 1-2165 < WILL>
A. Cross-references: EMBL: Z69361; PIDN: CAA93288.1; GSPDB: GN00022; CESP: F25H8.3

A. Experimental source: clone T13H10

C. Genetics: Lane
                                                                                                                                                                                                                                                                        hypothetical protein F25H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T21371; T24896
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226 HLVRKFDPMHFKSFDHLNSTSVNETETTVATWQDQWEDVIER-------KARSR
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478 MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGGG
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C; Species: Homo sapiens (man)
C; Decies: Tolorial protein Kian)
C; Decies: Tolorial protein Kian (man)
C; Decession: T00355
R; Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A; Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A; Reference number: 214142; MUID:98403880; PMID:9734811
A; Accession: T00355
A; Reference number: 214142; MUID:98403880; PMID:9734811
A; Residues: 1-837 <ISH>
A; Residues: 1-837 <ISH>
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A; Residues: 1-837 <ISH>
A; Residues: L8ML:Ab014588; NID:93327189; PIDN:BAA31663.1; PID:93327190
A; Experimental source: brain
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: thrombospondin type 1 repeat homology
F; 519-575/Domain: thrombospondin type 1 repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 GGALLGVLQYRGAELHLQPLEGGTPNSA--GGPGAHILRRK----SPASGQGPMCNV--- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                                                                                                                            HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWOKKL 299
                                                                                                                                                                                                                           347 GSHTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLLLGILTLAFAGRIAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 RYLLIVMAAAARAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 GETLLLELEQDSGVQVEGLTVQYLGQAPE-LLGGAEP--GTYLTGTINGDPESVASLHWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLE
                                                 GACVERHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 7.3e-93
88; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1336.5;
                                                                                                                                                                                                                                                                                                             RVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 45.1%;
Matches 265; Conservative
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Best Local
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                                                                                                                                                                                                            502
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A; Residues: 1-1444 <W12>
A; Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A; Experimental source: clone T07C5
C; Genetics:
A; Gene: CESP:C02B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:250004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone C02B4
                                                                                                                                                                                                                                                    Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Riblum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A; Reference number: 224379
A; Reference number: 244379
A; Reference number: Protein Many
A; Reference number: 147158
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-550 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18856; T24653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:AL162080
A; Cross-references: EMBL:AL162080
C; Experimental source: adult melanoma (MeWo cell line); clone DKF2p762C1110
C; Genetics:
A; Note: DKF2p762C1110.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DGNWGAWSPFGSCSRTCGTGV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SHWMASMLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDKPQNPIQLPGDLPGTSYDANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 ERHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                T47158
hypothetical protein DKFZp762C1110.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.6%; Score 684; DB 2; L 59.2%; Pred. No. 8.1e-44; ive 25; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted to the EMBL Data Library, July 1995
A;Reference number: 219031
A;Accession: T18856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1444 <WIL>
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1995
A; Reference number: 219917
A; Accession: T24653
524 'KGPPLDGTMCAPGKHCFKGHCIWLTPDILKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||| || ::||:|||||
RSCNLEDCPDN-NGKTFREEQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 RSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 59.2%
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
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                                                                                                                                                                                                                                                  procollagen N-endopeptidase (EC 3.4.24.14) I - bovine
NiAlternate names: procollagen N-proteinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T18517
R;Colige, A.; Nusgens, B.V.; Laplere, C.M.
submitted to the EMBL Data Library, February 1996
A;Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.
A;Reference number: 218941
A;Reference number: 218941
A;Reference number: 218941
A;Reference number: 218941
A;Reference number: 218941
A;Reference number: 218941
A;Reference sinenslated from GB/EMBL/DDBJ
A;Residues: 1-1205 <COL>
A;Cross references: EMBL:X96389; NID:e990769; PID:e228215; PIDN:CAA65253.1
A;Experimental source: skin
C;Genetics:
A;Gene: PC I-NP
C;Function:
A;Description: catalyzes cleavage of the propeptides of type I and II collagens prior
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : ::| :|:| : | HDGQGNRCGD---EVRLGSIMAPLVQAAFHRFHWSRCSQQELSRYLHS--YDCLRDDPFT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 VRTRRAAPAQIPGLSG-----SEEEDPGGRLFYNVTVFGRDLHLRLRPNARLVAPGATV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 KGL---AAKEAEQGRVHVVYHRPTTSRPPPLGGPQALDT---GISADSLDSLSRAL---- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYRHPSILNPINIVVVKVLLLRDRDSGPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDWP-ALPQ-LPGLHYSMNEQCRFDFGLGYMMCTAFRTFDPCKQLWCS-HPDNPYFCKTK 523
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                             EHLGVPLQGLTGGSSDLRRCFYSGDV-NAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 NASAPAAQRNSQG-AHLLQRRGVP-----GGPSGDPTSRCGVASGWNPAILRALDPYKP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 RRAGFGESRSRRRSGRAKRFVSIPRY-VETLVVADESMVKFHGAD-LEHYLLTLLATAAR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |: ||:||::|| | : || : || 354
    TRHFPWADGTSCGEGK--LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PDINGRRYYWRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFST 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%; Score 775; DB 2; Length 1205; 32.9%; Pred. No. 2.8e-50; Live 82; Mismatches 246; Indels 106;
                                                                                                                     627 LRDCDSPKPRNGGKYCVGQRERYRSCNTQECPWDT--QPYREVQ 668
                                                                                              540 RRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLLLGILTLAFAGRTAG------GFEPEREVVVPIRLD-
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Matches 213; Conservative
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A;Gene: CESP:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:U29378, NID:9868184, PID:9868185, PIDN:AAA68721.1, CESP:F08C
A,Experimental source: strain Bristol N2
   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T15976
R; Bentley, D.
submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmid F08C6.
A; Reference number: 218440
A; Accession: T15976
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-957 < BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                        365 PPGQLFTLDEQCEIFHG----ECWKHELKDGQTMQNICQMVWC---GNGEGVIRTAH-PA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 ADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWD--PYGPCSRTCG-----GGVQLAR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VETLVVADESM----VKFHGADLEHYLLTLLATAAR----LYRHPSILNPINIVVVKVLL 271
                                                                                           272 LRD----RDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTC 327
                                                                                                                                                                                                                                                                                     328 DILGMADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
                                                                                                                                                                                                                                                                                                                                                                                                   HMMSPTLIQIDRANPWSACSAAIITDFLDSGH-GD-----CLLD---OPSKPISLPE-D 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 LPGASYTLSQQCELAFGVGSKPC-----PYMQYCTKLWCTGKAKGQMVCQTRHFPW 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSD----LRRCFYSGDVNAEPD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPR--- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 ----YVETLVVADESMVKF----HG--AD--LEHYLLTLLATAARLYRHPSILNPINIVV 266
   Gaps
                                                                                                                                                                                                         216 QSDLIVELAVFVDENLWRHFSSKHGGMADRKLQDYTLTLLNNIQIMYYQPTASPPLTFRV
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   90;
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   161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F08C6.1 - Caenorhabditis elegans
   54; Mismatches
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   Matches 117; Conservative
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A;Map position: X
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566
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A;Molecule type: DNA
A;Residues: 1-860 <BEN>
A;Cross-references: EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CESP:T19D2
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A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3;
                                                                                                                                            24;
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20.5ep-1999 #sequence_revision 20.5ep-1999 #text_change 20.5ep-1999
C;Accession: T16892
R;Bentley, D.
R;Dentley, D.
R;Dentle
                                                                                                                                                                                                                                                                                                                 102 FYSGDVNAEPDSFAAVSLCGGLRCAFGYRGAËYVISPLPNASAPAAQRNSQGAHLLQRRG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 ----VETLVVADESMVKFHGAD------LEH------YLLTLL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 ATAARLYRHPSILNPINIVVVKVLLLRDRDS----GPKVTGNAALTLRNFCAWOKKLNKV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SD-KHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAH 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGHGDCLLDQPSKPISLPE----DLPGASYTLSQQCELAFGVGSK-PCP----YMQYCTK 467
                                                                                                                                                                                                   43 RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAP-AFSTEHLGVPLQGLTGGSSDLRRC 101
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                        468 LWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE-RHNLNKHRVDGSWAKWD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 IWCGNSGS---TISTAH-PALEGSWCGANKWCHKGQCTHWTFGLTPVPIDGEWSEWGGAE
                                                                                     Length 1444;
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                                                                                  Match 13.7%; Score 433; DB 2; Local Similarity 25.9%; Pred. No. 2.3e-24; les 156; Conservative 81; Mismatches 264,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%; Score 393; DB 2; 29.8%; Pred. No. 1.3e-21;
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Best Local Similarity
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REE 598
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                                                                                        Query Match
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Matches
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Jatainayiii C pircuisou. Jatainaca (iiiagument)
NyAlternate names: single chain botrocetin
NyContains: disintegrin-like 28K protein; hemorrhagic proteinase (EC 3.4.24.-)
(Species: Bothrops jararaca (jararaca)
C; Date: 20-Feb-1995 #sequence_revision 29-Aug-1997 #text_change 09-Jun-2000
C; Accession: S24789; JC2245; A44463; A37958; JC2373
R; Paine, M.J.I.
Submitted to the EMBL Data Library, August 1992
A; Reference number: S24789
A; Accession: S24789
A; Accession: S24789
A; Accession: S24789
A; Residues: 1-571 < PAIN
A; Residues: 1-571 < PAIN
A; Residues: 1-571 < PAIN
A; Residues: 1-571 < PAIN
A; Reference number: JC2245; MUID: 94256999; PMID: 8198592
A; Residues: JC2245; MUID: 94256999; PMID: 8198592
A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; Residues: 360-571 < Union A; 
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A; Molecule type: mRNA
A; Recession: A44463
A; Molecule type: mRNA
A; Recession: A44463
A; Molecule type: mRNA
A; Cross references: GB: X68251
A; Experimental source: venom gland
A; Cross references: GB: X68251
A; Experimental source: venom gland
A; Note: sequence extracted from WISI Dackbone (NUBIP:118104)
B; Fujimura Y: Titani, K: Usami, Y:; Suzuki, M:; Oyama, R.; Matsui, T.; Fukui, H.;
B; Fujimura Y: Titani, K: Usami, Y:; Suzuki, M:; Oyama, R.; Matsui, T.; Fukui, H.;
B; Fujimura Y: Titani, K: Usami, Y:; Suzuki, M:; Oyama, R.; Matsui, T.; Fukui, H.;
B; Fujimura Y: Titani, K: Usami, Y:; Suzuki, M:; Oyama, R.; Matsui, T.; Fukui, H.;
B; Fujimura Y: Titani, K:; Usami, Y:; Suzuki, M:; Oyama, R.; Matsui, T.; Fukui, H.;
B; Title: Isolation and chemical characterization of two structurally and functionally
A; Title: Isolation and chemical C; Superfamily: Moss meltrin alpha; disintegrin homology
C; Keywords: M; Mouse meltrin alpha; disintegrin homology
C; Keywords: h; Microse meltrin alpha; disintegrin homology
C; Keywords: h; Microse: metalloproteinase; venom; Zinc
F; 360-571/Product: jararhagin C #status experimental <AMT>F; 362-444/Pomain: disintegrin homology vols:
F; 295, 299, 305/Binding site: Zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP----S 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 NQCH-----CGANSCVMPSVLSDQPSKLFSDCSKKDYQTFLPVNNPQCILNKPLRTDTAS 400
                                                                                                                       SRRRSGRAKREVSIPRYVETLVVADESM-VKFHGAD--LEHYLLTLLATAARLYRHPSIL 259
                                                                                                                                                                                                                                                                                                                                                         374
318 RQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDD---GLPSAFTTAHELGHVFNMPHDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 NPINI--VVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFT
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Airtles Analysis and Sequence of fibrolase, a direct-acting fibrinolytic enzyme from Agist Airtles Annolacule type: Procein Sci. 1, 590-600, 1392
Airtles Annolacule procein AAI827
Ancessions S10-123, MUD:9278288; PMID:1304389
Airtles Annolacule type: Procein AAI827
Ancessione: 131-123, FMID:9276288; PMID:1304389
Airtles Annolacule type: Procein AAI827
Ancessione: 131-124, FMID:9276289; PMID:1898066
Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Procein Airtles Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Annolacule type: Ann
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                                                                                                                                                                                     334 DVGTMCDPKRSCSVIED---DGLPSAFTTAHELGHVFNMPHDNVKV-CEEVFGKLRANHM 389
                                                                                                                                                                                                                                          : || | | || : | : | | || || : | 306 RMRGMCSPSNSVGVIQDYCKNYLLVAITMAHELGHNLGMDHDNGNCNCPDTSCIMSAVAG 365
                                                                                                                                                                                                                                                                                                                                                             448
                                                                           366 PEPVF-----SFSNCSRNDYRSFRNSDQSKCIDNKPLKTDIVSPSVCGNYFVEVGEEC 418
                      274 DRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMA 3333
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26.4%; Pred. No. 1.6e-15;
tive 67; Mismatches 179; Indels
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Pactor   P	No. 2.7e-15;   A.
12 AGRTAGGFEBERVOVPILLOPDINGRRYVRRGPEDSGDGGLIFQITAFQEDF-YLHILTP 70	GGLIFQITAFQEDFYLHLTPDAQFIAPAFSTEH 83  : ::           :
1 ATRRGANOPRYED NOT THE STATE OF THE STATE O	DAMQYELKVNGEPVVLHÜERNKGLFSKDYSETH 85 DDSFAAVSLCGGLRGAFGYRGAEVVISPLENS 143
71 DAQFLAPAFSTEHLGVPLOGLTGGSSDLRRCFYSGDVAAEPDSFAAVSLCGGLRGAFGYR 130	
131 GABYUSPP. LPNASAPAAQRNSQGAHLLORRGYDGRSGDPTSRCGVASGWN 181  131 GABYUSPP-LPNASAPAAQRNSGGAHLLORRGYDGRSGDPTSRCGVASGWN 181  94 RETYFIELLELDSEAHAVEKYENVEKEDEAFWAGGYDWRKSYEPIKK 142  182PAILRALDYKPRRAGFGESRSRRSGRAKRFVSIPHYVETLVVADESNVKFHG 235  143 ASQLAFTAEQQRYXDPYK	PGGPSGDPTSRCGVASGWNPAILRALDPYKDRR 195
94 RETETEPLEADSEAHA	VVADESM-VKHGADLEHYLLTLATAARL 252  TVVADESM-VKHGADLEHYLLTLATAARL 252  TVVDHGMYTKYGGSDKIRQWYHQWYNTKES 230  KVTGNALTLENFCAWQKKLNKVSDKHPEY 309  AARHTLDSFGEWRERDLLHRISH 279  WCDPKRSCSVIEDDGLPSAFTTAHELGHY 366                                     MCDPKRSCSVIEDDGLPSAFTTAHELGHY 366                                     WCDPKRSCSVIEDDGLPSAFTTAHELGHY 366                                     WCDPKRSCSVIEDDGLPSAFTTAHELGHY 366                                     WCDPKRSCSVIEDGLGSAFTTAHELGHY 366                                   WCDPKRSCSVIEDGLGSAFTTAHELGHY 366                                       WCDPKRSTGVVEDHSKINFLNAVTMAHEWGHN 334                                     WCDPKLSTGVVEDHSKINFLNSVTMAHEWGHN 334                                     WCDPKLSTGVVEDHSKINFLNSVTMAHEWGHN 334
182PAILRALDPYKPRRAGFGESRSRRRSGRAKFFVSIPRYVETLVVADGESWYKFHG 235  143 ASQLAFTAEQORYDPYK.  236 ADLEHYLLTLATAARLYRHPSILNPI-NIVVKVLLLRDRDSGPKVTGNAALTLR 290  11	TUVVDHGMYTKINGDSDKIRGWHQMYNTMKES 230  *RVTGNAALTLENECAWOKKLNKVSDKHPEY 309
236 ADLEHYLLTLATAARLYRHPSILNPI-NIVVVKVLL-LRDRDSGPKVT-GNAALTIR 290 177 GDLDKIRARMYELANIVNEIFRYLXMHVALVGLEIWSNGDKITVKPDVYTLN 229 291 NFCAWOKKLNKVSDKHPEYWDTAILFTRODLCGATTCOTLGMADVGTMCDPKRSCSVIED 350 1	**WYGNAALTLRNFCAWOKKLNKVSDKHPEY 309
	MCDPKRSCSVIEDDGLDSAFTTAHELGHV 366
291 NFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTWCDPKRSCSVIED 350	
230 SFAEMRKTDLLTRKKHDNAQLLTAIDENGPTIGYAYIGSNCHPKRSVGIVQD 281 351DGLPSAFTTAHELGHVFNMPHDNVKVCEEVEGKLRANHMASPTLIQIDRANPWS 404  [	PTLIQIDRANDWSACSAAIITDFLDSGHGDCL 423    :
351DGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWS 404  282 YSPINLVVAVIMHEMGHNLGIHHDTGSCSCGDYPCIMGPT-ISNEPSKFFS 332  405 ACSALITDFLDSGHGDCLLLDQPGSCSCGDYPCIMGPT-ISNEPSKFFS 332  405 ACSALITDFLDSGHGDCLLLDQP	
405 ACSAAITTDFLDSGHGDCLLDQP	lamondback rattlesnake mondback rattlesnake) . 05-Dec-1998 #text_change 21-Jul-2000
402 ACSALITPELDSGRODGLLDQPSKPISLPEDLPGASYTLSQQCELAFGYGSKP 458	lamondback rattlesnake mondback rattlesnake) .05-bec-1998 #text_change 21-Jul-2000
459 CPYMQYCTKLMCTGKAKGOMVCQTRHFPNADGTSCGEGKLCLKGACVERHNLNKHRVD 516	lamondback rattlesnake mondback rattlesnake) .05-Dec-1998 #text_change 21-Jul-2000
517 GSWAKWDPYGPCSRTCGGGVQLARRQCINPTPANGGKYCEGVRVKYRSC 565   ::	<pre>mondback rattlesnake) 05-Dec-1998 #text_change 21-Jul-2000</pre>
423 ASMSECDPAEHCTGQSSECPADVFHKNGQPCLDNYG-YCYNGNCPIMYHQC 472	
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	
A.ittle: Molecular Cloning and expression of Carrocollastatin, a A.Reference number: S55264; MVID:95251603; PMID:7733877 A.Accession: S55270	10n OI Calrocollastatin, a snake-venom protein 603; PMID:7733877
Metalloproteinase (EC 3.4.24) precursor - southern copperhead A; Molecule type: mRNA C; Species: Agkistrodon contortrix contortrix (southern copperhead) C; Species: Agkistrodon contortrix contortrix (southern copperhead) C; Species: Agkistrodon contortrix (southern copperhead) A; Residues: 17-B69 (sequence_revision 13-Mar-1997 #text_change 22-Jun-1999 C; Accession: 566260; S74263	0353; PIDN:AAC59672.1; PID:g710354
	Sintegrin homology
Best Local Similarity 23:58; Pred. No. 5.8e-15; Matches 129; Conservative 80; Mismatches 218; Indels	
Qy 50 DQGLIFQITAFQEDFY	AFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNA 109
A;Cross-references: EMBL:U18234; NID:g603216; PIDN:AAC59704.1; PID:g603217  A;Accession: S74263	:    ::  DYSETHYSPDGREITTYPLVEDHCYYHGRIEN 111
A/MOLECULE Type: protein  OY 110 EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAORNSGGAHLLQRRGVPGGPS A7.Residues 1.08 = 1	
LI DADDIAGIAGIAGIAGIAGIAGIAGIAGIAGIAGIAGIAGIAGI	AX
F;19-187/Domain: propeptide #status predicted <pro> F;18-187/Domain: propeptide #status predicted <pro> F;18-407/Promain: propeptide #status experimental <pro> F;18-407/Promain: propeptide #status experimental <pro> F;18-44-351,346-368/Disalfide bm. #status experimental <pro> F;18-44-351,346-368/Disalfide bm. #status experimental <pro> F;18-44-351,346-368/Disalfide pm. #status experimental <pro> F;18-45-368/Disalfide pm. #status experimental <pro> F;18-56-368/Disalfide pm. #status experimental <pro> F</pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro>	AGFGESRSRRRSGRAKFVSIPRY 219
F;329,333,339/Binding site: zinc, catalytic (His) #status predicted  Qy 220 VETLVVADESMYKFHGADLEHYLITLLATAARLYRHPSILNPINIVVVKVLLLRDRD  F;330/Active site: Glu #status predicted  Db 200 VELELVVDRAMVTKNNGDLDKIKTRAYEIVVNVBIYRYMIHVALVGLETANSED	LLATAARLYRHPSILNPINIVVVKVLLLRDRD 276 ::   ::   :  :  : IVNTVNETYRYMYIHYALVGLEIWSNED 255

Db 265 NFLSWREQNLQGQHPHDNVQLITGVDFIGSTVGLAKVSALCS-RHSGAVNOD 315  Qy 351DGLPSAFTTAHELGHVFNMPHD-NVKVCEEVFGKLRANHMMSPTLIQIDR 399  316 HSKNSIGVASTMAHELGHVEAMPHD-NVKVCEEVFGKLRANHMMSPTLIQIDR 399  400 ANDWASACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG 439  371FSRCSKIDLESFYKPQTGCLLNVPDVNKFVGGPVCGNLFVEHGEQCDCGFPGDCN 427  Qy 440ASYTLSQQCEL	Search completed: April 29, 2003, 17:13:25 Job time : 17.4848 secs			
Qy         277 SGPKVTGNAALTLRNPCAMQKKLNKVSDKHPEYMDTAILFTRQDLCGATTCDTLGMAD 334           L:	RESULT 15 A60385 monocyte surface antigen MS2 precursor - mouse C;Species: Wus musculus (house mouse) C;Decies: Wus musculus (house mouse) C;Decies: Mas musculus (house mouse) C;Decies: Mas Masculus (house mouse) C;Dete: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 26-Aug-1999 C;Accession: A60386; R;YOshida, S.; Setoguchi, M.; Higuchi, Y.; Akizuki, S.; Yamamoto, S. Int. Immunol. 2, 585-591, 1990 A;Title: Molecular cloning of cDNA encoding MS2 antigen, a novel cell surface antigen A;Reference number: A60385; MulD:91197896; PMID:1982220 A;Residues: 1-826 cYOS- A;Residues: 1-826 cYOS- A;Cross-references: EMBL:X13335 C;Superfamily: mouse meltrin alpha; disintegrin homology C;Reywords: 91ycoprotein; surface antigen; transmembrane protein F;1-1-444/Domain: signal sequence #status predicted <imm>F;330/Active site: Glu #status predicted F;330/Active site: Glu #status predicted</imm>	Ouery Match 9.5%; Score 301; DB 2; Length 826; Best Local Similarity 22.1%; Pred. No. 1.1e-14; Matches 154; Conservative 87; Mismatches 237; Indels 218; Gaps 30; Qy 1 MLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGL 53	Oy 54 IFQITAFQEDEYLHLTPDAQFLADAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEDDS 113 :	

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2003, 17:10:24; Search time 7.18023 Seconds Run on:

(without alignments)
3367.676 Million cell updates/sec

US-10-009-332-1\_COPY\_1\_583

3163 1 MLLLGILTLAFAGRTAGGFE.....SCNLEPCPSSASGKSFREEQ Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID.	່ເກັ	ATS1_HUMAN	ATS1_RAT	ATS8_HUMAN	ATS4_HUMAN	ATS8_MOUSE	ATS5_MOUSE	ATS9_HUMAN	ATS5_HUMAN	ATS4_RAT	ATS7_HUMAN	AT10_HUMAN	AT12_HUMAN	ATS2_HUMAN	ATS2_BOVIN	ATS3_HUMAN	ATS6_HUMAN	ATS5_BOVIN	ATS4_BOVIN	AD08_HUMAN	AD28_MACFA	AD12_MOUSE	AD33_HUMAN	AD28_MOUSE	AD28_HUMAN	AD12_HUMAN	DIST_BOTJA	AD08_MOUSE	AD19_HUMAN	DISA_TRIGA	ACLA_AGKAC	AD19_MOUSE	HRTD_CROAT
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æ	Query	9.4	49.3	48.9	43.1	42.3	42.0	39.3	39.0	38.3	36.9	29.6	28.2	27.7	24.9	24.5	23.8	22.9	18.9	18.9	11.1	11.0	10.4	10.3	10.2	10.2	6.6	7.6	9.5	o .5	4.	4.6	6	0.6
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OTNOSNW SNW GALIKO	Q63180 rattus no	Q9p0k1 homo sapien	035227 mus musc	P34182 crotalus	Q923w9 mus musc	Q13444 homo sap	Q9h2u9 homo sap	Q28475 macaća fasc	P30403 agkistrodon			S
AD22_MOUSE	AD07_RAT	AD22_HUMAN	AD07_MOUSE	HRTE_CROAT	AD33_MOUSE	AD15_HUMAN	AD07_HUMAN	AD07_MACFA	DISR_AGKRH	AD22_XENLA	AD11_HUMAN	ALIGNMENTS
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857	789	906	788	478	797	814	754	176	478	935	169	
6.8	8.9	8.9	8.7	9.8	8.1	8.1	7.8	7.7	7.7	7.6	7.5	
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"Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene."; Inflammation associated gene."; Biol. Chem. 272:556-562(1997).
                                   ATSI_MOUSE STANDARD; PRT; 968 AA.
P97887; 054768;
30-MAY-2000 (Rel. 39, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin.motifs 1) (ADAM-TS 1) (ADAM-TS 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cathepsin L proteases.";
Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
-I- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLYED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Progesterone-regulated genes in the ovulation process: ADAMTS-1 and
                                                                                                                                                                                                                                                                                                         STRAIN=129/SvJ;
MEDLINE-98110583; PubMed=9441751;
MINO K., Lizasa H., Ohno S., Matsushima K.;
"The exon'hitron organization and chromosomal mapping of the mouse ADAWTS-1 gene encoding an ADAM family protein with TSP motifs."; Genomics 46:466-471(1997).
                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
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Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.;
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"ADAMTS-1 is an active metalloproteinase associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M.,
Ohno H., Matsushima K.;
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SEQUENCE FROM N.A.
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Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 274:18821-18826(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20389568; PubMed=10930576;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extracellular matrix.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                   ATS1_MOUSE
RESULT 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                            DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN'LIKE DOMAIN. SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                     CATALYTIC ÁCTIVITY: CLEAVES AGGRECAN AT THE 1691-GLU-1-LEU-1692 STIE, WITHIN THE CHONRACITIN SULFATE ATTACHMENT DOMAIN. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
                                                                                                          INDUCTION: INDUCED IN VITRO IN COLON ADENOCARCINOMA CELLS BY INTEREBURIAL., OR IN VIVO IN KIDNEY AND HEART BY LIPOPOLYSACCHARIDE. ALSO INDUCED BY LH STIMULATION IN GRANULOSA CELLS OF PREOVULATORY FOLLICLES.
VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SM00209; TSP1; J.
PROSITE; PS50215; ADAM_WEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix; Heparin-binding.
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
            CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY
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N -> S (IN REF. 2).
T -> S (IN REF. 2).
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TSP TYPE-1 3,
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(BY
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InterPro: IPR001762; D181ntegrin.
InterPro: IPR001762; D181ntegrin.
InterPro: IPR001590; Reprolysin.
InterPro: IPR0001894; TSP1.
InterPro: IPR000130; Zn_MTeptdse.
Pfam; PF004021; Reprolysin; J.
Pfam; PF01421; Reprolysin; J.
Pfam; PF01421; Reprolysin; J.
Pfam; PF01562; Pep_MI2B_Propep; J.
SWART; SM00209; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB001735; BAA24501.1; ALT_INIT.
EMBL; D67076; BAA11088.1; ALT_FRAME.
MEROPS; M12.222; -.
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ATSI_HUMAN STANDARD; PRT; 967 AA.
QUHTHS: QUPNBS: QPDRS: QPNSJ8;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondim motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).
ADAMTS1 OR METH1 OR KIAA1346.
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                                                        1 MLLLGILTLAFAGRTAGG--FEPEREVVVPIRLDPDINGRRYYWRGP-EDSGDQGLIFQI 57
                                                                           424 VTGDSHLMASMLSSLDHSQPWSPCSAXWVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLY
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Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi, Mammalia; Eulberia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Length 968;
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                              Indels
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 DB 1;
               50.4%; Pred. No. 3.2e-112; ive 79; Mismatches 154;
 49.4%; Score 1562.5;
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MEDLINE=99367466; PubMed=10438512;
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                              Conservative
                Similarity
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AF207664; AAF23772.1; -AB037767; BAA95284.1; ALT\_INIT.
AB001697; BAA95502.1; -AL162080; CAB82413.1; --

EMBL;

InterPro; IPR001762; Disintegrin. InterPro; IPR002870; Pep\_M12B\_pro

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R Interpro; IPR0012870; Peptingly.

R Interpro; IPR0012870; Peptingly.

R Interpro; IPR0012870; Reprolysin.

R Interpro; IPR00130; Zn_MTpeptdse.

R Pfam; PF00090; tsp_1; 6.

R Pfam; PF01421; Reprolysin; 2.

R Pfam; PF01562; Pep_M12B_propep; 2.

R RART; SM00209; TSP1; 3.

R PR051TE; PS50427; DISINTEGRIN_1; FALSE_NEG.

R PR051TE; PS00427; DISINTEGRIN_1; FALSE_NEG.

R PR051TE; PS00427; ZINC_PR0TEASE; 1.

R PR051TE; PS0424; ZINC_PR0TEASE; 1.

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MEDINE-20289799; PubMed=10830953;

MEDINE-20289799; PubMed=10830953;

MEDINE-20289799; PubMed=10830953;

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A Park H.-S., Toyoda A.A. Ishli K., Totoki Y., Choi D.-K., Soeda E.,

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Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Reichwald K., Rump A., Schillhabel M., Schudy A., Sakawa S.,

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Mincalia A., Schan A., Nordsiek G., Hornischer K., Brandt P.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Reichmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

Ramer J., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";

R. Nature 405:311-319(2000).
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNGTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER (BY SIMILARITY). HAS ANGIOGENIC INHIBITOR ACTIVITY. ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUS INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXLA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPPURE.
-! CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLU-!-LEU-1939
-!- CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1938-GLU-!-LEU-1939
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro.";
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Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S., Lombardo M., Iruela-Arispe M.L.;
"METH-1, a human ortholog of ADMYS-1, and METH-2 are members of family of proteins with anglo-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Endothelial cells;
MEDLINE-20247184; PubMed=10785405;
Glienke J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,
Rosenthal A., Thierauch K.H.;
"Differential gene expression by endothelial cells in distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 267:2820-2830(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
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ZINC (CATALYTIC) (BY SIMILARITY).

SIMILARITY

CYSTEINE SWITCH (POTENTIAL)

BY SIMILARITY.

ADAMTS-

2INC (CATALYTIC) (BY SIMILARITY).
2INC (CATALYTIC) (BY SIMILARITY).
DSINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.

967 198 401 402 402 411 559 616 616 849 908

DOMAIN DOMAIN DOMAIN

DOMAIN DOMAIN

ACT\_SITE METAL

METAL

PROPEP CHAIN SITE METAL

TSP TYPE-1 2. TSP TYPE-1 3. POLY-LYS.

DOMAIN CARBOHYD CARBOHYD

SPACER

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17;
                                                                                                                                                                                                                                                                                                                                                                                            61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
                                                                                                                                                                                                                                                                                                                        115 AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                            166 PSG-----DPTSRC-----GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GRAKREVSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV 267
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                              1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                                                               36 LLILLAAALLAVSDALGRPSEEDEELVVP-ELE------RAP---GHGTTRLRLHAF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 TCGVVDDEPRPTGKAETEDEDEGTEGEDEGPQWS------PQDPALQGVGQP-TGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 IRKKREVSSHRYVETMLVADQSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSLVVV
                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                  67;
                                                                                                                                                              Score 1560.5; DB 1; Length 967; Pred. No. 4.6e-112;
                                                                                                                                                                                                  160; Indels
                                                                                                                         105383 MW; C189389324741ED1 CRC64;
                                                                     P -> A (IN REF. 4 AND 5).
Q -> H (IN REF. 1).
S -> N (IN REF. 1).
                                                                                                                                                                                               73; Mismatches
                                                                                                                                                            49.3%;
                                                                                                                                                                                             Matches 320; Conservative
843
547
720
764
227
468
561
                                                                                                                                                                            Similarity
                                                                     CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                     CARBOHYD
                                                                                                                                                              Query Match
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EMBL; AF170084; AAF15317.1; -. EMBL; AF060152; AAD48080.1; ALT\_INIT.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley; TSSUE-Liver;
MEDLINE-20304099; PubMed-10847486;
Diamants I., Luethi M., Hoesli M., Reichen J.;
Diamants I., Luethi M., Hoesli M., Reichen J.;
Cloning of the rat ADAM'S-1 gene and its down regulation in endothelial cells in cirrhotic rats.";
Liver 20:165-172(2000).
-1- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. HAS ANGIOGENIC INHIBITOR ACTIVITY (BY SIMILARITY). ACTIVE METALLOPROTEASE, WHICH MAY BE ASSOCIATED WITH VARIOUG INFLAMMATORY PROCESSES AS WELL AS DEVELOPMENT OF CANCER CACHEXIA. MAY PLAY A CRITICAL ROLE IN FOLLICULAR RUPTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9WUQ1; Q9ERI1;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
ADAMYS-1 precursor (RC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1).
                                                                                                                                 447
                                                                                                                                                                                                                                                                     CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: CLEAVES AGGRECAN AT THE 1683-GLU-|-LEU-1684
STIFE, WITHIN THE CHONDROLIN SULFATE ATTACHMENT DOMAIN.
-1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                487
                                                                                                                                                                                                                                                                                                      DTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley, TISSUE-Brain,
Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.,
Little S.P.,
"Induction of a disintegrin and metalloprotease with the
thrombospondin type I motif (ADAMIS).",
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
                                                                                                                                                                    RHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARQCTNPTPANGGKYCEGVRVKYR
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INDUCTION: DOWN-REGULATED IN ENDOTHELIAL CELLS DERIVED FROM
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-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNAE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . .) (POTENTIAL)
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. . .) (POTENTIAL)
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5e-111;
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I -> T (IN REF. 2).
i; F93C864F6DCDB4CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | POLY - ARG. | POLY - ARG. | POLY - ARG. | P. LINKED (GLCNAC. . . ) | P. LINKED (GLCNAC. . . ) | P. LINKED (GLCNAC. . . ) | P. LINKED (GLCNAC. . . ) | P. LINKED (GLCNAC. . ) | P. LINKED (GLCNAC. . ) | P. Y (IN REF. 2) | P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82; Mismatches 165;
                                                                                                                                                                                                                                              Interpro; IRR001890; Pep_MIN2_propep.
Interpro; IRR001590; Reprolysin.
Interpro; IPR0001590; Reprolysin.
Interpro; IPR000184; TSP1.
Interpro; IPR000184; TSP1.
Interpro; IRR000180; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 6.
Pfam; PF001421; Reprolysin; 2.
Pfam; PF00162; Pep_MIN2B_propep; 2.
PR0SITE; PS50012; ADAM_MEPRO; 1.
PR0SITE; PS50012; ADAM_MEPRO; 1.
PR0SITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycop.
Repeat; Extracellular matrix; Popepmentary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (DISINTEGRIN-LIKE. TSP TYPE-1 1. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPACER.
TSP TYPE-1 2.
TSP TYPE-1 3.
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ZINC (CATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY. ADAMTS-1.
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Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
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                                                                                                                                                            EMBL; AF149118; AAD34012.1; -. EMBL; AF304446; AAG29823.1; -.
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962
967 AA;
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Matches 312; Conserv
                                                                                                                                                                                                            MEROPS; M12.222;
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MEDLING-20079168; PubMed=10610729;

Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;

Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;

"ADAM-TS8, a novel metalloprotease of the ADAM-TS family located on mouse chromosome 9 and human chromosome 11.";

Genomics 62:312-315(1999).

-I - FUNCTION: HAS ANTI-ANGIGENIC PROPERTIES.

-I - COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-I - SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similatity).

-I TISSUE SPECIFICITY: HIGLY EXPRESSED IN ADULT AND FETAL LUNG, LOWER EXPRESSION IN BRAIN, PLACENTA, HEART, STOMACH AND FETAL BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDNEY.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                               SIPRYVETLVVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS 8) (ADAM-TS 9)
GVPGGPSGD-----PTSRCGVASGWNPALLRALDPYKPRRAGFGESRSRRRSGRAKRFV 214
                                          VGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTL 394
                                                                                                                                                                                                                                                                                                                                                                               395 IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGV 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"METH-1, a human ortholg of ADAMTS-1, and METH-2 are members of process with angio-inhibitory activity.";
J. Biol. Chem. 274:23349-23357(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          890 AA.
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MEDLINE-99367466; PubMed-10438512;
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614 PDN-NGKTFREEQ 625
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ADAMIS8 OR METH2
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Q9UP79; Q9N
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ID ATSB_HUMAN

ID ATSB_HIM

DT 16-OCT-

DT 16-OCT-

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DE (METH-E)

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
E -> R (IN REF. 2).
YLTELINGGHGBOLLDAPGAALPLETGL -> FSGCHLQGW
IHFKYLCKCVSELKCDLAPP (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001362; Disintegrin.
InterPro; IPR002870; Pep_MA12B_propep.
InterPro; IPR0012870; Reprolysin.
InterPro; IPR001390; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
IPR001421; Reprolysin; 1.
IPR051TE; Ps001421; Reprolysin; 1.
IPR051TE; Ps00142; ZINC_FROTEASE; 1.
IPR05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 VSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGV
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PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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Pred. No. 7.2e-97
1; Mismatches 17:
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SPACER.
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N-LINKED
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Conservative 8
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MIM; 605175; -
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Best Local S:
Matches 284
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CARBOHYD
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ATS4_HUMAN STANDARD; PRT; 837 AA.
075173; OSUN83;
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 41, Last annotation update)
15-OCT-2001 (Rel. 44, Last annotation update)
MDAMYS-4 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS 4) (Adgrecanase 1)
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MEDLINE-99286303; PubMed=10356395;
Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M.,
Liu R.-G., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
Nagase H., Itch Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K.,
Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Irzaskos J.M., Arner E.C.; ^{\circ} *Purification and cloning of aggrecanase-1: a member of the ADAMTS
                                                                            SEGSCLPEEEVERPKPVVDGGWAPWGEVGSRTCGGGVQFSHRECKDPEPQNGGRYCLG
                 KVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT-T
                                                                                                                                                                                              CDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRA
                                                                                                                                                                                                                                                              NHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG--ASYTL
                                                                                                                                                                                                                                                                                                                               445 SQQCELAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTSCGEGKLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                              208 GRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV
                                                                                                                                                                                                                                                                                                                                                                                             500 LKGACVERHNLNKHR--VDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEG
177 ASGWNPAILRALDPYKPR---RAGFGESRSR.
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MEDLINE-98403880; PubMed-9734811;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site.

C -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

C -1- SUBCELLUIAR LOCATION: Secreted, Associated with the extracellular matrix (By similarity).

C -1- TISSUB SPECIFICITY: EXPRESSED IN BRAIN, LUNG AND HEART. EXPRESSED AT VERY LOW LEVEL IN PLACERTA AND SKELETAL WUSCLES.

C -1- INDUCTION: BY INTERLEUKIN-1.

C -1- INDUCTION: BY INTERLEUKIN-1.

C -1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT POR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.

C -1- PTM: THE PRECURSOR IS CLEAMED BY A FURIN ENDOPEPTIDASE.

C -1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.

C -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.

C -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.

C -1- CAUTION: HAS SOMETIMES BEEN REFERRED TO AS ADAMTS2.
                                                                                                                                                  Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross H.,
Burn T.C., Arner E.C.;
"The thrombospondin motif of aggrecanase-1 (AbAMTS-4) is critical for
aggreen substrate recognition and cleavage.";
J. Biol. Chem. 275:25791-25797(2000).
-I-FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGIYCAN, AND MAY BE
INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE
DESTRUCTION OF AGGRECAN IN ARTHATIC DISEASES. COULD ALSO BE A ONE
CRITICAL FACTOR IN THE EXACERBATION OF NEURODEGENERATION IN
ALZHEIMER, S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prant, Provoul30; Zn_MTpeptdse.

Prant, Pro0090; tsp_1; 1.

Prant, Pro10121; Repro1ysin; 1.

SMART; SM00209; TSP1; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00042; TSP1; 1.

PROSITE; PS00092; TSP1; 1.

PROSITE; PS00092; TSP1; 1.

PROSITE; PS00127; DISIMPGRIN_1; FALSE_NEG.

Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Extracellular matrix.

SIGNAL

DECORPORATE CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONT
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                        (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111111111111
Sawaji Y., Nagase H., Saklatvala J., Clark A.R.; "ADDANTS-4 genomic locus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ dat
                                                                                                                AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYS-RICH.
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                                                                                                                PARTIAL SEQUENCE, AND CHARACTERIZA:
MEDLINE-20400518; Pubmed-10827174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001762; Disintegrin.
Interpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB014588; BAA31663.1; -. EMBL; AF148213; AAD41494.1; -. EMBL; AX044847; AAL02262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M12.221; -.
Genew; HGNC:220; ADAMTS4.
MIM; 603876; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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                                                                                                                                                           12;
                                                                                                                                                                                                                                                                           61 QEDFYLHLIPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120
                                                                                                                                                                                                                                                                                                      180 WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMYKFHGADLE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KAPLGSPSPRPR--RAKRFASLSRFVETLVVADDKMAAFHGAGLK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 RYLLTVMAAARKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHELGHVFNMPHDNVKVCEEVFGKL-RANHMMSPTLIQIDRANPWSACSAAIITDFLDSG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 AHELGHVFNMLHDNSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0c7-2001 (Rel. 40, Created)
16-0c7-2001 (Rel. 40, Last sequence update)
16-0c7-2001 (Rel. 41, Last amoncation update)
ADAMTS-8 precursor (EC 34.24-.) (A disintegrin and metalloproteinase with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS 8) (ADAM-TS 8)
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                                                                                                                                                           Gaps
                                                                                                                                                                                             1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60
                                                                                                                                                                                                                     GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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MEDLING-20079168; PubMed=10610729;

Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;

Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;

"ADAM-TS8, a novel metalloprotease of the ADAM-TS family located mouse chromosome 9 and human chromosome 11.";

Genomics 62:312-315(1999).

-I- FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES (BY SIMILARITY).

-I- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                    43;
                                                                                                              DB 1; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQLARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
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  A -> T (IN REF. 1).
R -> Q (IN REF. 3).
G -> R (IN REF. 3).
; 5DF9C9AC137DF41F CRC64;
                                                                                                                                       2e-95
                                                                                                                                  Pred. No. 4.2e
88; Mismatches
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                                                                                                              Score 1338.5;
                                                                                                         Match 42.3%;
Local Similarity 45.1%;
Nes 265; Conservative 8
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CONFLICT
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ATS8_MA

DD ATS8_MA

DT 16-OCT

DT 15-OCT

DD 15-JUN

DE ADAMTS

OC BURSTY

                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                      MATCHIX (BY SIMILARILY).

TISSUE SPECIFICIALLY IN ADULT LUNG AND HEART AND LOW EXPRESSION DISTING MOUSE DEVELOPMENT.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 IFQITAPQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLLGILTL-----AFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AFHLSAFGQGFVLRLAPDASFLAPEFKIERLG-GSSAAAGGEPGLRGCFFSGTVNGERES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFACE...

TESP TYPE-1 2.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                              TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 1329.5; DB 1; Length 44.9%; Pred. No. 2.3e-94; ive 85; Mismatches 175; Indels
SUBCELLULAR LOCATION: Secreted. Associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
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(BY
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SINC (CAPALYTIC) (
ZINC (CAPALYTIC) (
DISINTEGRIN-LIKE.

CYS-RICH.

SPACER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50092; TSP1; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Metalloproteeaes; Zinc; Signal; Gly(Repeat; Extracellular matrix; Heparin-bhdding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
ADAMTS-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00209; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884; TSP1.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 2.
Pfam; PF01421; Reprojysin; 1.
SWART; SM00209; TSP1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1353468; Adamts8.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF175282; AAF25805.1; -.
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506
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905 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M12.226;
                                                                                                                   FOR A TIGHT
                                                                                                                                                              SIMILARITY)
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ACT_SITE
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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Developmental syage: Expressed Specifically in the Peri-
Implantation Period in Embryo and Trophoblast and at Low or
UNDECTABLE LEVEL THEREAFTER.

DOMIN: THE SPACER DOWAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACLLULAR MATRIX.

PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99385124; PubMed=10464288; Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.; Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.; Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.; Signal Propertion and ADAM-TS7, novel members of a new family of zinc metalloproteases."; J. Blod. Chem. 274:2555-25563(1999).

-1. FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY BE INVOLVED IN TIS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISBASES. MAY PLAY A ROLE IN PROTEOLYTIC PROCESSING MOSTLY DURING THE PERI-IMPLANTATION PERIOD.
-1. CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                 379
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                                                                                                                                                                                                             492
                                                                                                                                                                                                                                   516
                                                                                                                                                                                                                                                                    457 HSTLYELDQQCKQIFGPDFRHCPNTSVEDICVQLCARHRDSDEPICHTKNGSLLWADGTP
                        -----RAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILN
                                    PINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQD
                                                                                                                  321 LCG-ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE
                                                                                                                                                                           440 AS--YTLSQQCELAFGVGSKPCP---YMQYCTKLWCTGKAKGQMVCQTRH--FPWADGTS
                                                                                                                                                                                                                                                          CGEGKLCLKGACVERHNLN--KHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPAN
 REDP----GLAAAEVFPLPQGLEWEVEMGNGQGQERSDNEEDRKQDKEGLLKETEDSRKV
                                                                                                                                                               380 VFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                       930 AA
                                                                                                                                                                                                                                                                                                                    GGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADMP-2) (Implantin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                       ATS5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAMTS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NSQGAHLLQRRG-----VPGGPSGDPTSRCGVASGWNPAILRALDPY 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 KPRRAGFGESRSRRRSG-------RAKRFVSIPRYVETLVVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 ESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 IYGDGSSRILHVYNREGFSFEALPPRASCETPASPSG---------
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%; Score 1242; DB 1; 44.9%; Pred. No. 1.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISINTEGRIN-LIKE.
TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS50092; TSP1, 1.
PROSITE: PS00142; TSP1, 1.
PROSITE: PS00427; DISINTEGRIM.1; FALSE NEG.
Hydrolase: Metalloprotease; Zinc; Signal; GREPEA; Extracellular matrix.
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SPACER.
TSP TYPE-1 2.
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MGD, MGI.1346521; Adamts5.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001870; Pep_MI2B_propep.
InterPro; IPR001890; Reprolysin.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. ADAMTS-5.
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POLY-ARG.
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                                                                                                                                                            EMBL; AF140673; AAD56356.1; -.
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930 AA;
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Local s...
243;
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METAL
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DOMAIN
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Matches
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397 IEDDGLHAAFTVAHEIGHLLGLSHDDSKFCEENFGTTEDKRLMSSILTSIDASKPWSKCT 456
                                408 AAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTK 467
                                                  DPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREE 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         large proteins in vitc.";

Res. 7:65-73(2000).

Res. 7:65-73(2000).

COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFCITY: HIGHLY EXPESSED IN ALL FETAL TISSUES.

EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, LUNG, PALCENTA. ALSO DETECTED IN SILVAL CORD AND BRAIN. NOT DETECTED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                  LWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER----HNLNKHRVDGSWAKW 522
                                                                                                                                                                                  metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
MEDLINE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVI The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAKI R.A.;
"ADAMIS_9, a novel member of the ADAM-TS/Metallospondin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                          ATS9_HUWAN STANDARD; PRT; 1629 AA.
Q9P2N4; Q9NR29;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and me with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal;
MEDLINE~20396138; PubMed=10936055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 67:343-350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAMTS9 OR KIAA1312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |:| |||:: :::!|
47 EYEIVSPIRVNALGEPFPTNVHFKRTRRSINSATDPWPAFASSSSSSTSSQAHYRLSAFG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDFYLHLTPDAQFLAPAFSTEHLGVP----LQGLTGGSSDLRRCFYSGDVNAEPDSFAAV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR00084; TSP1.

Interpro; IPR000130; Zn_MTpeptdse.

R Interpro; IPR000130; Zn_MTpeptdse.

R Pfam; PF01421; Reprolysin; 1.

P Ffam; PF01562; Pep-M2B_propep; 1.

R SMART; SW00209; TSP1; 12.

R PROSITE; PS00427; DISINFERIN_1; FALSE_NEG.

R PROSITE; PS00427; TSP1; 9.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R Hydrolase, Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; W Repeat; Extracellular matrix; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Pred. No. 1.3e-86;
87; Mismatches 210; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
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SIMILARITY).
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ClC4CEFF58B8941F CRC64;
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N-LINKED GLCNAC...)
N-LINKED GLCNAC...)
N-LINKED GLCNAC...)
N-LINKED GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                          DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC.
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TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 7.
TSP TYPE-1 9.
TSP TYPE-1 10.
TSP TYPE-1 110.
TSP TYPE-1 110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                       ISP TYPE-1 1.
                                                                                                                         InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1629 AA; 182649 MW;
                                                         EMBL; AE261918; AAF89106.1; -. EMBL; AB037733; BAA92550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.0%;
                                                                                                     HGNC:13202; ADAMTS9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EREVVVPIRLDP----
                                                                    EMBL; AB037733; BAA9
HSSP; P15167; 1ATL.
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1184
1240
1332
1386
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                                                                                          MEROPS; M12.021
                                                                                                                 MIM; 605421;
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METAL
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Matches
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MEDLINE-20289799; PubMed-10830953; Hattori M., Yada T., Hattori M., Fujiyama A., Tajlor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBUNAC, OBUKP2;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
ADAMTS-5 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 5) (ADAM-TS 5) (ADAM-TS 11).
ADAMTSO OR ADAMTS1 11).
                                                                                                                                                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                           446
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                                                                                                                                                     343
                                                                                                                                                                                  327
                                                                                                                                                                                                                400
                                                                                                                                                                                                                                                                                                                                      HVMAPTLNFYTNPWMWSKCSRKYITEFLDTGYGECLLNEPESRPYPLPVQLPGILYNVNK 519
                                                                                                                                                                                                                                                                                                                                                                     QCELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                CVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
SLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abbaszade I., Liu R.-O., Yang F., Rosenfeld S.A., Ross O.H., Link J.R., Ellis D.M., Tortorella M.D., Pratta M.A., Hollis J.M., Whyn R., Duke J.L., George H.J., Hillman M.C. Jr., Murphy K., Wiswall B.H., Copeland R.A., Decicco C.P., Bruckner R., Nagase H., Ito Y., Newton R.C., Magolda R.L., Trzaskos J.M., Hollis G.F., Arner E.C., Burn T.C., "Cloning and characterization of ADAMTS11, an aggrecanase from the ADAMTS family."
                                                                                                                                                                                                                                                                                                                                                                                     QCELIFGPGSQVCPYMMQCRRLWCNNVNGVHKG---CRTQHTPWADGTECEPGKHCKYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                         --SRSRRKSG
                                                                                          227 EHKN----RHSKDKKKTRARKWGERINLAGDVAALNSGLATEAFSAYGNKTDNTREKRTHR
                                                                                                                                                                                    269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA-TTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  930 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 274:23443-23450(1999).
                                                               SGWNPAILRALDPYKPRRAGFGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99367476; PubMed-10438522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||| || SCNTEPCLKQK--RDFRDEQ 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 SCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATS5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
ATS5_HUMAN
                                                               178
                                                                                                                          503
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 274:2555-25563(1999).

-i. FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEGGLYCAN, AND MAY BE INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES. MAY PLAY A ROLE IN PROTECLYTIC PROCESSING MOSTLY DURING THE PERI.IMPLANTATION PERIOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix (By similarity).
TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL, PRIMARILY IN PLACENTA
BUT ALSO IN OTHER TISSUES, SUCH AS HEART AND BRAIN, AND ALSO
CERVIX, UTENTY, UTENDER, ESOPHAGUS, RIB CARTILAGE,
CHONDROBLASTOWA, FIBROUS TISSUE AND JOINT CAPSULE FROM AN
ARTHRITIC PATIENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shinitani A., Sasaki T., Magamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H. Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Fetal brain;
MEDLINE-99395124; PubMed=10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
Hurskainen T.E., AbM-TS6, and ADAM-TS7, novel members of a new family of zinc metalloproteases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00000; tsp_1; 2.

Pfam; PF01421; Reprolysin; 1.

Pfam; PF01421; Reprolysin; 1.

Pfam; PF01421; Pep_M12B_propep; 1.

SMART; SM00209; TSP1; 2.

PROSITE; PS500427; DISHWEGRIN_1; FALSE_NEG.

PROSITE; PS00042; TSP1; 1.

PROSITE; PS00042; TSP1; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Repeat; Extracellular matrix.

SIGNAL

PROPERTIAL.

16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001762; Disintegrin.
Interpro; IPR002870; Pep_M12B_propep.
Interpro; IPR001590; Reprolysin.
Interpro; IPR000884; TSPI.
Interpro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 413-930 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 605007;
                 TIME TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO SEA TO S
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                                                                                                                                                                                                                                                                                                                                                                                               RRAGFGES---RSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAA 250
                                                                                                                                                                                                                                                                                                                                                                                                          RLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLR---RCFYS 104
                                                                                                                                                                                                                                                                                                                GDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPL---PNASAPAAQRNSQGA----HLL 157
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 TSCGEGKLCLKGACVER----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                   ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINFERIN-LIKE.
TSP TYPE-1 1.
                                                                                                                                                                                                                                DB 1; Length 930;
            SWITCH (POTENTIAL)
                                                                                                                                                                         -> G (IN REF. 2).
-> H (IN REF. 3).
-> L (IN REF. 2).
B64281502F28193B CRC64;
                                                                                                                                                                                                                            Score 1212.5; DB 1;
Pred. No. 2.3e-85;
71; Mismatches 180;
                                                                                                             POLY-ALA.
POLY-ARG.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATS4_RAT STANDARD; PRT; 630 AA. 09ESP7; Q9ESP8; Q9ESP6; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                         SPACER.
TSP TYPE-1 2.
  ADAMTS-5.
CYSTEINE 5
                                                                                  CYS-RICH.
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                                                                                                                                                                                                         101715 MW;
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                                                                                                                                                                                                                                                 258; Conservative
                                                                                                                                                                                                        930 AA;
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AC Q9ES
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                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-4 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
                                                                                                                                                                                                                                                                                                       COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                   Satoh K., Suzuki N., Yokota H.;
"ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin
motifs) is transcriptionally induced in beta-amyloid treated rat
astrocytes.";
                                                                                                                                                                                                                      Neurosci. Lett. 289:177-180(2000).
-!- FUNCTION: CLEAVES AGGRECAN, A CARTILAGE PROTEOGLYCAN, AND MAY INVOLVED IN ITS TURNOVER. MAY PLAY AN IMPORTANT ROLE IN THE DESTRUCTION OF AGGRECAN IN ARTHRITIC DISEASES.
                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Cleaves aggrecan at the 392-Glu-|-Ala-393
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VLINKED (GLCNAC. . .) (POTENTIAL).
N-IINKED (GLCNAC. . .) (POTENTIAL).
63A428753167C7EF CRC64;
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PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

Hydrolase; Metalloprotease; Zinc; Glycoprotein; Zymogen;
Extracellular matrix.

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PROPEP <1 5 BY SIMILARITY.
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(BY
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EMBL, AB042271; BAB16473.1; -.
EMBL, AB042273; BAB16473.1; -.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001894; TSP1.
InterPro; IPR001894; TSP1.
Ffam; PF00190; tsp.1; 2.
Pfam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 1.
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                                                                                                                                             STRAIN-Wistar; TISSUE-Brain;
MEDLINE-20415831; PubMed-10961658;
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PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
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Genew; HGNC:
MIM; 605009;
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Matches 250;
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                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATIX (BY SIMILATITY).
TISSUE SPECFICITY: EXPRESED IN HEART, BRAIN, PLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.
DOMAIN: THE SPACER DOMAIN THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERRATION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-7 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAM-TS 7) (ADAM-TS?).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc Metalloproteases.";
J. Biol. Chem. 274:2555-25563(1999).
-1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular.
                                                                                                                                                                  329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRAN 387
                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                     448 CELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE 506
                                                                                                                                                                                                                                                                                              242 COLIFGPDSSHCPOLPPPCAALWCFGHLNGHAMCQTKHSPWADGTPCGPAQACMGGRCLH 301
                                                                                                                                                                                                                                                                                                                        507 RHNLNKHRVD - GSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRS 564
                                                                                                                                                                                                                                                                                                                                     102 VDQLKDFNIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTKPVPRNGGKYCEGRRTPFRS 361
                                                              209 RAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
                                                                                                                269 VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD 328
                                                                                                                                Gaps
                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-99395124; PubMed-10464288;
Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
"ADAM-TS5, ADAM-TS6, and ADAM-TS7, Novel Members of a New Family of
                                                                             2 RIKRFASLSRFVETLVVADDKMARFHGAGLKHYLLTVMAAAAKAFKHPSIRNPVNLVVTR
                                                                                                                                                                                                                                 HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                       5;
             Length 630;
                         ; Pred. No. 3.4e-82;
52; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
             DB 1;
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            36.9%; Score 1168.5; 54.9%; Pred. No. 3.4e
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Mammalia; Eutheria; Primates;
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                                     Conservative
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                            Similarity
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Q9UKP4;
              Query Match
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                                         Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 PARPGHAQ-PHVVYKRQAPERLAQRGDSSAP-STCGV------QVYPELESRRERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 APAFYELQYRGRE-----LRFNLTANQ-----HL-----LAPGFVSETRRG----GL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP TYPE-1 1.

CYS-RICH.
SPACE.
TSP TYPE-1 2.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50042; TSP1; 1.
PROSITE; PS500477; DISINTEGRIN 1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix.
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BY SIMILARITY.
LIC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
DISINTEGRIN-LIKE.
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                                                                                                                                                             Disintegrin.
Pep_M12B_propep.
Reprolysin.
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
SMART; SM00209; TSP1; 2.
                                                            EMBL; AF140675; AAD56358.1;
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InterPro; IPR002870;
InterPro; IPR001590;
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997 AA;
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AT12_HUMAN
ID AT12_HU
AC P58397;
DT 15-JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAWTS-10 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix (By similarity).
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By
                                          400 GSGNDCEPV-GK--RPFIMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDPPAKDI 456
373 -NVKVCEEVFGKLRANHAMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP- 430
                                                                                                                                                                                                                   513 GTRCGENKWCLSGECVP-VGFRPEAVDGGWSGWSAWSICSRSCGMGVQSAERQCTQPTPK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADAM-TS10: a novel member of the ADAM-TS family containing multiple
                                                                                        431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWAD
                                                                                                                       GTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50032; TSP1; 2.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS001427; DISINIEGRIN. 1; FALSE_NEG.
HYdrolase; Metalloprotease; Zinc; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1077 AA
                                                                                                                                                                                                                                                                          550 NGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                            InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR0001804; TSP1.
InterPro; IPR000130; Zn_MTeptdse.
Pfam; PF00090; tsp_1; 5.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF01562; Pep_M12B_propep; 1. SMART; SM00209; TSP1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF163762; AAG35563.1; -. MEROPS; M12.235; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:13201; ADAMTS10.
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AT10_HUMAN
Q9H324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apte S.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 YVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGV--ASGW--NPAILRALD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHG-ADLEHYLLTLLAT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL------NK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AHELGHVFNMPHDNVKVCEEVFG----KLRANHMMSPTLIQIDRANP--WSACSAAIITD 413
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 EVVVPIRLDPDINGR-----RYYWRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQF 74
                                                                                                                                                                                                                                                                                                                                                                                                          365 AHEIGHIFGMNHDGVGNSCGARGODPAKLMAAHITMKT-----NPFVWSSCNRDYITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 KAKGQMVCQTRHFPWADGTSCGEGKL----CLKGACVERHNLNKHRVDGSWAKWDPYGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 VSDKHPEYWDTAILFTRQDLC--GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 FLDSGHGDCLLDQPSK-PISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 KSNR---CIINSIPAAEGTLCQTHTIDKGWCYKRVCVP-FGSRPEGVDGAWGPWTPWGDC
                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                 Score 891.5; DB 1; Length 1077;
                                                       SIMILARITY).
                         WC (CATALYTIC) (BY SIMILARITY) SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 SRICGGGVQLARRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ
                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2e-60;
80; Mismatches 239; Indels
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N-LINKED GLCNAC...) (
N-LINKED GLCNAC...) (
N-LINKED GLCNAC...) (
N-LINKED GLCNAC...) (
N-LINKED GLCNAC...) (
                                                       (BY
                                                  ZINC (CATALYTIC) (ZINC (CATALYTIC) (DISINTEGRIN-LIKE.
                                                                                                               SPACER.

TSP TYPE-1 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 4.
SIMILARITY.
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P58397;
15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                              28.2%;
                                                                                                                                                                                                                                                                                                                                              36.8%;
                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 36.8
Matches 219; Conservative
                                                                                                                                                                                                        64
196
297
714
769
866
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196
297
297
714
769
769
866
866
1077 AA;
                      METAL
ACT_SITE
METAL
                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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SEQUENCE
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Matches
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                                                                                                                                    METAL
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                                                                                                                                                                                                                                                                                                      DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                      PTM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND TO A FRACHENT CONTAINING THE N-TERMINAL RECION INCLUDING THE METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND THE C-TERMINAL FRACHEN CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                      R InterPro; IPR00126; Disintegrin.
R InterPro; IPR0012870; Pep_M12B_propep.
R InterPro; IPR0012890; Reprolysin.
R InterPro; IPR000130; Zn_MTpeptdse.
R InterPro; IPR000130; Zn_MTpeptdse.
R Pfam; PF001421; Reprolysin; I.
R Pfam; PF01421; Reprolysin; I.
R Pfam; PF01421; Reprolysin; I.
R PR051TE; PS00209; TSD1; 8.
R PR051TE; PS001427; DISINTEGRIN_1; FALSE_NEG.
R PR051TE; PS010427; TSD1; 2.
R PR051TE; PS010427; TSD1; 2.
R PR051TE; PS010427; ZINC_PR0TEASE; 1.
R PR051TE; PS01042; ZINC_PR0TEASE; 1.
R PR051TE; PS01042; ZINC_PR0TEASE; 1.
          15-JUN 2002 (Nel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-
                                                                                                                                                                                                                                                          matrix (By similarity).
TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is wid
expressed in gastric carcinomas and in cancer cells of diverse
                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMITARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISINTEGRIN-LIKE TSP TYPE-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY. ADAMTS-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPACER 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
  15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                 IISSUE=Fetal lung;
MEDLINE=21264577; PubMed=11279086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ250725; CAC20419.1; -. Genew; HGNC:14605; ADAMTS12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Extracellular matrix.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
465
465
597
701
827
886
                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 606184;
                                                                                                                                                                                                                                                                                                origin.
                                                               ADAMTS12.
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPD--SFAAVSLCGGLRGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVNQGFLSNSYIMEKRYGNLSHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGWNPAILR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                       PEREVVVPIRLD------PDINGRRYYWRGPEDSGDQGLIFQITAFQEDFYLHL 68
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPEYWDTAILFTRODLCGA - - TTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTRHFPWADGTSCGEGKLCLKGACVERHNLNK--HRVDGSWAKWDPYGPCSRTCGGGVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGAD-LEHYLLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 NPVHHDVAVLLTRKDICAGFNRPCETLGLSHLSGMCQPHRSCNINEDSGLPLAFTIAHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHVFNMPHDNVK-VCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 LLDQPSKP-ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQ-YCTKLWCTGKAKGQMVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 LDDIPKKKGLKSKVIAPGVIYDVHHQCQLQYGPNATFCQEVENVCQTLWCSVKG----FC
                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                   Length 1593;
                                                                                                           (BY SIMILARITY)
                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 230; Indels
                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 ARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSTEINE SWITCH (POTENT)
BY SINC (CATALYTIC) (BY SIN
BY SINC (CATALYTIC) (BY SIN
ZINC (CATALYTIC) (BY SIN
N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                   Score 876.5; DB 1
Pred. No. 2.7e-59;
                        TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 8.
TYPE-1
                                                                                 POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                      2/.
36.6%; --
92; }
                                                                                                                                                                                                                                                                                                                                                         AA; 177545 MW;
                                                                                                                                                                                                                                                                                                                                                                                   27.78;
                                                                                                                                                                                                                                                                                                                                                                                                                214; Conservative
                                                                                 Similarity
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1371
1378
1503
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METAL
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               DOMAIN
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                                                          16-OCT-2001 (Rel. 40, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
ADANTS-2 precursor (E. 3.4.24.14) (A disintegrin and
metalloproteinase with thrombospondin motifs 2) (ADAM-TS2)
(Procollagen I/II amino-propeptide processing enzyme) (Procollagen I/II amino-propeptide processing enzyme) (Procollagen I/II amino-propeptide processing enzyme)
(Procollagen I/II amino-propeptide processing enzyme)
ADAMTS2 OR PCINP OR PCPNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO COLLAGEN TYPE XIV (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND AORTA AND AT LOW LEVELS IN THYMUS AND BRAIN.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPERTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: Defects in ADAMTS2 are the cause of Ehlers-Danlos syndrome type VIIC (EDS-VIIC), a recessively inherited connectivetissue disorder characterized clinically by severe skin fragility and joint hypermobility and biochemically by the presence in skin of procellagen incompletely processed at the N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mertelecki W., Sieron A.L., Las.-W., Schwarze U., Petty E.,
Nertelecki W., Wilcox W., Krakow D., Cohn D.H., Reardon W.,
Nertelecki W., Wilcox W., Prockop D.J., Nusgens B.V.,
"Human Ehlers-Danlos Syndrome type VII c and bovine dermatosparaxis
are caused by mutations in the procollagen I N-proteinase gene.",
Am. J. Hum. Genet. 65:308-317(1999).
I. FUNCTION: Cleaves the propeptides of type I and II collagen prior
to fibril assembly. Does not act on type III collagen. May also
play a role in development that is independant of its role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATTIX (BY SIMILATITY).
ARE TRENATIVE PRODUCTS: 2 ISOFORMS; LPNPI (SHOWN HERE) AND SPNPI;
ARE PRODUCED BY ALTERNATIVE SPLICING. SPNPI HAS NO SIGNIFICANT N-
PROCOLLAGEN PEPTIDASE ACTIVITY.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN SKIN, BONE, TENDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen biosynthesis.
CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains at Ala-|-Gln.
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO PERTIDASE FAMILY M12B.
-1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
-1- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
    1211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99347935; PubMed-10417273;
                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ003125; CAA05880.1; -.
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; M12.301; -.
Genew; HGNC:218; ADAMTS2.
                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Skin;
ATS2_HUMAN
                     095450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
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InterPro; IPR001762; Disintegrin. InterPro; IPR002870; Pep\_M12B\_propep.

604539; -

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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 YSGDVN--AEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG-AHLLQR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336
                                                                                                                                 Hydrolase, Metalloprotease, Zinc, Signal, Glycoprotein, Zymogen, Repeat, Collagen degradation, Extracellular matrix, Heparin-binding, Alternative splicing; Ehlers-Danlos syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----INGRR-----YYW 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 GPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 MSLIEIGNPSOSLENVCRWAYLQOKPDTGHDEYHDHAIFLIRQDF-GPSGMQ--GYAPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 -VETLVVADESMYKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 NIEVLLGVDDSVVQFHGKEHVQKYLLTLMNIVNEIYHDESLGAHINVVLVRIILLSYGKS
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1211;
                                                                                                                                                                                                          ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                  SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                            CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLGGGGRWIA (IN ISOFORM SPNPI).
567 1211 MISSING (IN ISOFORM SPNPI).
1211 AA; 134722 MW; BECEEF25C23CAD2D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246;
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                                                                                                                                                                                                                                                                                                                TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
                                                                                                                                                                                  BY SIMILARITY. ADAMTS-2.
                                                                                              PROSITE; PSS0092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 788.5;
Pred. No. 1.1
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                                                                                                                                                                       POTENTIAL.
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InterPro; IPR001590; Reprolysin.
InterPro; IPR000843; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PR00190; tsp_1, 4.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1, 4.
PROSITE: PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                       SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%;
34.9%;
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METAL
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Matches
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matrix (By similarity).

TISSUE SPECIFICITY: ENZYMATIC ACTIVITY IS DETECTED AT HIGH LEVEL
IN ALL TYPE I COLLAGEN-RICH TISSUES SUCH AS SKIN, BONES, TENDONS
AND AORTA AND AT LOW LEVEL IN BRAIN AND THYMUS. THE MRNA LEVELS
WERE DISPROPORTIONATELY HIGH IN HEARY, LIVER, RETINA AND MUSCLE.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-10W-2002 (Rel. 41, Last annotation update)
15-10W-2002 (Rel. 41, Last annotation update)
ADAMTS-2 precursor (EC 3.4.24.14) (A disintegrin and metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (Procollagen I/II amino-propeptide processing enzyme) (Procollagen I N-proteinase) (PC I-NP) (Procollagen N-endopeptidase) (pNPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBUNIT: MAY BELONG TO A MULTIMERIC COMPLEX. BINDS SPECIFICALLY TO
COLLAGEN TYPE XIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA cloning and expression of bovine procollagen I N-proteinase: a new member of the superfamily of zinc-metalloproteinases with binding sites for cells and other matrix components."; proc. Natl. Acad. Sci. 0.S.A. 94:2374-2379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
384 GMCHPVRSCTLNHEDGFSSAFVVAHETGHVLGMEHDGQGNRCGD---EVRLGSIMAPLVQ 440
                                                                                                                505
                                                                                                                                                                                                             607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Cleaves the N-propeptide of collagen chain alpha-1(I) at Pro-|-Gln and of alpha-1(II) and alpha-2(I) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                    GVGSKPCPYMQY ----CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACV----
                                                                                                                                                                              --- ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARROCINPTPANGGKYCEGVRVKY
                                                   396 QIDRANPWSACSAAIITDFLDSGHGDCLLDQP---SKPISLPEDLPGASYTLSQQCELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE-97225960; PubMed-9122202;
Colige A., Li S.W., Sieron A.L., Nusgens B.V., Prockop D.J.,
Laplere C.M.;
                                                                                                                                                                                                                                                                                                                                                        PRT; 1205 AA
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                                                                                                                                                                                                                                             RSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                          QLCSRODCPDSLA--DFREEQ 626
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                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P79331;
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                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                        --- DISEASE: DEPECTS IN ADAMTS2 ARE THE CAUSE OF DERMATOSPARAXIS, A RECESSIVELY INHERITED DISORDER CHARACTERIZED BY SEVERE SKIN FRAGILITY AND BIOCHEMICALLY BY THE PRESENCE IN SKIN OF PROCOLLAGEN INCOMPLETELY PROCESSED AT THE AMINO TERMINUS.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
--- SIMILARITY: CONTAINS 1 DISINTEGRINELING.
--- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
--- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Collagen degradation; Extracellular matrix; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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TSP TYPE-1 3.
TSP TYPE-1 4.
CELL ATTACHMENT SITE (POTENTIAL).
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX. PTM: THE N-TERMINUS IS BLOCKED. PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1205;
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY
ZINC (CATALYTIC) (BY SIMILARITY
DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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(GLCNAC. . .)
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BY SIMILARITY.
ADAMTS-2.
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PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X96389; CAA65253.1; -.
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82 EHLGVPLOGLTGGSSDLRRCFYSGDV-NAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLP 140
                  141 NASAPAAQRNSQG-AHLLQRRGVP-----GGPSGDPTSRCGVASGWNPAILRALDPYKP 193
                                                                                                                                                                                                  252 LYRHPSILNPINIVVVKVLLLRDRDSGPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
                                                                                                                                                                                                                                                   311 DTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP 370
                                                                                                                                                                                                                                                                                                                      428 -SKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQY---CTKLWCTGKAKGQMVCQTR 483
                                                                                                                                                                                                                                                                                                                                                                                                      484 HFPWADGTSCGEGKLCLKGACV-----ERHNLNKHRVDGSWAKWDPYGPCSRTCGGGV 536
                                                                   194 RRAGFGESRSRRRSGRAKRFVSIPRY-VETLVVADESMVKFHGAD-LEHYLLTLLATAAR 251
                                                                                                                                                                138 ---GVLEERVNSSRRRARRHAADDDYNIEVLLGVDSVVQFHGTEHVQKYLLTLMNIVNE 294
                                                                                                                                                                                                                  295 IYHDESLGAHINVVLVRIILLSYGKSMSLIEIGNPSQSLENVCRWAYLQQKPDTDHDEYH 354
                                                                                                                                                                                                                                                                   371 HDNV-KVCEEVFGKLRANHMASPILIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP-- 427
                                                                                                                                                                                                                                                                                                                                                                      ------PDINGRRYYWRGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFST 81
                                                                                                                   537 QLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
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Search completed: April 29, 2003, 17:14:04 Job time: 11.1802 secs

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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: April 29, 2003, 17:10:24 ; Search time 35;5509 Seconds (without alignments)
3378.970 Million cell updates/sec

Title: US-10-009-332-1_COPY_1_583

Perfect score: 3163
Sequence: 1 MillioitzinlarAggre.....SCNLEPCPSSASGKSFREEQ 583
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Sequence: 1 MilligilTlaFaGRTaGGFE.....SCNLEF
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL\_21:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_lungi:\*
4: sp\_human:\*
5: sp\_lunvertebrate:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_phage:\*
10: sp\_varues:\*
11: sp\_rodent:\*
12: sp\_varues:\*
13: sp\_varues:\*
14: sp\_unclassified:\*
15: sp\_varues:\*
16: sp\_archeap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description		08te58 homo sapien	019791 caenorhabdi	09w493 drosophila	OBTACO CICCOLINE	004154 000000	Option Printingua	Marean Homo sapien	Q8sxb0 drosophila	O8te57 homo sapien	Ogvf61 drosophila	ORte59 homo sanien	OBWAS homo sanien	08+455 homo sanion	Cottons monitoring	Coreyo nomo sapien	Q96137 homo sapien	095n24 equips cabal	095n23 equus cabal	1
DUMMAKIES					<b>~</b>							_				-						_	
Š			ΙD		Q8TE58	019791	Q9W493	OBTES	0961.54	084400		OBSABU	Q8TE57	Q9VF61	OSTE59	08WXS8	08TE55	CATEVA		מחסבט	Q95N24	<b>095N23</b>	
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		Query	Length		950	2165	1054	1095	269	1081	1007	TODG	1072	1229	1207	1223	1223	1159	1100	1757	192	187	
	dР	Query	Match	1 1	99.7	29.8	27.4	25.4	25.2	25.1	10	0.07	24.1	23.9	23.8	22.6	22.6	22.6	0 0	0 1	17.6	16.4	
			Score	1 1	3155	941.5	865.5	803.5	196	793	700	0 0	762	757.5	753.5	715.5	715.5	714	200	0 0	258	518	
		Result	No.		_	7	e	4	Ŋ	G		- (	80	6	10	11	12	13	7.	r 1	T	16	

O9w1z6 drosophila			Q22580 caenorhabdi	08t458 drosophila				Q91ax7 aqkistrodon						09vi19 agkistrodon		09yi20 agkistrodon				092032 agkistrodon	09glk6 oryctolagus	Oğiab0 aqkistrodon	090282 crotalus at					-
09W1Z6	019204	017591	Q22580	Q8T458	Q8UVF1	ODM460	Q8UVF2	Q9IAX7	Q98SP2	Q9PW78	Q9W6M5	093523	Q8QG88	Q9Y119	Q9PVK9	Q9Y120	090499	092031	Q9IAX6	092032	Q9GLK6	Q9IAB0	090282	042138	Q9IAY0	Q8R3D3	Q8VHK4	005060
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444	442.5	433	393	357.5	335.5	332.5	331	326	322	319.5	314.5	313.5	313.5	310	310	309.5	309	307	307	304	303	303	302.5	300	299.5	298.5	298	297
17	18	19	20	21	22	23	24	22	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

IPF.000130; Zn\_MTpeptdse.

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Query Match
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                                                                                                                                                                                                             Matches
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Bonfield J., Burton J., Conneil M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mage J., Thomas K., Yaudin M., Yaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                        480
                                                                                                                                                                      300
                                                                                                                                                                                                             360
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                           241 YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN
                                                                                                                                                                                                                                                                                                                                                                                          DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVC
                                                         NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEH
                                                                                                                                    241 YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN
                                                                                                                                                                                                                                                                                          HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gajadsty S.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-94150718; Pubmed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z69361; CAA93288.1; -. EMBL; Z69360; CAA93288.1; JOINED. EMBL; Z69360; CAA93287.1; -. EMBL; Z69361; CAA93287.1; JOINED. HSSP; P15167; IDTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
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08,
19,
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1)
F25H8.3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                         181
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425
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                                                                                                                                                                                                                                                                       CFYSGDVNAEPDSFAAVSLC---GGLRGAFGYRGAEYVISPLPNASA---PAAQRNSQGA 154
                                                                                                                                                                                                                                                                                                                                                                     HLLQRRGVPGGPSGDPTSRCGV------ASGWNPAILRALDPYKPRRAGFGESRSR 204
                                                                                                                                                                                                                               Gaps
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                                                                                                                                                                                                                                                                         226 HLVRKFDPMHFKSFDHLNSTSVNETETTVATWQDQWEDVIER-------KARSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 VVVKVLLLRDRDSGPRVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-TCDILGMADVGIMCDPKRSCSVIEDDGLPSAFTIAHELGHVFNMPHDNVKVCEEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------FGKLRAN---HMMSPTLIQIDRANPWSACSAAIITDFLDSGHG--DCLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 QPSKPISLPE----DLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRHFPWADGTSCGEGK --LCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA
                                                                                                                                                                                                                                 65;
                                                                                                                                                                                 Length 2165;
                                                                                                                                                                                   29.8%; Score 941.5; DB 5; Length 38.7%; Pred. No. 5.3e-69; Live 75; Mismatches 181; Indels
                                                                                                                                        FCC3DA8AAA9C4888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 LRDCDSPKPRNGGKYCVGQRERYRSCNTQECPWDT--OPYREVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRQCINPIPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1054 AA
                                                                                                                     UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 14.
SNART; SM00209; TSP1; 18.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 6.
PROSITE; PS00142; ZINC_PROTEASE; UN SEQUENCE 2165 AA; 244397 MW; FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                           al Similarity
203; Conserv
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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rallaw R., Bazua A., Bandaria D., Bayaktaroglu L., Beaaley B.M., Bealew R., Basua A., Bandaria D., Blandaria D., Bolshakov S., Bencos P.V., Bernan B.P., Bhandaria D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Cadler S., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Rohery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dong Z., Mays A.D., Dew I., Dietz S.W., Rosler K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borlen R.J., Beacher R., Garg M., Bouch I. C., Ferraz C., Ferriera S., Fleischmann W., Rabler R., Gorrell J.H., Gu Z., Guan P., Harris M. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M. J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Radlock A., Gong F., Marland T.J., Red M.-H., Ibegwam C., Barli M., Kalush F., Karpen G. H., Ke Z., Kenlison J.M., Ketchum K.A., Jalali M., Kalush F., Karpen G. H., Ke Z., Kenlison J.M., Kalush F., Karpen G. H., T., Iz., Liang Y., Lin X., Liu X., Mattel B., McIntcoh T.C., McLeod M.P., Mocherson D., Lai X., Mattel B., McIntcoh T.C., McLeod M.P., Parla M., Nelson D.L., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Balazzolo M., Pithang G.S., Pan S., Pollard J., Mon, R., Nang Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B., Spier B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 NAEPDSFAAVSLCGGL------PNASA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 RGQPATNVAISTCAGLVSCPNFCVLPELITLCQVGHIRTAGNEYFIEPSKEHEPHPVNGH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P--AAQRNS-QGAHLLQRRG--VPGGPSGD--PTSRCGVASGWNPAILRALDPYKPRR-- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETRLEWQARGKVKVQGGRQIRRHHHHHHHHHHHKKYRHHQQKISRVPHTKFKYETQFQTE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- AGFGES 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 GGVRPLYGLHSDELVAGEGOLVVPRRVHPDGAFMTHOLEYAHELDHRRHRORRSLNSEHD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGFEP------EREVVVPIRLDPD------INGRRYYWR----GPED 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 865.5; DB 5; Length 1054; 33.4%; Pred. No. 4.1e-63; Live 76; Mismatches 226; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1.
DC1545555CB6212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR00287); Pep_M12B_propep.
Interpro; IPR001509; Reprolysin.
Interpro; IPR001509; Reprolysin.
Interpro; IPR000130; Zn_MTpeptdse.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00099; tsp_1; 2.
SMART; SM00209; TSP1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROFEASE;
SEQUENCE 1054 AA; 118616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0029791; CG4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003435; AAF46065.1;
HSSP; P15167; 1ATL.
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              g
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                   309 PDHAEIPRRRSISSPRHVETLIVADATMSAFH-RDLNGYLLTIMNMVSALYKDPSIGNS 367
                                                                    INIVVVKVLLLRDRDSGPK--VTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQ 319
                                                                                      DLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKV-CE 378
                                                                                                                                                                                                         379 EVFGKLRANHMMSPTL----IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPI--- 431
                                                                                                                                                                                                                                                                           SLPEDLPGASYTLSQQCELAFG-----VGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHF 485
                                                                                                                                                                                                                                                                                               595 PTAPGTLCGRNKWCQNGKCVRREEL -- AAVNGGWGDWSEWSECSRSCGGGVSTQQRECDN 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 DS-----GDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 RR-GVPGGPSGD---PTSRCGVASGWNPAILRALDPYKPRRAGFGE-SRSRRRSGRAKRF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LYLPYLLLLYWGLDPGTAYGDAAADYEVYLPWRYRPDDYHLPPLPAAPGPRRRRRPRTPP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLLGILTLAF----AGRTAGGFEPEREVVVPIRLDPDI-------NGRRYYWRGPE 46
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopez-Otin C.; "Cloning, expression analysis, and structural characterization seven novel human ADAWTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002). EMBL; AJ315735; CAC86016.1; -.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 17, with thrombospondin domains.
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Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.4%; Score 803.5; DB 4; Length 33.5%; Pred. No. 6.2e-58; ive 93; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1095 AA; 121099 MW; A5C6540484754D5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1095 AA.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Matches 212; Conservative
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SEQUENCE 1095 AA;
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Best Local Similarity
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Conservative
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01-JUN-2002 (TrEMBLrel.
ADAMTS18 protein.
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nes 211; Conserv
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Goad D.L., Goad M.E.;
"Molecular cloning of lapine aggrecanase-2 (ADAMTS-11) from articular
                                                                                                                                                                                                                                                                402
                                                                                                                                                                                                                                                                                                       432
                                                                                                                                                                                                                                                                                                                                      403 HSSCAGRSHIMSGEWVK--GRNPSDLSWSSCSRDDLENFLKSKVSTCLLVTDPRSQHTVR 460
                                                                                                                                                                                                                                                                                                                                                                                   LPEDLPGASYTLSOOCELAFGVGSKPCPYMOY - - CTKLWCTGKAKGOMVCOTRHFPWADG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 TSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPAN 550
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        273 RDRDSGPKVTGNAALTLRNFCAWQKK-----LNKV--SDKHPEYWDTAILFTRQDL 321
                                                                                                                                                                        Gaps
                                                                                        348 CVHKDEPCDTVGIAYLGGVCSAKRKCVLAEDNGLNLAFTIAHELGHNLGMNHD-----DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 VSIPRYVETLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLL
                                                                                                                                                                                                                           322 C -- GATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEE
                                                                                                                                                                                                                                                                                                       380 VFGKLRANHMMSPTLIQIDRANP----WSACSAAIITDFLDSGHGDCLL---DQPSKPIS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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EMBL; AF317415; AAG33062.1; -.
HSSP; Q9PW35; 1BUD.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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        182 RKWSLTPSPSAEAQRPEQLCKVLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLIPDAQFLAPAFSTEHLGVPLQGLTGGSS----DLRRCFYSGDVNAEPDSFAAVSLCGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 LRGAFGYRGAEYVISPLP-----NASAPAAQRNSQGAHLLQR------RGVPG- 164
                         121 NITEGPEYTVCPGMDVCARLWCAVVRQGQMVCLTKKLPAVEGTPCGKGRICLQGKCVDKT 180
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AGGFEPEREVVVPIRLDP-----DI--NGRRYYWRGPEDSGDQGLIFQITAFQEDFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 GRNYPGYSPSHIPHASQSRETEYHHRRLQKQHFCGRRKKYAP------KPPTEDTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAMTS18.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 ELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER-
MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
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EMBL, AJ311903; CAC83612.1; -. SEQUENCE 1081 AA; 119655 MW; 0438BF64567646IE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-21856482; Pubmed-11867212;
Call S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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ICHMLGLAELGTVCS-SSSCSIVQDTGLPTAFTMAHELGHILNMNHDDDDKCMPYVTRQN 614
                                                                                                   440 ASYTLSQQCELAFGVGSKPCPYMQYCTKLWC---TGKAKGQMVCQTRHFPWADGTSCG-E 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : : : | |:| || || || QGSLRSHRNSSVALSTCQGLSGMIRTEEADYFLRPLPSHLSWKLGRAAQGSSPSHVLYKR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSS------DLRRCFY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 SGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG---AHLLQRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------CGVASGWNPA-----ILRA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEPHAPGASEVLVTSRTWELAHQPLHSSDLRLGLPQKQHFCGRRKKYMPQPPKEDLFIL 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AN---HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLPG
                                                                                                                                                              496 GKLCLKGACVERHNLNKH----RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 16 with thrombospondin type I motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression analysis, and structural characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin; Protease.
SEQUENCE 1072 AA; 119491 MW; 081EEFF78F47D061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada
Lopez-Otin C.;
                                                                                                                                                                                                                           552 GKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                             Created)
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EMBL; AJ315734; CAC86015.1;
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                                                                                  497
                                                                                                                                                                      QTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLAR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 FQITAFQEDFYLHLIPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| | :|||||: | :|||||: | 355 VEDDPHSMVSVSLCGGWTGYIKTSFGALLIQPVNRTSSDEVLHRVFRKSQRNAR--HAVS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAP-----AAQRNSQGAHLLQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 KFEL-------GLDDFMSKLEQVQEEEQKSKSRKLNRKKHYA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIPRYV---ETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRDRDSGPKV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT--- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGE----SRSRRRSGRAKRFV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawee M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                            :|: | |:|| || | | | | || || ETKFMPAAEGTVCGLSMWCRQGQCVKFGELGPRPIHGQWSAWSKWSECSRTCGGGVKFQE
SK--PISLPEDLPGASYTLSQQCELAFGVGSKPCP---YMQYCTKLWC--TGKAKGQMVC
                                                                                                                                    KQAGQYKYPDKLPGQIYDADIQCKWQFGAKAKLCSLGFVKDICKSLWCHRVGHR-----C
                                              MPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; Score 790; DB 5; Length 1688; 33.4%; Pred. No. 1.5e-56; ive 93; Mismatches 194; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY094716; AAM11069.1; -SEQUENCE 1688 AA; 189867 MW; 48FB8DD4DE0CA4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ
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                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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hes 191;
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        RAMENINE-ZOUGHOUS PUNDEG-10/J1143;

RA Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,

Radams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA Adams A.D., Celniker S.E., II P.W., Hoskins R.A., Galle R.F.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Radion R.C., Rogers Y.H.C., Blazef R.G., Change M., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendal J., Bayaxlaroglu L., Basaley E.M.,

RA Besson K.Y., Bacos P.V., Barman B.P., Bhandari D., Bosinhakov S.,

RA Burtis R.C., Busem D.A., Bulter H., Cadleu E., Center A., Chandra I.,

RA Burtis R.C., Busem D.A., Bulter H., Cadleu E., Center A., Chandra I.,

RA Burtis R.C., Evalue S., Dahlke C., Davemport L.B., Davies P.,

RA Burtis R.C., Cabriellan A., Dan R., Galbart W.M., Glasser K.,

RA Burtis N.L., Barvey D., Helman T.J., Herray B., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kentlacta S., Plaischmann W.,

RA Hostin D., Houston K.A., Helman T.J., Well M.-H., Ibeywan C.,

RA Jasko P., Lei Y., Levitsky A.A., Li J., Ravyey D., Melman P., Harris M.L.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li A., Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Radazollo M., Pittemen G.S., Pan S., Pollard J., Puri V., Reese M. G.,

RA Shue B.C., Stadling A.C., Stapleton M., Strong R., Shen H.,

RA Sher E., Spradling A.C., Stapleton M., Strong R., Shen H.,

RA Sheng X.H., Robong T., Wenter E., Wang A.H., Wang X.,

RA Sheng X.H., Zhong F.N., Zhon M., Zhon G., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhon M., Zhon G., Zhu X., Smith H.O.,

RA Jheng C. W., Where E. W., Welner E., Wang G., Zhu X., Smith H.O.,

Ra Jenec E., Spradling G.M., Shon G., Zhu X., Zhu X., Zhu X., Smith R.,

Ra Jenec E., Spradling G.M., Subor C., Worter E., Wang G., Zhu X., Smith R.,

Ra Jenec S. R., Wooden S., Shon M., Shong G., Zhu X., Smith R.,

Ra Jenec S. R., Reger G., Shon 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                             436 GHNFGMIHDGEGNMCKKSEG-----NIMSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAIC 490
                                                                                                                     423 LLDQPSKPI---SLPEDLPGASYTLSQQCELAFGVGSKPCPY---MQYCTKLWC--TGKA 474
                                                                                                                                                     534
           GHVFNMPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDC 422
                                                                                                                                                                                                                                                                    475 KGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGG
                                                                                                                                                                                                                                                                                                                                                   535 GVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618 SGHWCQRGKCVS----NKHGYGRQVNGGWGPWTPFTPCSLTCGGGVQESRRECNQPVPEN 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 LRDRDSGPKV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRODLCGAT--- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-----DININDQTHSSNEMLKHFCQF---INQSGYER----DTAMLITREPICGSVPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 ICHMLGLAELGIVCS-SSSCSIVQDTGLPTAFTWAHELGHILNMNHDDDDKCMPYVTRQN 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 VNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAP-----AAQRNSQGAHLLQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 DVDNQYYTLEVLIAVDNSMKQFHGEDLQPYILILMSIVSSIFADASIGNSIRILLVRLIS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 FQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 RRGVPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGE----SRSRRRSGRAKRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 AN----HMMSPTL-IQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLP---EDLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 SIPRYV---ETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.9%; Score 757.5; DB 5; Length 1229; Best Local Similarity 33.3%; Pred. No. 4.9e-54; Matches 191; Conservative 91; Mismatches 184; Indels 107;
R Flybase; FBgn003340; CG6107.

R InterPro; IPR001590; Reprolysin.

R InterPro; IPR001590; Reprolysin.

R InterPro; IPR000184; TSP1.

R InterPro; IPR000184; TSP1.

R InterPro; IPR000184; TSP1.

R Ffam; PF01421; Reprolysin; 1.

R Ffam; PF01421; Reprolysin; 1.

R Pfam; PF001421; Reprolysin; 1.

R PROSITE; PS50025; TSP1; 2.

R PROSITE; PS50025; TSP1; 2.

R PROSITE; PS50032; TSP1; 2.

R PROSITE; PS50034; ZINC_PROTEASE; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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ADAMTS19.
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disintegrin-like and metalloprotease with thrombospondin
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            14 precursor.
                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                  HLGVPLQGLTGGSSDLR-----RCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYV 135
                                                                                                                                                                                                                                                                                            LDPYKPRRAGFGESRSRRRSGRAKRF-VSIPR--YVETLVVADESMVKFHGAD-LEHYLL 243
                                                                                                                                                                                                                                                                                                                                                                                    TLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQ-KKLNKV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGLPSAFTTAHELGHVFNMPHDN-VKVCEEVFGKLRANHMMSPTLIQIDRAN--PWSACS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAIITDFLDSGHGDCLLD---QPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQY 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 KEDLERFLRSKASNCLLQTNPQSVNSVMVPSKLPGMTYTADEQCQILFGPLASFCQEMQH 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKW 522
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                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                           136 -ISPLPNASAPAA-----QRNSQGAHILQRRGVPGGPSGDPTSRCGVASGWNPAILRA 187
                                                                                                                                                                                                                                     --YYWRGP-----EDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21866482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
EMBL: AJ311904; CAC84565.1; -.
SEQUENCE 1207 AA: 134061 MW; AF36F6BF5886FDE2 CRC64;
                                                                                                                                                                                                                                                                                                                                         255 FIEPLNDIMAITGHPHRVYRQKRSMEEKVŢEK-----SALHSHYCGIIS-----
                                                                                                                                                                   Indels 133;
                                                                                                                                           Query Match 23.8%; Score 753.5; DB 4; Length 1207; Best Local Similarity 31.5%; Pred. No. 1e-53; Matches 208; Conservative 86; Mismatches 234; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
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                                                                                                                                                                                         AGGFEPEREVVVPIRLDPDINGRR------
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                     SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WXS8;
01-MAR-2002 (
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Q8WXS8
ID Q6WXS
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DT 01-MA
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DT 01-MA
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                                                                                                                                                                                                         Euteleostomi;
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A BOLZ H., Ramirez A., von Brederlow B., Kubisch C.;

Bolz H., Ramirez A., von Brederlow B., Kubisch C.;

"Characterization of Adamys14, a novel member of the ADAMYS

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                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                         Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Lopez-Otin C.;
"Cloning, expression analysis, and structural characterization
seven novel human ADAMTSS, a family of metalloproteinases with
disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
EMBL; AJ345098; CAC87943.1; -.
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                                               Created)
Last sequence update)
Last annotation update)
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31.2%; Pred. No. 1.5e-50;
Live 86; Mismatches 238;
                        1223 AA
                                                                                   Metalloprotease-disintegrin protease.
                       PRT;
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MEDLINE-21856482; PubMed-11867212;
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RESULT 13

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MEDLINE-21839041; PubMed-11741898;
MEDLINE-21839041; PubMed-11741898;
Colige A., Vandenberghe I., Thirty M., Lambert C.A., Van Beeumen J.,
Li S.W., Prockop D.J., Laplere C.M., Nusgens B.V.;
"Cloning and Characterization of ADAMTS-14, a Novel ADAMTS Displaying
High Homology with ADAMTS-2 and ADAMTS-3.";
J. Blol. Chem. 277:5756-576(2002).

EMBL; AP366351; AAL79814.1;
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SEQUENCE 1159 AA; 127336 MW; A5B130149BF7FF34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.6%; Score 714; DB 4; Length 115
Best Local Similarity 31.4%; Pred. No. 1.9e-50;
Matches 176; Conservative 87; Mismatches 239; Indels
                                                                                                    Created)
Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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"Structure of von Willebrand Factor-cleaving Protease (ADAMTS13), a metalloprotease Involved in Thrombotic Thrombocytopenic Purpura.";

"J. Balol. Chem. 276:41059-41063(2001).

"REMBL; AY055376; AAL17652.1;

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196 TQLGGACSPIWSCLITEDIGFDLGVITAHEIGHSFGLEHDGAPGS----GCGPSGHVMAS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 TLIQIDRANP-----WSACSAAIITDFLDSGHGDCLLD----QPSKPISLPEDLPGASYT 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 LKGACVERHNLNK-HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE.
1427 AA; 153632 MW; EB1BC3AABC1A4442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 CGFLLGCWGPSHFQQSCLQALEPQAVSSYLSPGAPLKGRPPSPGFQRQRQR-----RA 75
                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 18.0%; Score 568.5; DB 4; Length 1427; Best Local Similarity 31.0%; Pred. No. 3.2e-38; Matches 143; Conservative 50; Mismatches 199; Indels 69;
                                                                                                                                                                                                                                                                                                       Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E.,
Fujikawa K.;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Von Willebrand factor-cleaving protease precursor.
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1427
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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192 AA.

PRT;

PRELIMINARY;

Q95N24 Q95N24;

Q95N24 ID Q AC Q

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121 TFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGKDYDADROCOL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 MADVGIMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGK-LRANHMM 390
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 192;
                                                                                                                                                                                                                                                                               Flannery C.R., Little C.B.;
"Expression and activity of equine aggrecanases.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, #F36821, ARK53425.1;
MEROPS; MI2.221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20670 MW; 9013B0E19FCE8C56 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.6%; Score 558; DB 6; ilarity 51.0%; Pred. No. 1.5e-38; Conservative 26; Mismatches 64.
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InterPro; IPR000130, Zn_MPpeptdse.
PROSITE: PS50215; ADAM MEPRO; I.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_I.
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                                                                                      Aggrecanase-1 (Fragment). Equus caballus (Horse).
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192 AA;
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les 98; Conserv
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Human PRO1563 (UNQ
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Human ADAMTS-SI pr
Human protease, PR
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Human protease #3
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AAB86950
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16-MAY-2000; 2000JP-0144020.
 10-NOV-2000; 2000WO-JP07917
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N-PSDB; AAH41003.
WO200134785-A1.
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  Human protease #2.
Human protease PRT
Rat metalloprotein
Human protease #3.
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Mouse metalloprote
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                                                                                            (without alignments) 2738.218 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                             1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
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19: /SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:*
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3163
1 MLLGILTLAFAGRTAGGFE.....SCNLEPCPSSASGKSFREEQ
                                                                                                                                                                                                                                  908470
            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                           908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAU72899
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Gapop 10.0 , Gapext 0.5
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                                 This invention relates to a metalloprotease with aggrecanase activity. The invention includes protein and DNA sequences of the metalloprotease, vectors containing the DNA, host cells transformed by the vectors and antibodies directed against the metalloprotease. The antibodies, protein and DNA sequences can be used in the treatment and prevention of joint diseases, particularly osteoarthritis. The treatment may result in osteopathic and antiarthritic activity. The present sequence represents the metalloprotease of the invention termed MDTS6.
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                                                                                                                                     100.0%; Score 3163; DB 22;
100.0%; Pred. No. 7.4e-255;
.ive 0; Mismatches 0;
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osteoarthritis
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                                                                                                                                                Similarity
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in threateners of an abstance, attraction, an appropriate of polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to careen for substances (S) that may modulate its activity. Administering a screen for substances (S) that may modulate its activity. Administering (is disorder selected from cancers (e.g., of tissues, of blood or heamatopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72910 represent human processes amino acid sequences of the invention.
                          colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
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aspartyl protease; cysteine protease;
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Pred. No. 3.3e-254;
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Payne V;
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                                                                                                                                                                                                                                                                                                                                                    bl human protein; NHP; protease; biological disorder; obesity; pressure; arthritis; connective tissue disorder; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid encoding a human protease, useful as a hybridization for screening libraries and assessing gene expression patterns -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is novel human protein (NHP), human protease. WHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
                  KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA 360
                               HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG 420
                                                                        QTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLAR 540
                                                                                                                                                           DCLLDQPSKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVC 480
YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN 325
                                                                                                                RQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 36-38; 41pp; English.
                                                                                                                                                                                                                                                               AAE22541 standard; Protein; 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001; 2001WO-US30350.
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                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                  Human; novel human pr
high blood pressure;
gene therapy; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-372123/40.
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                                                                                                                                                                                                                                                                                                                                                 novel human
                                                                                                                                                                                                                                                                                                                               Human protease #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Length 950;

Score 3155; DB 23; Pred. No. 3.4e-254;

99.78;

Best Local Similarity

Query Match

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                                                                                                                       GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW 180
  Gaps
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                        MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
                                     YLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLN
                                                                                                                                                                                                                                    KVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA
                                                                                                                                                                                                                                                                                   NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEH
                                                                                                                                                                                                                                                                                                                        HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
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  Indels
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2000US-213955P.
2000US-215396P.
2000US-216821P.
2000US-218946P.
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 Conservative
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22-JUN-2000; 2
29-JUN-2000; 2
07-JUL-2000; 2
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582;
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481
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                                                                                                                                                                                                                                                                                                       The present invention relates to twenty one new human proteases, referred to as PRTS-1 to PRTS-21. The PRTS polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and myocardial infarction, autoimmune/inflammatory e.g. acquired myocardial infarction, autoimmune/inflammatory e.g. acquired proliferative e.g. cancer, developmental e.g. Duchenne and Becker muscular dystrophy, epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzheimer's disease and reproductive e.g. infertility and endometriosis disorders. Numerous other examples of each disorder are given in the specification. The present protein sequence represents the human protease PRTS-11 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                            Twenty one human proteases (referred to as PRTS-1 to PRTS-21), useful in the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative (e.g. cancer)disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEH 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM; Delegeane AM, Baughn MR, Nguyen DB. Lee EA, Hafalia A, Khan FA; Walle NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT; Azimcai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%; Score 3155; DB 23; Length 952; 99.8%; Pred. No. 3.4e-254; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                              Claim 1; Page 144-146; 177pp; English.
                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.8 Matches 582; Conservative
                                                                                                                                                WPI; 2002-090437/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 AA;
                                                                                                                                                                 N-PSDB; ABK12894.
                                                                                                 Azimzai Y,
Kallick DA;
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The present sequence is rat metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenessis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 QGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQ 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; ADAWIS-5; metalloproteinase; ADAM; a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
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                                                               Query Match
79.0%; Score 2497.5; DE
Best Local Similarity 93.5%; Pred. No. 1e-199;
Matches 462; Conservative 8; Mismatches 2
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                                                                                                                                                                                                                                                                                                                 AAB21257 standard; Protein; 505
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N-PSDB; AAA95827.
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Length Indels

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blood pressure, arthritis, connective tissue disorders and infertility. They are also used in gene therapy.
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                                                                                                                                                                                                          GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
                                                                                                                       1 MLILGILTLAFAGRTAGGSEPEREVVVPIRLDPDINGRRYYWRGPEDSGDGGLIFQITAF
                                                                                                          1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF
                                                                                                                                                                                                                                                                        181 NPAILRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEH
                                                                                                                                                                                                                                                                                                                                                            KVSDKHPEYWDTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTA
                                                           23;
                                                           Score 1913; DB 2. Pred. No. 4e-151;
                                                                                   0; Mismatches
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304
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308
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                                                          tch 60.5%;
al Similarity 99.7%;
363; Conservative
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                                    367 AA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid encoding a human protease, useful as a hybridization probe for screening libraries and assessing gene expression patterns -
                                                                                                                                                                   ELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERH 508
                    TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 388
                                                                                                                  NLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARR--QCTNPTPANGGKYCEGVRVKYRSCN 566
                                                                                                                                                                                                                                                                RAKREVSIPRYVETLYVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVK 268
                                                      VLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is novel human protein (NHP), human protease. NHPs share structural similarity with animal proteases particularly zinc metalloproteases. Sequences of the invention are useful in therapeutic, diagnostic and pharmacogenomic applications. NHP polynucleotides are used as hybridisation probes for screening libraries and assessing gene expression patterns. They can also be used for treating related biological disorders such as obesity, high
                                                                                                                                                    MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 39-40; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          AAE22542 standard; Protein; 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LEXI-) LEXICON GENETICS INC
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                                                                                                                                                                                                                                                                                                                   LEPCPSSASGKSFR 505
                                                                                                                                                                                                                                                                                                      LEPCPSSASGKSFR 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protease #3.
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N-PSDB; AAD35570.
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Homo sapiens.
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                                            04-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                      The present sequence is human metalloproteinase ADAMTS-5. The ADAMTS family of proteins is closely related to the ADAM (A Disintegrin and Metalloproteinase Domain) family. Members of the ADAMTS family contain a thrombospondin domain in addition to the disintegrin and metalloproteinase domains found in the ADAMS. ADAMTS polypeptides are useful for the manufacture of medicaments for treating conditions associated with neuroinflammation and/or neurodegeneration, such as Alzheimer's disease, Parkinson's disease and stroke. They are also useful for treating conditions associated with cell proliferation, cell migration, inflammation and/or anglogenesis, such as cancer, arthritis and autoimmune diseases. They can be used to treat patients afflicted with an invasive tumour, a brain tumour or brain injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 COTRHEPWADGTSCGEGKFCLKGACVEXHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLA 300
                                                                                                                                                                                                                                                                                                                                                                                             240 HYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                          300 NKVSDKHPEYWDTAILFTRQDLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTT 359
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHELGHVFNMPHDNVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGH
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                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                 Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1767; DB 21;
Pred. No. 6.3e-139;
3; Mismatches 18;
                        (NEUR-) NEUROCRINE BIOSCIENCES INC.
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                                                                                                                                                   Claim 12; Fig 23; 129pp; English.
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                                              Maki RA;
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llarity 93.3%;
Conservative
99US-0264585
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                                              Clark M,
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                                                                   WPI; 2000-594326/56.
N-PSDB; AAA95831.
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                                                                                                                                                                                                                                                                                                                            381 AA;
 08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                         322;
                                              Kelner GS,
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Best Local S
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Matches
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Novel nucleic acid encoding a human protease, useful as a hybridization probe for screening libraries and assessing gene expression patterns -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB21265 standard; Protein; 896 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    5; Page 34-35; 41pp; English.
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                                                                                                                  (LEXI-) LEXICON GENETICS INC
27-SEP-2001; 2001WO-US30350.
                                                          29-SEP-2000; 2000US-236689P.
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                                                                                                                                                                               Hilbun
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N-PSDB; AAD35568.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding novel members of a disintegrin, metalloproteinase and thrombospondin domain protein family used to prevent and treat Alzheimer's disease, cancer and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLC 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 TAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGS-----SDLRRCFYSGDVNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 EPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNAS----APAAQRNSQGA----HLLQRRG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RRGSGGAKCGVMD------DETLPTSDSRPESQNTRNQWPVRDPTPQDAGKP 226
               a disintegrin and metalloproteinase domain; thrombospondin domain; vaccine; nootropic; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; cancer; arthritis; autoimmune disease; brain tumour; brain injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LLLLASITMLLCARGAHGRPTEEDEELVLP-SLE-----RAPGHDSTTTRL--RL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRR--------
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                                                                                                                                                                                                                                                                                                                   (NEUR-) NEUROCRINE BIOSCIENCES INC.
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                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594326/56.
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                                                                                                                                                                WO200053774-A2.
                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                              08-MAR-1999;
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AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; infilammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangloma; detection; arterial-venous malformation; immune deficiency.
                                                                                                                                                                                      TLSQQCELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLK
                                                              407 VTGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLY
                                              KLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASY
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RVRYRSCNIEDCPDN-NGKTFREEQ 609
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(HAST/) HASTINGS G A.
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(YAMA ) YAMANOUCHI PHARM CO LTD.

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09-JUL-1999; 09-JUL-1999;

23-JAN-2001

JP2001017183-A. Homo sapiens

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17;
                  immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and actue conditions. The products can also be used for detection and diagnosis. AA332002 to AA332080, and AA49503 to AA495511 represent sequences given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                              49.3%; Score 1560.5; DB 20; Lengt.
51.6%; Pred. No. 3.7e-121;
ive 73; Mismatches 160; Indels
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A Disintegrin And Metalloprotease; cancer; arthritis.
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mobilisation (chemotaxis) of immune cells.
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                                                                                                                                                                                                                                                                             Metalloprotease)-type metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 genes, the recombinant production of MDTS4 and MDTS5, and antibody specific for MDTS4 or MDTS5, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. The present
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51.6%; Pred. No. 3.7e-121;
ive 73; Mismatches 160; Indels
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                                                                                                                                                                                                  A new metal protease and its preparation for anti-arthritic therapeutic -
                                                                                                                                                                                                                                           Claim 1; Page 12-14; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                            sequence represents human MDTS4.
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Best Local Similarity 51.6 Matches 320; Conservative
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                                                                                                                                                                                Human; METHI; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; Osler-Webber syndrome; plaque neovascularisation; telangiectasia; hemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jonak ZL,
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BETH ISRAEL DEACONESS MEDICAL CENT.
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Ā
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                                                                                                  AAB50002 standard; Protein; 950
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99US-0147823.
99US-0373658.
99US-0171503.
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                            564 SCNLEPCPSSASGKSFREEQ
                                        SCNLEDCPDN-NGKTFREEQ
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HASTINGS G A.
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JONAK Z L.
TRULLI S H.
FORNWALD J A.
TERRETT J A.
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Fornwald JA, Te
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22-FEB-2000;
                                                                                                                                           19-MAR-2001
                                                                                                                                                              Human METH1
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(SMIK ) S
(BETH-) E
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(HAST/)
(RUBE/)
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angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque meovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METHI can also be used in birth control. METHI can also be used in diagnostic methods for the prognosis of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOOLDLELRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DILGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN 387
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                     950 AA;
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Human; METH1; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular anglogenic disease; rheumatoid arthritis; psoriasis; wound healing; endomerriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; plaque neovascularisation; telangiectasis; haemophiliac joint; anglofibroma; fibromuscular dysplasia; wound granulation; crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human METH1 and METH2 (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). METH can be used for inhibiting angiogenesis in an individual, and for
RHNLNKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYR 563
                                                   METHI and METH2 polynuclectides and encoded polypeptides, inhibit angiogensis in the treatment of disorders such as rheumatoid arthritis and psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Pages 759-763; 768pp; English.
                                                                                                                                                                                      AA.
                                                                                                                                                                                      AAB50011 standard; Protein; 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHKLINE BEECHAM CORP
                                                                                                          SCHLEDCPDN-NGKTFREEQ 625
                                                                                              SCNLEPCFSSASGKSFREEQ 583
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99US-0147823.
99US-0373658.
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22-FEB-2000; 2000US-0183792.
                                                                                                                                                                                                                                           (first entry)
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Fornwald JA, Terrett JA;
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JONAK Z L.
TRULLI S H.
FORNWALD J A.
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(TERR/) TERRETT J A.
                                                                                                                                                                                                                                                                  ID 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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10-AUG-1999;
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(SMIK ) S
(BETH-) H
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                                                                                                                                                                                                                                                                                                                                             This represents a human integrin ligand polypeptide ITGL-TSP. ITGL-TSP polypeptides can be used in the treatment of anglogenic diseases such as cancer, cancer metastasis, chronic inflammatory disorders, rheumatoid attributis, atherosclerosis, macular degeneration or diabetic retinopathy, restenosis, Alzheimer's disease and tissue remodeling. They can be used to treat a subject in need of enhanced activity or expression of the ITGL-TSP polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QEDFYLHLTPDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114
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tissue
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to
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                                                                                                                                                                                                                                                                      DNA encoding integrin ligand polypeptide ITGL-TSP - used anglogenic diseases, restenosis, Alzhelmer's disease and
                                                                                                                                                                                            Terrett JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.3%; Score 1560.5; DB 1
51.6%; Pred. No. 3.8e-121;
                                                                                                                                                                                         Fronwald JA, Hastings GA, Jonak ZL,
Trulli SH;
                                                                                                                                                                                                                                                                                                                            Claim 11; Pages 6-9; 24pp; English.
                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                               97US-0845496.
                                                                                    98EP-0300575
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                                                                                                                                                                                                                                 WPI; 1998-544643/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              967 AA;
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           Homo sapiens.
                                                                                                               24-APR-1997;
                                                                                     27-JAN-1998;
                                   EP874050-A2
                                                            28-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Best Local S:
Matches 320,
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treating cancer, benign tumours, an ocular angiogenic disease, rheumatcid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemnic limb angiogenesis, osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer. The present sequence is a protein isolated in the present invention.
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                                                                                                                                                                                                                           Length 968;
                                                                                                                                                                                                                         ; Score 1560.5; DB 22; Length; Pred. No. 3.8e-121; 73; Mismatches 160; Indels
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51.6%;
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Matches 320; Conservative
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The present sequence represents human Tango-71. Tango polypeptides are useful for identifying compounds which bind the polypeptide via direct binding, competition binding assays or Tango-71, -73, -74, 76 or -83-mediated signal transduction. Tango polypeptides are also useful for identifying modulating compounds by determining effect on Tango activity. Tango polypeptides and nucleic acids are useful for diagnosing diseases related to aberrant expression of Tango, and Tango polypeptides are useful for raising antibodies which can be used in diagnostic assays for detection of Tango, and also for generating anti-idiotype antibodies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S2 DQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 136
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tuman; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEDFYLHLTPDAQFLAPAFSTEHLG - - - - - VPLQGLTGGSSDLRRCFYSGDVNAEPDSF
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                                                                                                                                                                                                                                                                                                                       and nucleic acids encoding them - useful for treating disorders caused by aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Score 1559.5; DB 2 Local Similarity 51.6%; Pred. No. 4.6e-121; les 320; Conservative 73; Mismatches 160;
                                                                                                                                                                                                               (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig 1; 84pp; English.
                                                                                                                                      98WO-US16502
                                                                                                                                                                  97US-0058108
97US-0054966
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                                                                                                                                                                                                                                                                                                                        New TANGO polypeptides
diagnostic agents and f
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N-PSDB; AAX19955.
                                                                                                                                                                                                                                                                                                                                                   expression of TANGO
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                                               Homo sapiens
                                                                          409907850-A1
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                                                                                                                                                                                 06-AUG-1997;
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                 detection.
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1 MLLGILTLAFAGRTAGGFE.....SCNLEPCPSSASGKSFREEQ 583
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	491-2 Sequence 2, Appl	2 Sequence 2.	Sequence 9.	Sequence 2.	15 Sequence 15	Sequence 13	3 Sequence 13	Sequence 15,	-7 Seguence 7.	Sequence 5,	Segmence 4.	17	1 Sequence 11	Sequence 5,	Sequence 16,	1 Sequence 1	-22 Sequence 22,	7 Sequence 7,	80	-2 Sequence 2,	-2 Sequence 2.	Sequence 4,	4	Sequence 3.	7 Sequence 17.	3 Sequence 3, 7	190-1 Company 1 App
SUMMARIES	ID	US-09-130-49	US-09-122-126B-	US-09-369-364A-9	-09	US-09-122-126B-1	US-09-130-49	us-09-369-36	US-09-369-364A-1	US-09-369-364A-	US-09-491-522-	US-09-930-87	US-09-369-364A-	US-09-491-522-1	US-09-369-364A-	US-09-130-491-16	US-09-369-364A-	US-09-369-364A-	US-09-491-522-	US-09-130-491-	US-09-930-872	US-09-632-098	US-09-632-098-4	US-09-411-329C-1	US-09-411-32	US-09-411-32	US-08-836-44	27-808-00-21
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dР	Query Match Length	967	837	905	930	930	608	1882	874	997	1211	1224	1081	1205	859	551	245	518	266	481	491	802	812	464	462	462	529	616
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	Score	1560.5	1338.5	1329.5	1240	1212.5	1136	1121	1087.5	932.5	782.5	763	750.5	739	712.5	687	662.5	629	576.5	493.5	441	326	326	303	301	301	292	269
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Sequence 6, Appli Sequence 14, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 20, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli	TANGO-76, AND TANGO-83	4; Length 967; ;; Indels 67; Gaps 17;	WRGPEDSGDQGLIFQITAF 60 	VPLQGLTGGSSDLRRCFYSGDVNAEPDSF 114    :                 1 TPLPETDLAHCFYSGTVNGDPSSA 136	AHLLQRRGVPGG 165                 APLQFHLLRRNRQGDVGG 196	WNPAILRALDPYKPRRAGFGESRSRRRS 207  :	ARLYRHPSILNPINIVVV 267     :       ::      ARLYKHPSIRNSVSLVVV 307
621 4 US-09-026-001A-6 592 4 US-09-026-001A-14 814 4 US-09-920-0048-4 815 4 US-09-920-048-4 855 4 US-09-920-048-2 855 4 US-09-920-048-2 613 4 US-09-026-001A-10 335 4 US-09-026-001A-10 335 4 US-09-026-001A-10 335 4 US-09-026-001A-10 336 4 US-09-026-001A-10 337 4 US-08-313-28B-20 3391 4 US-08-313-28B-20 391 4 US-08-313-28 769 1 US-08-477-407-4 770 1 US-08-833-823-2 470 2 US-08-833-823-2 470 2 US-08-833-823-2	ALIGNMENTS 2, Application US/09130491 2, 6416974 INFORMATION: TT: GOOGBATION Andrew D.J. TRIGOGBATION TANGO-71, TANGO-73, TANGO-74, FERENCE: 09404/041001 APPLICATION NUMBER: US/09/130,491 FILING DATE: 1998-08-07 APPLICATION NUMBER: US 60/058,108 FILING DATE: 1997-09-05 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: 1997-08-06 APPLICATION NUMBER: US 60/054,961 FILING DATE: HOW SEVENTE US 60/054,961 FILING DATE: HOW SEVENTE US 60/054,961 FILING DATE: HOW SEVENTE US 60/054,961 APPLICATION NUMBER: US 60/054,961 FILING DATE: HOW SEVENTE US 60/054,961 FILING DATE: HOW SEVENTE US 60/054,961	49.3%; Score 1560.5; DB 4 51.6%; Pred. No. 1.5e-130; ative 73; Mismatches 160;	MLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYWRGPEDSGDGGLI:	VPLQGLTG    RKSGSETPLP	AAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHIJQRRGVPGG   :     :	GVASG     TEDEDEGTEGEDEG	GRAKREVSIPRYVETLVVADESNYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVV 
28 268.5 8.5 29 30 255.5 8.1 32 255 8.1 33 255 8.1 34 255 8.1 35 29.5 7.3 36 229.5 7.1 41 225.5 7.1 44 225.5 7.1 45 225.5 7.1	RESULT 1 US-09-130-491-2 Sequence 2, Application US/09130. Patent No. 6416974 GENERAL INO. 6416974 APPLICANT: HOLTMAN, DOUGLAS A. TITLE OF INVENTION: TANGO-71, TITLE OF INVENTION: TANGO-71, TITLE OF INVENTION: TANGO-71, TITLE APPLICATION NUMBER: US/CHRENT APPLICATION NUMBER: US/CHRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: US/CHRENT FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 EARLIER FILING DATE: 1997-09-05 TOTOMORER FILING DATE: 1997-09-09-09-09-09-09-09-09-09-09-09-09-09-	Query Match Best Local Similarity 51. Matches 320; Conservative	1 MLLLGILTLAFAGF :    36 LLLLAAALLAVSDA	61 QEDFYLHLTPDAQFLAPAFSTEHLG :                 : ::  82 DQQLDLELRPDSSFLAPGFTLQNVG	115 AAVSLCGGLRGAFG   :     :     137 AALSLCEGVRGAFY	166 PSGDPTSRC-           1 197 TCGVVDDEPRPTGKAE	208 GRAKRFVSIPRYVE 
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                                                          CELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVE
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 DTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRAN
                                              HMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQ
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                                                                                                                                                                                                                                                              Sequence 2. Application US/09122126B
Patent No. 6451575
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FLING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SSQ ID NO SSC 21
LENGTH: 837
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ORGANISM: Homo sapiens
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Best Local Simi
Matches 265;
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                                                                                  -----RAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILN
                                                             MVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVD--GSWAKWDPYGPCSRTCGG
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                                                                                                                                                                     42.0%; Score 1329.5; DB 4; 44.9%; Pred. No. 5.6e-110; ive 85; Mismatches 175;
                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: HICKAINEN, Tilna L.
APPLICANT: HICKAINEN, TAILA E.
TITLE OF INVENTION: Nucleic Acids Encoding Zin;
FILE REFERENCE: 26473,44007,10:30-00
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9.
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Best Local Similarity 44.9%;
Matches 284; Conservative
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US-09-369-364A-9
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218 -PQESPSVHSRSRRSALAPQLLDHSAFSPSGNAGPQTWWRRRRSISRARQVELLLVAD 276
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181 IYGDGSSRILHVYNREGFSFEALPPRASCETPASPSG------------
                                                                                                                                                        APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hurskainen, Tilna L.
APPLICANT: Hirohata, Satoan
TILLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
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44.7%; Pred. No. 5.6e-102;
tive 70; Mismatches 153;
                                                  577 GGRFCLGERVKYQSCNTEECP--PNGKSFREQQ 607
                                    551 GGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ
                                                                                                                      Sequence 2, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              ORGANISM: mus musculus ADAMTS-5
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LENGTH: 930
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APPLICANT: Goodearl, Andrew D.J.
IIILE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE. REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 SGGGKVGYLVYAGGRRFLLDLERDGSVGIAGF-----VPAGG--GTSAPWRHRSHCFYR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTVDASPRSLAVFDLCGGLDGFFAVKHARYTLKPLLRGPWAEEEKGRVYGDGSARILHVY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 QRRG----VPGGPS------GDPTSRCGVASGWNPAIL--RALDPYKP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 RRAGFGES----RSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 -AGGSGPQTWWRRRRRS-----ISRARQVELLLVADASMARLYGRGLOHYLLTLASIAN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYW 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 SGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLR---RCFYS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPL---PNASAPAAQRNSQGA----HLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTAILFTRODLCGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMP
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 930;
                                                                                 GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES;
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                              38.3%; Score 1212.5; DB 4;
44.6%; Pred. No. 1.6e-99;
tive 71; Mismatches 180;
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                                          ; Sequence 15, Application US/09122126B ; Patent No. 6451575
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Patent No. 6416974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 44.6
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
RESULT 5
US-09-122-126B-15
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                                                                                                                                                                                                                                                                        SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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297 KKLNKVSDKHPEYWDTAILFTRQDLCGA-TTCDTLGMADVGTMCDPKRSCSVIEDDGLPS 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DSGHGDCLLDQP-SKPISLPEDLPGASYTLSQQCELAFGVGSKPCPYMQYCTKLWC---T 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRC 174
                                                                                                                                                                                                                             203 AALNSGLATEAFSAYGNKTDNTREKRTHRRT---KRFLSYPRFVEVLVVADNRMVSYHGE 259
                               EYEIVSPIRVNALGEPFPINVHFKRTRRSINSATDPWPAFASSSSSSSSAHYRLSAFG 108
                                                                 EDFYLHLTPDAQFLAPAFSTEHLGVP----LQGLTGGSSDLRRCFYSGDVNAEPDSFAAV 117
                                                                                                                                                                        156 RLCQYQLRAHG------RHQPLLRNEHKNRHSKDKKKTRARKWGERINLAGDV 202
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                                                                                                                                                                                                                                                                              237 DLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQ
                                                                                                                                                                                                                                                                                                                                                                    472 GKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRT
---DINGRRYYW----RGPEDSGDQGLIFQITAFQ
                                                                                                                                                                                                            178 SGWNPAI-LRALDPYKPRRAGFGESRSRRRSGRAKRFVSIPRYVETLVVADESMVKFHGA
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APPLICANT: Apte, Suneel

APPLICANT: Hirchata, Satoshi

TITLE OF INVENTION: Nucleic Acids Encoding 2inc Metalloproteases

FILE REFERENCE: 26473/4007/10-30-00

CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 CGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                           RESULT 8
US-09-369-364A-15
; Sequence 15, Application US/09369364A
; Patent No. 6391610
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Matches 217; Conserv
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     EREVIVPIRLDP-
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                                                                                                                                                                                                                                                                                                                                                                        329 TLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANH 388
                                                                                                                                                                                                                                                                                                                                                                                              64 ILGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                           389 MMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKPISLPEDLPGASYTLSQQC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 ELAFGVGSKPCP-YMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLCLKGACVER 507
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40.0%; Pred. No. 6.2e-91;
Live 86; Mismatches 199; Indels 70
                                                                                                                                                                                                                                      Length 608;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                    Query Match 35.9%; Score 1136; DB 4; Best Local Similarity 63.0%; Pred. No. 5.9e-93; Matches 201; Conservative 39; Mismatches 7?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Apte, Suneel
APPLICANT: Hirokatan, Tilna L.
APPLICANT: Hirokatan, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zir
FILE REFERENCE: '264734007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 13
     CURRENT FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: US 60/058,108

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09369364A Patent No. 6391610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: HOMO Sapiens ADAMTS-9
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| CNLEDCPDN-NGKTFREEQ 320
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LOCATION: (468)
COCHER INFORMATION: Xaa = C
NAME/KEY: MOD_RES
LOCATION: (521)
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US-09-369-364A-13
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Best Local Similarity 40.0
Matches 237; Conservative
                                                                                                                                SEQ ID NO 13
LENGTH: 608
TTYPE: PRT
OCANISM: Mus musculus
US-09-130-491-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           269
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255 HPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAI 314
                                    280 DPSIGNPIHITIVRLVLLEDEEEDLKITHHADNTLKSFCKWOKSINMKGDAHPLHHDTAI 339
                                                                        315 LFTRQDLCGATT--CDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHD 372
                                                                                          373 -NVKVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQPSKP- 430
                                                                                                                                                                 ISLPEDLPGASYTLSQQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQMVCQTRHFPWAD 489
                                                                                                                                                                                                                                       457 IDFPSVPPGVLYDVSHQCRLQYGAYSAFCEDMDNVCHTLWCSVGT----TCHSKLDAAVD 512
                                                                                                                                                                                                                                                                                    GTSCGEGKLCLKGACVERHNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPA 549
                                                                                                                                                                                                                                                                                                        APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF OVERESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 782.5; DB 4;
Pred. No. 5.2e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Mindows OPERATING SYSTEM: Mindows Version 2.0b SOFTWARE: Fast-SEQ for Windows Version 2.0b CURRENT APPLICATION DATA: US/09/491,522 APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                           550 NGGKYCEGVRVKYRSCNLEPCPSSASGKSFREEQ 583
                                                                                                                                                                                                                                                                                                                                                                               8389-0060-988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICALLO...
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09491522
Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.7%;
34.9%;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1211 amino acids
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US-09-491-522-5
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                  VVKVLİLRDRDSGPKVTGNAALTLRNFCAWQKKLNKVSD-KHPEYWDTAILFTRQDLCGA 324
                                                                                       180 IVNLVVIHNEQEGPYINFNAQTTLKNFCQMQHSKNYLGGIQH----DTAVLVTREDICRA 235
                                                                                                                                                                                                                             TLSQQCELAFGVGSKPCPYMQYCTKLWCT---GKAKGQMVCQTRHFPWADGTSCGEGKLC 499
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GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hirohat, Satcshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
CURRENT FILIG DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
LENGTH: 997
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39.3%; Pred. No. 1.7e
ive 69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             560 VKYRSCNLEPCPSSASGKSFREEQ 583
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Matches 249; Conserv
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US-09-369-364A-7
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                                                     SCDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG---AHLLQRR 160
                                                                            G----VPGGPSGDPTSR-----ILRA 187
                                                                                                                                                                                                                                                                        247 ATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-NKVSDK 305
                                                                                                                                                                                                                                                                                                                                              HPEYWDTAILFTRODLCG--ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHEL 363
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                                                                                                                                                               STEPHAPGASEVLVTSRTWELAHQPLHSSDLRLGLPQKQHFCGRRKKYMPQPPKEDLFIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TIILE OF INVENTION: UNCleic Acids Encoding Zinc Metalloproteases
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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US-09-369-364A-17
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LENGTH: 1081
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Patent No. 644838
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Brin
APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUD NO 4
LENGTH: 1224
 27;
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                                                                                                                                                                                                                                                                                                                           220 VE-TLVVADESMVKFHGAD-LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDS 277
                                                                                                          RGPEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCF 102
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78; Mismatches 247; Indels
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Best Local Similarity 34.0%; Pred. No. 2.9e-59;
Matches 200; Conservative 74; Mismatches 227; Indels
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                                    LAFAGRTAG --- GFEPEREVVVPIRLDPD ----
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Conservative
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ORGANISM: homo sapiens
Matches 217;
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US-09-41-522-11
Sequence 11, Application US/09491522
Sequence 11, Application US/09491522
Sequence 11, Application US/09491522
Sequence 11, Application US/09491522
APPLICANT: Colige, Alain
APPLICANT: Laplare, Charles M.
APPLICANT: Laplare, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITT: New York
...
                                                                                                                                        KL-----NKVSDKHPEYWDTAILFTRQDLC--GATTCDTLGMADVGTMCDPKRSCSVI 348
                                                                                                                                                             518 SWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVKYRSCNLEPCPSSASGK 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KGRPWWLRTLKP--PPARPLGNETERGOPG-LKRSVSRERYVETWDVADKMAVAYHGRRD 237
                                                                                  349 EDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFG----KLRANHMMSPTLIQIDRANP-- 402
                                                                                                                                                                                                                                                                                                      WSACSAAIITDFLDSGHGDCLLDQPSK-PISLPEDLPGASYTLSQQCELAFGVGSKPCPY 461
                                                          LEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQK 297
                                                                                                                                                                                                                                                                                                                                                                                   MQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKL----CLKGACVERHNLNKHRVDG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 amino acids
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COUNTRY: USA
ZIP: 10036-2811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshl
; TILLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases;
FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEC ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
: LENGTH: 859
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                                                                                                                                                                                                                                                                                                               Query Match 23.4%; Score 739; DB 4; Length 1205; Best Local Similarity 32.5%; Pred. No. 3.9e-57; Matches 212; Conservative 81; Mismatches 242; Indels 118;
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ORGANISM: Homo sapiens ADAWTS-6
FEATURE:
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                            ; TOPOLOGY: linear
US-09-491-522-11
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US-09-369-364A-5
                                                                                                                                                                                                                                                                                                                                    Query Match
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FALCHIN NO. 0410974

FALCIN NO. 0410974:

APPLICANT: HOILZMAN, DOUGIAS A.

APPLICANT: GOOGMAIL AND TANGO-71, TANGO-73, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT APPLICATION NUMBER: US/09/130,491

CURRENT FILING DATE: 1998-08-07

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-09-05

BARLIER FILING DATE: 1997-09-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FALLING DATE: 1997-08-06

SEQ ID NO 16

LENGTH: 551
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                                                                                                                                                                                       KKL-----NKVSDKHPEYWDTAILFTRQDLCGATT--CDTLGMADVGTMCDPKRSCSV 347
                                                                                                                                  DAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSF-AAVSLCGGLRGAFGY 129
                                                                                         Gaps
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                                                                                         Indels 119;
                                                             Length 859;
                                                             22.5%; Score 712.5; DB 4; 30.2%; Pred. No. 5.7e-55; ive 89; Mismatches 215;
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                     OTHER INFORMATION: Xaa - L
US-09-369-364A-5
                                                               Query Match
Best Local Similarity 30.23
Matches 183; Conservative
NAME/KEY: MOD_RES
LOCATION: (450)
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                                                                                                                          9
                                                     Length 551;
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                                                 Query Match
21.7%; Score 687; DB 4;
Best Local Similarity 56.4%; Pred. No. 5.8e-53;
Matches 119; Conservative 29; Mismatches 57
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Job time : 13.4569 secs
            ; ORGANISM: Rattus rattus US-09-130-491-16
TYPE: PRT
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